GENETIC ANALYSIS OF YIELD, YIELD COMPONENTS AND WATER USE EFFICIENCY TRAITS UNDER ORGANIC AND INORGANIC FERTILIZER MANAGEMENTS IN GROUNDNUT (*Arachis hypogaea* L.)

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B.Sc. (Ag.)

MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)

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BY
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THESIS SUBMITTED TO THE
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(GENETICS AND PLANT BREEDING)

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DECLARATION

I, **Ms. GOWRA MEGHALA DEVI**, hereby declare that the thesis entitled “**GENETIC ANALYSIS OF YIELD, YIELD COMPONENTS AND WATER USE EFFICIENCY TRAITS UNDER ORGANIC AND INORGANIC FERTILIZER MANAGEMENTS IN GROUNDNUT (*Arachis hypogaea* L.)**” 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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Ms. **GOWRA MEGHALA DEVI** has satisfactorily prosecuted the course of research and that thesis entitled "**GENETIC ANALYSIS OF YIELD, YIELD COMPONENTS AND WATER USE EFFICIENCY TRAITS UNDER ORGANIC AND INORGANIC FERTILIZER MANAGEMENTS IN GROUNDNUT (*Arachis hypogaea* L.)**" 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 her for a degree of any University.

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This is to certify that the thesis entitled **“GENETIC ANALYSIS OF YIELD, YIELD COMPONENTS AND WATER USE EFFICIENCY TRAITS UNDER ORGANIC AND INORGANIC FERTILIZER MANAGEMENTS IN GROUNDNUT (*Arachis hypogaea* L.)”** 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. GOWRA MEGHALA DEVI,** 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.

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LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
µg ml^{-1}	:	Microgram per millilitre
ANOVA	:	Analysis of variance
cm	:	Centimetre
cm^{2} g^{-1}	:	Centimetre square per gram
CV	:	Co-efficient of variation
DAS	:	Days after sowing
et al.,	:	And others
FYM	:	Farm yard manure
g	:	Gram
G × E	:	Genotype × environment interaction
g kg^{-1}	:	Gram per kilogram
g l^{-1}	:	Grams per litre
GA	:	Genetic advance
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Co-efficient of variation
h^{2}(bs)	:	Heritability in broad sense
ha	:	Hectare
i.e.	:	That is
ICRISAT	:	International Crops Research Institute for the Semi-Arid Tropics
Kg	:	Kilogram
mg g^{-1}	:	Milligram per gram
nm	:	Nanometre
PCV	:	Phenotypic Co-efficient of variation
r	:	Correlation coefficient

RARS	:	Regional Agricultural Research Station
RWC	:	Relative water content
S. No	:	Serial Number
SCMR	:	SPAD chlorophyll meter reading
SLA	:	Specific leaf area
SMK	:	Sound mature kernel
SPAD	:	Soil Plant Analytical Development
t ha^{-1}	:	Tonnes per hectare
via	:	Through
viz.,	:	Namely
vs.	:	Against

Title of thesis : **GENETIC ANALYSIS OF YIELD, YIELD COMPONENTS AND WATER USE EFFICIENCY TRAITS UNDER ORGANIC AND INORGANIC FERTILIZER MANAGEMENTS IN GROUNDNUT (*Arachis hypogaea* L.)**

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ABSTRACT

The present investigation was conducted at dryland farm of S.V. Agricultural college, Tirupati, during *kharif* 2017 to study the variability and genetic parameters, character association and path analysis in thirty groundnut genotypes under organic and inorganic fertilizer managements.

Analysis of variance revealed significant differences for all the characters studied under both fertilizer managements indicating the presence of ample amount of variability among the genotypes. Mean performance of genotypes revealed that TCGS-1157, ICG-10384, ICG-11322, ICG-7153, TCGS-1330, Dharani under organic fertilizer management and ICG-7153, K-9, ICG-11322, TCGS-1330, K-7 bold and Dharani under inorganic fertilizer management were found promising for yield, water use efficiency and quality traits.

Higher estimates for GCV and PCV were observed for number of immature pods per plant, kernel yield per plant, pod yield per plant and total free amino acids under both fertilizer managements whereas number of pegs per plant, number of mature pods per plant and number of pods per plant showed high GCV and PCV in only inorganic fertilizer management.

The characters total free amino acids and carbohydrate content exhibited high heritability coupled with high genetic advance as percent of mean under both fertilizer managements whereas SLA at 60 DAS and hundred kernel weight showed high heritability coupled with high genetic advance as percent of mean in organic fertilizer management and plant height, number of pegs per plant, number of mature pods per plant, number of pods per plant and kernel yield per plant in inorganic fertilizer management indicating the preponderance of additive gene action and the selection for these traits will be effective.

Using D^2 analysis thirty genotypes of groundnut were grouped into seven and five clusters under organic and inorganic fertilizer managements. The characters oil content in organic and plant height in inorganic fertilizer management contributed more towards genetic divergence. The crosses TCGS-1157 X K-7 bold, TCGS-1157 X K-1789, TCGS-1330 X K-7 bold and Dharani X K-7 bold under organic fertilizer management and K-9 X ICG-11651, Dharani X ICG-11651, K-9 X K-7 bold, Dharani X K-7 bold and TCGS-1330 X ICG-11651 under inorganic fertilizer management can be utilized for development of transgressive segregants for yield, water use efficiency and quality traits.

Character association analysis revealed that the characters viz., number of primary branches, number of pegs per plant, number of mature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SCMR at 40 DAS and SCMR at 60 DAS showed significant positive correlation with pod yield per plant under both fertilizer managements. Path analysis revealed that kernel yield per plant under organic fertilizer management and kernel yield per plant and number of pods per plant in inorganic fertilizer managements exhibited high positive direct effect on pod yield per plant. Other traits also showed high indirect effects through these traits indicating the importance of these traits during selection process in groundnut.

Chapter ~ I

Introduction

Chapter I

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is an important protein rich oil seed crop belonging to the family Fabaceae which ranks 6th in world oil seed crops and 13th in world food crops. It is also known as peanut, earthnut, monkeynut, goober etc. It is a native of South America (Brazil) and grown in over 100 countries, between 40^{o} N to 40^{o} S latitude in tropical warm climate. It is a self-pollinated annual legume crop and a segmental allotetraploid (2n=40).

Groundnut has its importance both as grain legume and as an oil seed crop. It contains 36-54 % of edible oil, 22-36% of easily digestible protein and 18 % of carbohydrates in its seeds. Apart from this, groundnut kernels contain many health enhancing nutrients such as minerals, antioxidants, vitamins and are rich in mono-unsaturated fatty acids. They contain antioxidants like *p*-coumaric acid and resveratrol, Vitamin E and many important B-complex groups of thiamine, pantothenic acid, vitamin B-6, folates, and niacin.

China, India and Nigeria are the major groundnut producing countries in the world and in India, Gujarat and Andhra Pradesh are the major groundnut growing states. In India groundnut is cultivated in an area of 49.07 lakh ha with production of 82.17 lakh tonnes and productivity of 1674 kg ha^{-1}. In Andhra Pradesh it is grown in an area of 7.38 lakh ha with production of 10.09 lakh tonnes and productivity of 1367 kg ha^{-1}. (AICRP, Annual report, 2017).

Indiscriminate use of chemical fertilizers in conventional farming system is causing soil degradation, pollution of surface and ground water, atmospheric pollution leading to adverse effect on human health.

Considering these ill effects, organic farming is the need of the hour to ensure safe food production, to keep the land in healthy condition, to prevent over exploitation of natural resources and excessive chemicalization of agriculture. Hence organic farming is gaining impetus in recent years.

Organic farming is an agricultural system that aims to mimic processes in natural ecosystems for the provision of nutrients and pest control, instead of relying on chemical inputs (Andersen *et al.*, 2015). It is designed to enhance biological diversity within the production system, increase soil biological activity and maintain long term soil fertility. In India groundnut being an important exportable commodity there may be demand for organic groundnut in the national and international markets.

In organic farming, the major constraint is lack of suitable varieties specifically bred for organic farming. The different requirements for varietal characteristics clearly highlight the importance of breeding and selecting varieties under organic conditions that will be suitable for organic farming. The varietal trials under organic farming conditions shows that the modern varieties are not in all cases the best for organic agriculture. Hence, organically-bred plant varieties are needed to develop both the potential of organic agriculture and its integrity (Martin, 2002).

Groundnut is mainly cultivated under rainfed conditions. Even in irrigated areas, groundnut is frequently exposed to drought because water supply is not sufficient which has its adverse effect on yield, productivity and quality. It was also confirmed that substantial genotypic variation for water use efficiency exists in groundnut. Hence the physiological traits like SLA, SCMR, and relative water content will be useful for the selection of genotypes having high water use efficiency.

As groundnut is an important oilseed crop used for confectionary purpose, there is a need to improve the quality traits of groundnut. Value addition through quality enhancement will earn huge foreign exchange. Hence selection for quality traits in groundnut is necessary in breeding programmes.

Yield is a complex character influenced by a number of other yield contributing characters. Hence the study of different genetic parameters of these traits is necessary to know the variability present in the genotypes. A thorough knowledge of genetic variability present in the different groundnut cultivars, heritability of various characters and probable genetic advance to be expected from selection of superior lines aids in the effective selection of desirable genotypes under target environments.

To use the genotypes in breeding programmes the information on their genetic diversity is very much essential. In self - pollinated crops like groundnut, the genetic divergence of the parents involved solely determines the success of hybridization. D^2 statistics is an extensively used measure of genetic diversity to identify genetically divergent parents, which can be utilized in hybridization programmes.

Information on association of characters would help in developing efficient breeding programme in the target environment which can be achieved through the studies of correlation coefficients and path coefficients. Correlation coefficients helps in estimation of degree of association between yield and its attributes which helps in selection for improvement of yield. Path co-efficient analysis further partitions the correlation coefficients of each trait into direct and indirect effects upon yield.

Keeping in view the above perspectives, the present research work was formulated with the following objectives:

1. To estimate the variability, heritability and genetic advance for yield, yield components and water use efficiency traits in groundnut under organic and inorganic fertilizer managements.
2. To study the genetic divergence using Mahalanobis D^2 statistics under organic and inorganic fertilizer managements.
3. To estimate the extent of association existing among different component characters with yield and among themselves under organic and inorganic fertilizer managements.
4. To study magnitude of direct and indirect effect of yield components and water use efficiency traits on yield under organic and inorganic fertilizer managements.

Chapter ~ II

Review of Literature

Chapter II

REVIEW OF LITERATURE

The available literature related to the objectives of present investigation in groundnut (*Arachis hypogaea* L.) was reviewed briefly and presented hereunder.

2.1 COMPARATIVE STUDIES AND SELECTION STRATEGIES FOR DIFFERENT FERTILIZER MANAGEMENTS

Groundnut (*Arachis hypogaea* L.) is an annual herbaceous legume crop cultivated throughout the tropical, sub-tropical and warm temperate regions of the world and primarily grown for high quality edible oil (36-54%) and easily digestible protein (22-36%) in its seeds. Recently organic farming has emerged as an important priority globally in view of growing demand for safe and healthy food. Besides safety, organic farming also has favourable effects on the physical, chemical and biological properties of soil and nutrient availability. But the major constraint is the unavailability of suitable varieties specifically bred for the organic farming practices. Hence there is a need to develop varieties which perform well in organic farming conditions since the varieties selected under conventional agricultural management practices may not possess traits that allow for optimal production in organically managed systems.

Marimuthu *et al.* (2002) analysed the effect of different sources of vermicompost on groundnut and reported superior performance of ornamental garden waste vermicompost over other sources *viz.*, organic waste, common weed biomass, water hyacinth, chopped young *Prosopis juliflora*, coir pith and FYM. The treatment with ornamental garden waste vermicompost reported highest plant height, leaf area index, dry matter production and number of nodules per plant.

Chaithanya *et al.* (2003) studied effect of different types of organic manure on groundnut and concluded that the recommended dose of NPK fertilizers and other organic manures significantly increased the dry matter production, 100 pod weight and pod yield over control.

Field trials of Kumawat *et al.* (2010) on groundnut-cumin and clusterbean-cumin cropping systems under foliar application of panchagavya and 1:1 solution of panchagavya plus leaf extracts of neem (*Azadirachta indica*), datura (*Datura metel*) and tumba (*Citrullus colocynthis*) revealed that foliar application of neem plus panchgavya at branching and flowering stages increased yield of crops in both the cropping systems. The increase in groundnut and cumin yield was 118 and 156% higher, respectively, under groundnut-cumin system.

Lokanath (2010) studied effect of organic fertilizers on the productivity of groundnut and its residual effect of succeeding safflower for three seasons and observed higher dry pod yield of groundnut in organic farming with heavy application of FYM compared to inorganic farming during first season wherein a low rainfall dry spell situation occurred at early growth stage. During next two seasons where moisture stress was not present higher pod yield of groundnut was observed in inorganic fertilizer amended plots. They concluded that groundnut showed greater response to the application of organic manures (i.e., organic farming) under low rainfall with dry spell situations occurring at early growth stages. Organic amendments to a groundnut crop during *kharif* and no organic manures and fertilizers to safflower during *rabi* in groundnut safflower sequence cropping system (double cropping system) produced 13.24 to 22.69 % higher seed yield of safflower over treatment with the inorganic fertilizers to groundnut crop during *kharif* and no organic manures and fertilizers to safflower during *rabi*.

Experiments of Ravi *et al.* (2011) on integrated organic nutrient management practices for quality and economics of groundnut revealed that the protein content, oil and protein yield are significantly high with the application of FYM (7.5 t ha^{-1}) + *Rhizobium* + PSB + Panchagavya spray (3% at 30, 60 and 75 DAS).

Three bambara groundnut landraces (white seed coat, black seed coat and light red seed coat) were evaluated by Wamba *et al.* (2012) under organic and inorganic fertilizer managements and concluded that application of poultry manure @ 12 t ha^{-1} significantly increased the number of pods per plant, the number of seeds per pod, 1000 grain weight, grain yield and pod yield in light red seed coat landraces.

Effect of organic practices on the yield and yield attributes of groundnut were studied by Yogendra *et al.* (2013) and reported significantly higher pod yield with the application of farmyard manure (7.5 t ha^{-1}) inoculated with microbes (biofertilizers + bio-pesticides) 15 days before sowing and seed treatment with biofertilizers + bio-pesticides at the time of sowing.

Latha and Sharanappa (2014) studied the effect of organic nutrient management systems in groundnut-onion cropping system and reported significantly higher pod and kernel yield, number of pods per plant and shelling percent for groundnut under the treatment of enriched biodigested liquid organic manure at 25 kg N equivalent/ ha + 3 sprays of 3% panchagavya.

Studies of Sarathi and Sinha (2014) on the response of organic sources of nutrients on growth, net photosynthesis and seed yield of groundnut showed that combined application of poultry manure @ 2.5 t ha^{-1}

+ neem cake @ 2.5 t ha^{-1} + vermicompost @ 2.5 t ha^{-1} + phosphocompost @ 2.5 t ha^{-1}significantly improved dry matter, crop growth rate, leaf area index and net photosynthesis which ultimately helped in producing more seed yield. They have also observed that the sole application of organics recorded lower growth attributes and seed yield.

Choudhary *et al.* (2015) studied the effect of foliar application of neem, oak, glyricidia and custard apple leaf extracts in 1:1 combination with panchagavya on growth, yield and economics of groundnut and recorded significantly higher plant height, number of nodules, and number of branches with the foliar application of combination of panchagavya + neem leaf extract as compared to control.

Krishnamurthy *et al.* (2015) studied 147 RILs of direct crosses and 20 RILs of reciprocal crosses of TG 49 x GPBD 4 under organic farming system (received nutrients in the form of FYM (1/3), vermicompost (1/3) and green leaf manure (1/3)) and observed high genotypic and phenotypic variation for pod yield (kg/plant) and shelling percent indicating the presence of considerable amount of genetic variability for these traits whereas in oil content and protein content there was low GCV and PCV. In GPBD 4 X TG 49 population there was a significant and positive correlation between protein and oil content but negative correlation in the TG 49 X GPBD 4 population. Highly significant positive correlation was observed between 100-seed weight and pod yield per plant in both the population indicating that breeding for high yield can be achieved without compromising the large seed size.

Nabil *et al.* (2015) analysed two groundnut cultivars under eight fertilizer treatments (integrated use of organic, inorganic and biofertilizers) and recorded highest values of pods number per plant, weight of pods per plant, seed index, weight of seeds, seed oil, seed protein, seed P and seed K from the treatment 1/2 NPK + 12 tonnes compost + Bio fertilizer with Gregory cultivar.

Kenchanagoudar *et al.* (2016) evaluated 10 groundnut genotypes for yield and quality traits under organic, inorganic and integrated cultivation and recorded higher pod yield under organic cultivation in Dh 4-3, GPBD 4 and TGLPS-3. Mutant-III and GPBD-5 showed significantly higher test weight. The oil content was significantly more in GPBD 4 and TGLPS 3 followed by Dh 86, Dh 4-3, JL 24 and mutant II. The genotypes GPBD 4, Dh 4-3, Dh 2000- 1 and GPBD 5 recorded high protein content in organic cultivation. Finally, they identified three genotypes Dh 4-3, TGLPS 3 and GPBD 4 that were suitable for organic farming. These genotypes performed very well under organic and integrated compared to inorganic cultivation practices.

Correlation and path analysis conducted by Manjubhargavi *et al.* (2016a) on 44 groundnut genotypes under organic and conventional environments revealed significant positive association of kernel yield with pod yield per plant, mature pods per plant, number of pods per plant, primary branches per plant, days to 50% flowering, harvest index, 100 seed weight, shelling percentage and protein content whereas oil content showed significant negative correlation in both the environments. Path analysis revealed high positive direct effects of pod yield per plant and shelling percentage on kernel yield per plant under both organic and conventional fertilizer managements.

Manjubhargavi *et al.* (2016b) studied genetic variability of 44 groundnut genotypes under organic management and recorded high heritability coupled with high genetic advance as percent of mean for plant height indicating preponderance of additive gene action. Moderate heritability coupled with high genetic advance as per cent of mean was recorded for the characters primary branches per plant, number of pods per plant, pod yield per plant, kernel yield per plant, mature pods per plant, harvest index and 100 seed weight indicating that improvement can be brought about in these traits through simple pedigree method of breeding and phenotypic selection would be effective.

Aparna *et al.* (2017b) evaluated 168 germplasm lines and 5 checks of groundnut for character association and path analysis under organic fertilizer management and reported that pod yield was positively and significantly associated with kernel yield per plant followed by number of mature pods per plant, total number of pods per plant, harvest index, 100 seed weight, days to maturity, number of pegs per plant, days to 50% flowering and shelling percentage. They also reported high positive direct effect of kernel yield per plant on pod yield per plant.

2.2 VARIABILITY AND GENETIC PARAMETERS

The amount of variability present for different characters in a population and its efficient management determines the success of any breeding programme. The genetic co-efficient of variability is a useful measure of the magnitude of genetic variance present in the population. Estimation of genetic variability alone cannot indicate the possible improvement achieved through selection, but it should be used in conjunction with heritability and genetic advance. The degree of success depends on the magnitude of heritability as it measures the relative amount of the heritable portion of variability. Genetic advance under selection gives an idea about how much of the genetic gain obtained was due to selection. Hence, the estimates of genetic variability, heritability and genetic advance had an immense value in identifying superior genotypes.

Thirty two strains of groundnut genotypes were evaluated by Patil *et al.* (1982) and they observed high estimates of phenotypic and genotypic co-efficients of variation for number of secondary branches followed by yield per plant, number of developed pods per plant and number of pegs per plant. They also noticed high heritability accompanied with high genetic advance as per cent of mean for all the characters studied, except number of primary branches per plant indicating involvement of additive gene action and more scope for their improvement through selection.

Twelve Spanish bunch groundnut varieties were studied by Kandaswami *et al*. (1986) and they recorded high heritability estimates for plant height, number of secondary branches, pod to peg ratio and number of primary branches. On contrary, moderate heritability estimates were registered for number of mature pods, number of nodes on main stem axis, sound mature kernel per cent, shelling per cent, harvest index and pod yield and low heritability estimates for weight of mature pods, 100 kernel weight and 100 pod weight. Further, they also reported high GCV values for number of secondary branches, plant height and pod yield and high genetic gain for number of secondary branches and plant height whereas, shelling per cent, number of nodes on main stem axis and weight of mature pods recorded lowest genetic gain.

Manoharan and Ramalingam (1993) studied fifty Virginia groundnut genotypes and observed high PCV values than GCV for all the characters studied. They also observed higher heritability and genetic advance estimates for height of the main stem, 100 pod and kernel weights indicating that these traits are controlled by additive gene action and hence phenotypic selection can be exercised to improve the traits.

Francies and Ramalingam (1996) evaluated F_2 generation raised from 55 selected F_1^s obtained from 8 interspecific hybrid derivatives and reported low heritability coupled with medium estimates of genetic advance for the traits number of primaries, number of secondaries and nodes on primary branch indicating the involvement of both additive and non-additive gene action. Moderate heritability accompanied by low genetic advance was observed for oil content.

Jayalakshmi *et al.* (1998) assessed F_4 progenies of eight crosses of groundnut and identified high heritability and moderate genetic advance for specific leaf area and harvest index in ICGV 86031 X JL 24 and high heritability and greater genetic advance for total dry matter in ICGV 86031 X TG 26, TAG 24 X TPT-1 and ICGV 86031 X TAG 24 indicating the presence of additive gene effects. They also identified TAG 24 X TPT-1 and TG 26 X JL 24 as superior crosses for improvement of pod weight.

Khan *et al.* (2000) studied 13 geographically diverse peanut genotypes and reported low heritability value for seeds per pod and high heritability value for 100-kernel weight.

Genetic variability studies conducted by Nath and Alam (2002) on fifteen exotic groundnut genotypes revealed that phenotypic coefficient of variations were slightly higher than the genotypic coefficient of variations for all the characters studied except pod yield per plant indicating lower environmental effect for these traits. They also reported high heritability with high genetic advance for the traits plant height, pods per plant, 100-pods weight, shelling percent, harvest index and pod yield per plant indicating that these traits are governed by additive gene effects.

Jayalakshmi and Reddy (2003) studied 21 groundnut hybrids for two seasons (rainy and post rainy) and observed high GCV for shoot biomass, harvest index and immature pod number per plant in both the seasons and for kernel yield during rainy season. Specific leaf area and pod yield recorded low GCV during both the seasons. High heritability coupled with high GAM was obtained for shoot biomass, harvest index and immature pod number per plant during both the seasons.

Mahalakshmi *et al.* (2005a) evaluated 50 groundnut genotypes and recorded high heritability estimates combined with high genetic advance for the traits number of secondary branches, number of unproductive pegs, number of immature pods, number of mature pods, total number of pods, total number of gynophores, maturity index, shelling percentage and hundred kernel weight indicating that these characters are governed by additive genes.

Studies conducted on 48 diverse large seeded groundnut genotypes by Parameshwarappa *et al.* (2005) indicated higher genetic variability for number of primary branches, pod yield per plant, kernel yield and plant height. They have also reported that the traits kernel yield, sound mature kernels and 100-kernel weight showed high heritability coupled with high genetic advance indicating that additive genes govern these characters.

Hundred germplasm accessions were evaluated by John *et al.* (2006) for seven characters and found high PCV and GCV for pod yield per plant. They also found high heritability along with high GAM for the characters *viz.,* plant height, pod yield per plant and SCMR indicating the importance of additive gene action in the inheritance of these characters.

Kadam *et al.* (2007) evaluated 40 groundnut genotypes to assess the amount of genetic variation, heritability and genetic advance and reported high PCV and GCV for kernel yield per plant followed by pod yield, number of pods, number of branches, plant height and harvest index. They also reported that the traits pod yield and kernel yield showed high heritability coupled with high genetic advance and oil content showed high heritability with low genetic advance.

The F_2 population of six single crosses and parents were studied by John *et al.* (2008) and reported high heritability along with high genetic advance as percent of mean for the traits plant height, number of secondary branches per plant, number of mature pods per plant, pod yield per plant, kernel yield per plant, haulm yield per plant and harvest index in all the crosses.

John *et al.* (2009) assessed 60 genotypes of groundnut for 17 characters and reported that the traits number of secondary branches per plant, number of immature pods per plant, shelling percentage, 100-kernel weight, sound mature kernel weight, total number of pods, total number of gynophores, maturity index, reproductive efficiency and pod yield showed high heritability along with high genetic advance as percent of mean indicating additive gene action and phenotypic selection for these characters will be effective.

Genetic variability studies conducted by Korat *et al.* (2009) on 80 diverse groundnut genotypes revealed high PCV and GCV for number of secondary branches per plant and number of aerial pegs per plant. They have also observed high heritability along with high genetic advance as per cent of mean for number of secondary branches per plant and number of aerial pegs per plant and indicated that these characters were governed by additive gene action.

Meta and Monpara (2010) evaluated fifty elite genotypes of bunch groundnut and noticed high magnitude of GCV and PCV for pods per plant, kernel yield per plant and pod yield per plant which indicated large extent of genetic variability for these traits. High heritability was accompanied by high genetic advance for plant height and 100-pod weight, whereas, moderate heritability was associated with high genetic advance for pods per plant and kernel yield per plant, indicating involvement of additive gene action for these traits.

Channayya *et al.* (2011) evaluated 180 mutant lines of groundnut derived from two Spanish Bunch groundnut cultivars, viz. TPG-41 and

GPBD-4 and reported that the traits number of primary branches per plant, 100-kernel weight, SMK% and shelling per cent recorded high estimates of genetic variability, heritability and genetic advance.

Nandini *et al.* (2011) studied variability, heritability and genetic advance for 10 yield and physiological traits related to water use efficiency in 196 F_8 RIL population developed using parental lines NRCG12568 and NRCG12326 and recorded maximum GCV for pod yield per plant followed by kernel yield per plant, number of pods per plant, sound mature kernel percentage, Specific Leaf Area, number of branches per plant, shelling percentage, plant height, SCMR and days to fifty percent flowering indicating that individual plant selection can be followed for characters having high GCV. A moderate to high degree of heritability and genetic advance was observed for pod yield per plant, kernel yield per plant, pods per plant, sound mature kernel percentage, plant height, number of branches per plant and SLA indicated involvement of additive gene action in control of these traits. Low heritability and moderate genetic advance as per cent of mean was observed for SPAD Chlorophyll meter reading (SCMR).

Vekariya *et al.* (2011a) assessed 50 diverse genotypes of bunch groundnut and reported high estimates of PCV and GCV for number of mature pods per plant, protein content, kernel yield per plant, harvest index and 100 kernel weight. They have also reported high heritability with high GAM for number of mature pods per plant, kernel yield per plant and pod yield per plant indicating that these traits were mainly governed by additive gene action and responsive for further improvement.

Twenty eight F_2 populations were evaluated for genetic parameters of 23 characters by John *et al.* (2012) and found that the traits days to 50% flowering, plant height and number of secondary branches exhibited high heritability while moderate heritability was observed for number of primary branches per plant, specific leaf area, harvest index and oil percentage. High heritability and moderate GAM was recorded for days to 50% flowering; moderate heritability and high GAM for number of mature pods per plant and harvest index; moderate heritability and moderate GAM for number of primary branches per plant and specific leaf area; low heritability and moderate GAM for plant height indicating additive gene effect and scope of selection for genetic improvement.

Madhura and Kenchanagoudar (2012) studied 182 accessions of groundnut comprising *hypogaea* bunch (42), *hypogaea* runner (39), Spanish bunch (63) and *fastigiata* (38) types and observed highest heritability for pod yield per plant and oil content in all the four botanical types and also for test weight but was moderate in Virginia bunch type; moderate heritability for shelling per cent, sound mature kernel percent; low heritability in case of days to 50 per cent flowering and days to maturity. They have also recorded high genetic advance for pod yield per plant, test weight; moderate for shelling percent, sound mature kernel and oil content whereas low genetic advance for days to 50% flowering.

Genetic variability studies for nine characters conducted in eighteen groundnut genotypes by Narasimhulu *et al.* (2012) revealed high heritability along with high GAM for pod yield per plant, kernel yield per plant, test weight and shelling percentage which indicated the importance of additive gene action and the ample scope for improvement in these traits through simple selection.

Mohan *et al.* (2013) studied eight parents and their 28 cross combinations of groundnut for 16 characters and recorded high GCV accompanied by high heritability and high genetic advance as percent of mean for number of secondary branches and number of immature pods per plant indicating predominant role of additive gene action useful for phenotypic selection in early generations. Number of mature pods per plant and pod yield per plant recorded high GCV and moderate heritability and GAM.

Mukesh *et al.* (2014) evaluated 15 groundnut genotypes for 13 quantitative characters and observed high to moderate estimates of GCV and PCV for kernel yield, pod yield per plant and plant height. The traits seed index, days to 50% flowering, sound mature kernels, plant height, seed yield per plant and pod yield per plant exhibited high heritability. Moderate heritability was observed for days to maturity and number of primary branches and low heritability was noticed for shelling percentage. High heritability coupled with high genetic advance as percent of mean was recorded for kernel yield indicating additive gene effects and scope for selection in improvement of this character.

Patil *et al.* (2014) investigated variability of 58 Spanish bunch groundnut genotypes for 16 characters and found maximum broad sense heritability for days to 50% flowering followed by plant height and 100-kernel weight. The traits days to 50% flowering, plant height, 100-pods weight, 100-kernels weight, shelling percent and harvest index showed moderate to high heritability coupled with moderate to high genetic advance.

Variability studies were conducted on fifteen groundnut genotypes by Krishna *et al.* (2014) for 14 quantitative parameters and recorded higher PCV than GCV for all the parameters. Plant height, seed index, days to 50% flowering, shelling percentage, pod yield per plant, kernel yield, seed yield per plant, pod yield q ha^{-1} exhibited high values of heritability (broad sense). Kernel yield also exhibited high values of genetic advance as percent of mean.

Fifty groundnut genotypes of groundnut were studied by Rao *et al.* (2014) and observed high PCV than GCV for all the characters indicating the role of environmental variance in the total variance. They also observed moderate to high PCV and GCV for number of pods per plant, plant height, kernel yield, dry pod yield, hundred kernel weight, and dry haulm yield. High heritability coupled with high genetic advance as percent of mean was observed for hundred 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 and revealed better scope for improvement of these traits through direct selection.

Satish (2014) studied 16 genotypes of groundnut and recorded high estimates of PCV than GCV for all the characters indicating the influence of environment upon these traits. He also recorded high heritability for 100 seed weight followed by pod yield, number of pods per plant, number of branches per plant, plant height and days to 50 % flowering. The character number of pods per plant and pod yield showed the high genetic advance along with high heritability indicating additive gene effect.

Variability studies were conducted on 14 groundnut genotypes by Satyanarayan *et al.* (2014) for 14 quantitative characters and reported high GCV and PCV for seed yield per plant, kernel yield, pod yield per plant, pods per plant and plant height. High heritability coupled with high genetic advance was noticed for pod yield per plant and seed yield per plant indicating that these traits are less influenced by the environment.

Fifty genotypes of groundnut were studied by Dewangan *et al.* (2015) and inferred that PCV is slightly higher than GCV for all the traits studied. The traits plant height, seed index, pod yield per plant and days to 50% flowering showed high heritability coupled with high genetic advance suggesting that these are favorable traits for improvement through selection.

Sixty diverse genotypes of Virginia groundnut were evaluated by Gupta *et al.* (2015) for variability parameters and observed high PCV and

GCV for plant height, number of primary branches per plant, number of mature pods per plant, 100 pod weight, 100-kernel weight, kernel yield per plant and harvest index. The traits 100-kernel weight, 100-pod weight, biological yield per plant and kernel yield per plant showed high heritability coupled with high genetic advance indicating the preponderance of additive gene action and these traits possess high selective value. High heritability with moderate or low genetic advance was observed for days to 50% flowering, oil content and protein content.

Venkataramana *et al.* (2015) assessed variability, heritability and genetic advance of 21 crosses of groundnut for 13 traits and recorded highest PCV and GCV for number of secondary branches per plant followed by kernel yield per plant, pod yield per plant, number of kernels per plant and harvest index. High heritability coupled with high genetic advance as percent of mean for traits viz., days to 50% flowering, harvest index, kernel yield per plant and number of kernels per plant indicated that these were predominantly influenced by additive gene action. High heritability coupled with moderate genetic advance as percent 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 indicated the role of both additive and non-additive gene action with preponderance of additive genetic variance.

Balaraju and Kenchanagoudar (2016) evaluated 54 interspecific derivative lines and 6 recombinant inbred lines for yield, yield components and disease resistance and observed that PCV is higher than GCV for all the traits. The traits number of secondary branches per plant, number of pods per plant, pod yield per plant, pod yield per hectare, harvest index and per cent of disease incidence at harvest exhibited high PCV and GCV. The high heritability with high genetic advance as percent over mean was observed for plant height, secondary branches per plant, pod yield per plant, test weight, pod yield per hectare, harvest index and percent of disease incidence; low genetic advance was estimated for shelling percentage.

Twenty Spanish bunch groundnut genotypes were evaluated for variability, heritability and genetic advance by Bhargavi *et al.* (2016) and found high PCV and GCV estimates for pod yield per plant and pod yield per hectare indicating the greater variability and scope for improvement of high yielding genotypes The estimates of heritability and genetic advance as per cent of mean were high for number of mature pods per plant, biological yield per plant, pod yield per plant, biological yield per hectare, pod yield per hectare, harvest index, kernel yield per plant, kernel yield per hectare, 100 kernel weight and oil yield per hectare indicated that these characters were less influenced by environment and governed by additive gene action which may be exploited through simple selection methods.

Three F_2 populations derived from crosses *viz.*, KCG-6 X ICGV-91114, KCG-6 X TG-69 and TMV-2 X ICGV-00350 were assessed by Shashikumara *et al.* (2016) and found high PCV and GCV for pod yield, kernel yield, total pods, matured pods and oil yield per plant in all the crosses indicating wide range of variability. High heritability coupled with high genetic advance of mean (GAM) was noticed for matured pods, kernel yield, oil yield and pod yield per plant and harvest index and shelling per cent in all the three crosses which indicated the involvement of additive gene action in controlling these traits.

Srivalli and Nadaf (2016) studied the genetic variability of 299 RILs for physiological traits under drought stress conditions and noticed that RWC at 30 days after stress had moderate to high heritability and genetic advance as percent of mean indicating that selection for this trait is effective at later stages of stress. SLA and SCMR showed moderate to low heritability and genetic advance as percent of mean indicating expression of these traits are influenced by environment restricting the scope of selection.

Bhavya *et al.* (2017) evaluated F_4 and F_5 experimental material of a cross GKVK-16 X KCG-2 for WUE related traits, yield and its component characters and inferred higher estimates of PCV and GCV for pods per plant, kernel yield per plant and pod yield per plant in both the generations; moderate estimates of PCV and GCV for plant height, SLA and SMK percentage in F_4 generation and for primary branches per plant and shelling percent in F_5 generation. High heritability accompanied with high genetic advance as per cent mean was recorded for plant height, pods per plant, kernel yield per plant, SMK and pod yield per plant; high heritability accompanied with low to moderate genetic advance as percent of mean was noticed for traits like days to first flowering, primary branches per plant, SCMR, SLA and shelling percent.

Chavadhari *et al.* (2017) evaluated 70 groundnut genotypes for quantitative and yield parameters and observed high GCV for kernel yield per plant followed by the number of branches per plant, harvest index and biological yield per plant. High estimates of heritability coupled with high genetic advance expressed as percentage of mean was observed for kernel yield per plant, 100-kernel weight, plant height, 100 pod weight, biological yield per plant, harvest index and number of branches per plant indicating the preponderance of additive gene action.

Kamdi *et al.* (2017) evaluated eighteen local collections of groundnut and reported higher phenotypic coefficients of variations than genotypic coefficient of variations. They also observed small differences between genotypic and phenotypic variability for number of mature pods per plant, weight of dry haulm per plant and weight of dry pods suggesting that these characters were less influenced by the environment.

Variability studies by Mukesh and Lal (2017) on 40 genotypes of groundnut revealed high genotypic coefficient of variation for plant height at

20 DAS and high heritability coupled with high genetic advance for plant height at 60 DAS and kernel uniformity.

Omprakash and Nadaf (2017) evaluated 130 advanced breeding lines of groundnut and recorded significant variation for all the traits. They also recorded moderate to high variability among genotypes for pod yield and kernel yield indicating greater scope for improvement; low to medium variability for 100 kernel weight whereas low variability for shelling per cent, protein content and oil content. Moderate to high PCV and GCV associated with high heritability and high genetic advance as per cent mean was recorded for pod yield, LLS score, rust score, linoleic acid.

Sixteen groundnut genotypes were evaluated for twelve quantitative parameters by Yusuf *et al.* (2017a) and observed high heritability accompanied by high genetic advance for the traits 100 seed weight, number of branches per plant, plant height, number of mature pods, number of seeds per pod, harvest index and kernel yield indicating the predominant role of additive gene action and the possibilities of effective selection for the improvement of groundnut genotypes based on these characters. Low heritability and genetic advance was observed for shelling percentage and number of seeds per plant.

Studies of Aparna *et al.* (2018) on 168 germplasm lines and five checks for 14 characters revealed high estimates of PCV and GCV for the traits number of immature pods per plant, kernel yield per plant, number of primary branches per plant, number of mature pods per plant, pod yield per plant, number of pegs per plant and number of pods per plant. They also recorded high heritability coupled with high genetic advance as percent of mean for the traits number of immature pods per plant, days to 50% flowering, number of primary branches per plant, shelling percentage, number of pods per plant, number of mature pods per plant, plant height and 100 kernel weight.

Hussein *et al.* (2018) studied eight groundnut cultivars and recorded high estimates of GCV and PCV for number of branches per plant, number of pods per plant, number of seeds per plant, pod yield per plant, seed yield per plant and 100- seed weight while moderate estimate for plant height was recorded. They also recorded high heritability coupled with high genetic advance for number of pods per plant, number of seeds per plant, pod yield per plant, seed yield per plant and 100 seed mass.

Among the 13 different characters studied on 144 groundnut genotypes by Mahesh *et al.* (2018b), plant height, number of primary branches per plant, number of mature and immature pods per plant, kernel yield per plant, hundred kernel weight, haulm yield per plant and dry pod yield per plant showed high GCV, PCV, heritability and genetic advance as the percent of mean indicating the presence of additive gene effects and improvement of these characters can be done by effective phenotypic selection.

2.3 GENETIC DIVERGENCE

Estimation of 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 statistics. Selection of parents for hybridization programme based on Mahalanobis's D^2 statistics is more reliable method as the requisite knowledge in respect of a number of characters is available prior to crossing programme.

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

Sigamani (1986) grouped 144 genotypes of groundnut into 16 clusters using Mahalanobis's D^2 statistics and also observed that days to flowering and maturity were the important characters for differentiating genotypes into different clusters.

Venkateswarlu (1988) evaluated 57 intra and inter sub-specific cross derivatives of groundnut and grouped them into 12 clusters. The grouping pattern was at random and either botanical grouping or parentage showed no influence. The characters harvest index, 100-pod weight, number of nodes on main axis, number of secondaries and number of immature pods per plant contributed more towards divergence.

Using D^2 analysis, Rajkumar (1991) grouped 48 groundnut genotypes into eleven clusters and also reported that the characters harvest index and shelling percent contributed more towards genetic divergence.

Yadava *et al.* (1991) grouped 39 genotypes of groundnut into 10 clusters using Mahalanobis D^2 statistics. The genotypes TG-9, MH-111, ICGV-86008, ICGS-11, ICGS-1 and JL-24 were identified as the most promising genotypes for further breeding work.

Eighteen genotypes of groundnut were grouped into eight clusters by Katule *et al.* (1992) using D^2 analysis. D^2 values ranged from 26.88 to 493.23 indicating wide range of diversity among the genotypes for the characters studied.

Varman and Raveendran (1996) studied 60 three way cross F_1 hybrid populations derived from 6 bunch groundnut varieties and grouped them into five clusters using Mahalanobis D^2 analysis. They also observed that crosses originating from the same grandparental combinations were scattered in different clusters.

Based on D^2 analysis for nine characters John and Mylaswamy (1998) grouped the groundnut genotypes into three clusters and the clustering pattern did not show any relationship with the geographic origin.

A set of 144 groundnut genotypes were analysed by Venkataravana *et al.* (2000) using Mahalanobis D^2 analysis for 15 characters and grouped them into seven clusters. They found that the distribution of genotypes into different clusters was not according to their geographical origin.

Based on Mahalanobis D^2 analysis Vijayasekhar (2002) grouped 65 genotypes into 10 clusters. The mode of distribution of genotypes of various clusters was at random suggesting that there was no correlation between geographical distribution and genetic diversity. Maximum contribution towards genetic divergence was 100-seed weight and shelling percentage.

Hemanth (2004) studied 54 genotypes of groundnut and grouped them into 11 clusters based on morphological and biochemical characters whereas 17 clusters based on physiological characters, respectively. They also observed that mode of distribution of genotypes into different clusters for morphological and biochemical characters was at random and independent of each other suggesting that there was no relationship between geographical origin and genetic diversity.

Using Mahalanobis D^2 analysis Muralidharan and Manivannan (2004) grouped 19 genotypes of bunch groundnut into nine clusters and showed that characters total number of flowers, primary and secondary branches contributed more towards total divergence.

Mahalakshmi *et al.* (2005b) grouped 57 groundnut genotypes into seven clusters using Mahalanobis D^2 statistics and observed that days to first flowering followed by shelling percentage contributed maximum to the total divergence.

Lakshmidevamma *et al.* (2006) studied 81 genotypes of groundnut for genetic divergence analysis using Mahalanobis D^2 analysis and grouped them into 16 clusters. They also reported that test weight, days to maturity and oil content were the most potential traits contributing to the total divergence.

Suneetha (2007) conducted genetic divergence studies on 29 released and prereleased cultures of groundnut and grouped them into nine and eight clusters based on morphological, yield and yield attributes and physiological characters respectively. The characters harvest index, days to emergence, length of main axis, leaf area duration, leaf area index, crop growth rate and net assimilation rate contributed maximum towards genetic divergence.

Genetic diversity studies by Sudhakar (2008) using Mahalanobis D^2 analysis revealed that there is no relationship between geographical distribution and genetic diversity. They grouped 74 groundnut genotypes into 12 clusters and also reported that the characters 100-kernel weight, shelling percentage and harvest index contributed maximum towards genetic divergence.

Zaman *et al.* (2010) experimented 34 groundnut genotypes for genetic divergence and classified them into 5 clusters. They observed that cluster V has high intra-cluster distance indicating more divergence within the cluster whereas inter-cluster distance was maximum between cluster IV and III followed by V and III indicating that genotypes from these clusters can be selected for hybridization programme.

Venkateswarulu *et al.* (2011) evaluated 74 genotypes using Mahalanobis D^2 statistics and grouped them into 12 clusters and also reported that the characters 100-kernel weight, shelling percentage and harvest index contributed maximum towards genetic divergence.

Ravikumar *et al.* (2012) grouped 50 genotypes of groundnut into five and seven clusters using D^2 and metroglyph methods, respectively. They concluded that the distribution of genotypes from different clusters was at random and independent of their geographical origin and D^2 analysis was more effective compared to metroglyph analysis.

Nirmala *et al.* (2013) grouped 30 genotypes of groundnut into 14 clusters using D^2 analysis and also reported that number of secondary branches per plant contributed maximum towards genetic divergence followed by CGR at 75 DAS to harvest, CGR at 30-75 DAS, 100 seed weight, plant height, SCMR and harvest index.

Ganapati *et al.* (2014) evaluated 191 accessions of groundnut and grouped them into 15 clusters. They observed that cluster I was large with 100 accessions followed by cluster II and VII with 72 and 12 germplasm accessions, respectively and all other clusters are monogenotypic clusters. Maximum intra-cluster distance was observed for cluster VII and I indicating wide genetic divergence within cluster. Inter cluster distance was maximum between cluster X and XV followed by cluster IX and XV, XI and XV and cluster XI and XIII indicating genotypes from these clusters can be used in further hybridization programme.

By conducting genetic diversity studies Yadav *et al.* (2014) grouped 60 genotypes of groundnut into 12 clusters. They found maximum inter cluster distance between cluster III and X carrying one and two genotypes respectively and maximum intra-cluster distance for cluster V indicating high divergence within the cluster.

Fourty genotypes of groundnut were studied by Mukesh and Lal (2015) for diversity and grouped into seven clusters. Maximum inter cluster distance was observed between cluster IV and VII whereas intra cluster distance was maximum for cluster IV and the traits plant height at 60 days and kernel uniformity contributed more to the diversity.

Vasanthi *et al.* (2015) grouped 29 genotypes of groundnut into eight clusters based on data of 10 physiological traits. The highest inter-cluster distance was recorded between cluster VI and VII indicating more divergence between genotypes of these clusters. Leaf area duration at 54 DAS contributed maximum to the diversity followed by leaf area index at 72 DAS.

Vivekananda *et al.* (2015) estimated genetic divergence among 31 genotypes of groundnut and grouped them into seven clusters and the trait 100-kernel weight contributed maximum towards divergence followed by dry pod yield per plant.

Ashutosh *et al.* (2016) conducted divergence studies on 29 breeding lines of groundnut and classified them into eight clusters where maximum inter-cluster distance was observed between cluster VI and cluster VIII followed by cluster VI and cluster VII indicating that genotypes from these clusters could be selected as parents for hybridization. Shelling percentage contributed maximum to the divergence followed by harvest index.

Jayashree and Laxmidhar (2016) evaluated 28 groundnut mutant cultures along with its parent Smruti for genetic diversity and grouped them into six clusters. Cluster I was the largest consisting of 18 genotypes and inter cluster distance was highest between cluster III and VI followed by cluster II and VI and lowest between cluster II and V. The traits 100-kernel weight and kernel yield per plant contributed maximum towards genetic divergence whereas days to 50 percent flowering contributed least.

Singh *et al.* (2016) evaluated 50 groundnut genotypes using Mahalanobis's D^2 statistics and grouped them into 27 clusters. The clustering pattern of genotypes showed that the genotypes of different origins were clubbed into one cluster, whereas the genotypes belonging to same origin were grouped into different clusters indicating that the geographic distribution was not the sole criterion of genetic diversity.

Fifty drought tolerant groundnut genotypes were evaluated for their genetic diversity by Venkatesh *et al.* (2016) and classified them into nine clusters. They revealed maximum inter-cluster distance between cluster VI and VIII and intra-cluster distance for cluster VIII indicating the existence of high variability. The traits 100-kernel weight and haulm yield per plant contributed 92.25 percent towards total genetic divergence.

Thirty drought tolerant groundnut genotypes were evaluated for genetic diversity by Lokeshwar *et al.* (2017) and classified them into six clusters. Inter-cluster distances revealed maximum diversity between genotypes of cluster I and VI and intra-cluster distance was highest for cluster IV. They have also revealed that oil content, free proline content and protein content contributed to 94.94 per cent of the total genetic divergence indicating that these traits should be given importance in selection of parents for hybridization programme.

Twenty one Spanish bunch groundnut genotypes were studied by Saikat *et al.* (2017) and grouped into four distinct non-overlapping clusters. They found that pod yield was the key contributor towards the genetic divergence followed by days to maturity. Highest inter cluster distance was observed between cluster II and IV followed by cluster II and III indicating that genotypes from these clusters could be used as parents for hybridization.

Genetic divergence of 36 genotypes comprising of four parents and their 32 progenies was studied by Sardar *et al.* (2017) and revealed that haulm yield per plant contributed maximum to the divergence followed by pod yield per plant, kernel yield and kernel number per plant whereas shelling percent contributed least to divergence. They grouped the genotypes into 10 clusters in which cluster X was the largest containing 10 genotypes.

Tulsiram *et al.* (2017b) analysed 93 groundnut genotypes for genetic divergence using D^2 analysis and classified them into eight clusters. They have also observed that genotypes from same origin showed no tendency to be in same cluster.

Waghmode *et al.* (2017) evaluated 121 groundnut genotypes for genetic diversity and grouped them into seven clusters. Cluster I had maximum genotypes of 109 and all other clusters have two genotypes each. Maximum intra cluster distance was exhibited by cluster VII followed by cluster VI and I while maximum inter cluster distance was recorded between cluster VI and VII, followed by cluster II and VII, and cluster III and VII indicating a wide divergence between these clusters. Based on cluster means they have also revealed that dry pod yield per plant, number of kernels per pod, shelling percentage, 100 kernel weight and number of pods per plant were the main characteristics contributing to divergence.

Mahesh *et al.* (2018a) measured the genetic diversity among 144 genotypes of groundnut for 13 characters using D^2 statistics and grouped them into 16 clusters. The maximum inter cluster distance was observed between Cluster XI and XVI followed by IV and XVI indicating that crossing between these clusters helps in production of transgressive segregates or better recombinants.

2.4 STUDIES ON CHARACTER ASSOCIATION

Genetic improvement of yield is the primary concern to plant breeder as overall 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 the yield is essential for improving the yield. 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 available literature on the association of the characters in groundnut is presented here under.

Correlation studies by Patil *et al.* (1982) on 32 strains of groundnut revealed that yield per plant was positively correlated with number of developed pods per plant, number of primary branches per plant and height of the plant. Negative relationship of yield per plant was observed with number of pegs per plant and number of undeveloped pods per plant.

A set of 45 groundnut genotypes were studied by Reddi *et al.* (1986) for character association and reported that pod yield was positively and significantly associated with number of mature pods per plant, number of secondary branches per plant, 100 kernel weight and shelling percent.

Prasanthi *et al.* (1990) analysed 40 crosses in advanced segregating generations of groundnut and observed that the character pod yield per plant was positively and significantly associated with kernel yield, pods per plant and harvest index.

Reddy and Gupta (1992) studied 46 diverse genotypes of groundnut in three environments and revealed that pod yield was positively and significantly associated with number of mature pods, kernel yield, shelling outturn and harvest index in all the three environments indicating the importance of these characters in formulating a selection criteria to improve groundnut yields.

In a study of F_2 population, Manoharan *et al*. (1993) observed that pod yield had positive and significant association with number of primaries, dry matter production, harvest index, pod number and 100- pod weight. Plant height had positive but non-significant association with pod yield. Among the component characters, dry matter production was positively correlated with plant height and number of primaries. Similarly, pod number was positively associated with number of primaries and dry matter production whereas plant height was negatively correlated with number of primaries.

Sumathi and Ramanathan (1995) evaluated F_3 and F_4 generations of seven groundnut genotypes and their respective 33 hybrids and observed that pod yield was positively correlated with number of mature pods, 100-kernel weight and number of flowers.

Character association studies by Francies and Ramalingam (1997) in 55 genotypes of groundnut in F_2 generation revealed that kernel yield, number of kernels, number and length of secondary branch, nodes on primary and secondary branch, number of mature pods, mature pod percent and number of pegs were strongly associated with pod yield.

Jayalakshmi *et al.* (2000) conducted correlation studies in seven parents and 21 F_1 hybrids and observed highly significant and positive association of mature pods per plant, harvest index and specific leaf area with kernel yield per plant in both parents and hybrids, while oil content had negative association with kernel yield in parental genotypes. Specific leaf area had positive association with harvest index, while root dry mass had a negative association with harvest index.

While analyzing 15 genotypes of Spanish bunch groundnut, Johar and Mohinder (2001) reported high phenotypic correlation of number of pods with pod yield per plant followed by harvest index and number of fruiting nodes per plant. Further they also reported that main shoot height, number of secondary branches and 100- kernel weight were negatively correlated with protein content.

Jayalakshmi and Reddy (2003) analysed 21 groundnut hybrids for two seasons and inferred that kernel yield exhibited significant and positive phenotypic and genotypic correlations with harvest index, mature pod number per plant and pod yield during both the seasons. However, specific leaf area had significant positive phenotypic and genotypic association with kernel yield only during rainy season.

Mahalakshmi *et al.* (2005a) studied 57 groundnut genotypes for correlation analysis and recorded significant and positive association of kernel yield per plant with days to 50 per cent flowering, plant height, number of secondary branches, number of unproductive pegs, number of immature pods, number of mature pods, SMK weight, SMK number, total number of pods, total number of gynophores, shelling percentage, 100-kernel weight and pod yield.

Analysis of 48 diverse large seeded groundnut genotypes by Parameshwarappa *et al.* (2005) indicated positive and significant association of pod yield with shelling percent, sound mature kernels, 100-kernel weight and oil content whereas negative association was observed with protein content. They have also reported that number of pods exhibited positive association with shelling per cent, sound mature kernels and oil content and the association of kernel weight with oil content was positive but negative with protein content.

Correlation studies by Regina and Angela (2005) on three cultivars and six lines of groundnut showed that grain yield was influenced positively by the number of pods per plot and weight of 100- seeds and negatively by the number of seeds per pod.

Patil *et al.* (2006) evaluated 13 groundnut genotypes along with four checks (JL-24, GPBD-4, Dh-86 and Dh-3-3-30) for association analysis and revealed that pod yield per plant had significant positive association with number of pods per plant, shelling percent and SMK percent. Hundred kernel weight and oil content had non-significant association with pod yield per plant in positive and negative directions, respectively.

Venkateswarlu *et al.* (2007) evaluated 28 F_1's derived from 8 X 8 diallel and observed that pod yield per plant had highly significant and positive association with harvest index, number of well filled and mature pods per plant and kernel yield per plant indicating that they could be used as selection criteria for higher pod yield.

Parameshwarappa *et al.* (2008) studied two segregating populations of groundnut crosses TKG 19A X J11 and J11 X TGLPS 3 and revealed positive significant association of total number of pods, number of well filled pods, 100 kernel weight, SMK % and days to flowering towards pod yield in both the crosses whereas shelling percent showed significant positive association towards pod yield only in the cross J11 X TGLPS 3.

Character association studies by Giri (2009) in 20 groundnut genotypes indicated higher genotypic correlation coefficients than the corresponding phenotypic correlation coefficients suggesting strong inherent association among the characters studied. They have reported that pod yield had positive significant association with days to 50 percent flowering, days to maturity, kernel yield, test weight and oil content, whereas negative significant association was displayed with late leaf spot disease severity and reducing sugars.

Korat *et al.* (2010) evaluated 80 bunch groundnut genotypes and observed that biological yield per plant, 100-kernel weight and harvest index had positive and significant association with pod yield per plant at phenotypic level. Phenotypic interrelationship between days to maturity and pod yield per plant was negative and significant.

Channayya *et al.* (2011) assessed 12 different quantitative traits in the mutants derived from two Spanish Bunch groundnut cultivars and found that pod yield was positively and significantly associated with number of primary branches, pod weight per plant, 100-kernel weight, sound matured kernel percent and oil yield.

Jogloy *et al.* (2011) conducted experiment on 200 breeding lines in the F_6 generation of 10 peanut crosses and recorded positive association of pod yield with seed size and harvest index with high and significant correlation coefficients but negative association with maturity.

Vekariya *et al.* (2011b) evaluated 50 diverse groundnut bunch genotypes of bunch groundnut for correlation analysis and observed higher magnitude of genotypic correlation coefficients compared to the corresponding phenotypic correlation coefficients for most of the characters studied indicating least environmental effects on the expression of the traits. They also observed pod yield per plant had highly significant and positive correlations at phenotypic level with number of mature pods per plant, 100-pod weight, 100-kernel weight, kernel yield per plant, biological yield per plant and harvest index.

A study of character association among nine characters in 18 selected groundnut genotypes by Narasimhulu *et al.* (2012) revealed that pod yield per plant had significant positive association with kernel yield per plant, shelling percentage and SMK percent at both genotypic and phenotypic levels.

Seyyed and Seyyed (2012) studied interrelationship between oil yield and its components in 23 peanut genotypes and reported high positive correlation of seed yield, total number of kernels per plant, plant height and 100- kernel weight with oil yield.

Correlation coefficients among nine yield and yield attributing characters were investigated in F_3 generation of three crosses of groundnut by Shoba *et al.* (2012) and revealed that kernel yield was significantly and positively correlated with number of pods per plant, pod yield per plant, shelling percentage and hundred kernel weight for all the crosses.

A set of 66 groundnut genotypes were analysed for correlations among yield and yield attributing characters by Pavan *et al.* (2013) and observed significant positive correlation of kernel yield with pod yield per plant, number of mature pods per plant, shelling percentage, harvest index, sound mature kernel percentage, specific leaf weight after 60 DAS, protein content and oil content indicating the possibility of selection of these traits to improve the kernel yield.

Rao *et al.* (2014) evaluated 50 groundnut genotypes and observed significant positive correlation of pod yield with kernel yield, number of pods per plant, hundred kernel weight and dry haulm yield and significant negative association with days to 50% flowering.

Satish (2014) studied 16 groundnut genotypes and recorded significant positive genotypic correlation of pod yield with number of pods per plant, number of branches, days to 50% flowering and 100- kernel weight, whereas they recorded negative and non-significant correlation of pod yield with plant height.

John and Reddy (2015) studied 15 quantitative traits in 28 F_2s for character association and recorded significant positive association of pod yield per plant with days to 50 percent flowering, days to maturity, number of well-filled and mature pods per plant, shelling per cent, sound mature kernel per cent, 100-kernel weight, protein per cent and kernel yield per plant. They have also reported significant and positive association of kernel yield per plant with number of secondary branches per plant, number of well filled and mature pods per plant, shelling per cent, 100-kernel weight, and protein per cent.

Rathod *et al.* (2015) conducted correlation studies in 18 groundnut genotypes and inferred that pod yield per plant exhibited positive significant association with number of pods per plant, total sugar, kernel yield, non-reducing sugar, test weight, SCMR, harvest index, oil content and shelling per cent, whereas, LLS severity, reducing sugar, stomata frequency and size showed negative significant association.

Character association studies was done by Shashikumara *et al.* (2015) among 14 characters in F_2 segregating generations of three groundnut crosses and revealed that specific leaf area had significant negative correlation with SCMR, total pods per plant, matured pods per plant, kernel yield and pod yield. They have also observed significant positive correlation of traits SCMR, matured pods per plant, harvest index, kernel yield, oil yield and sound mature kernel percent with pod yield.

Shreya *et al.* (2015) analysed correlation for yield and yield contributing characters in F_3 generation derived from four crosses of groundnut and observed that pod yield was significantly and positively associated with number of primary branches per plant, plant height, pegs number per plant, total biomass per plant, shoot weight per plant, root weight per plant, number of mature pods per plant, number of immature pods per plant, harvest index and kernel weight per plant for all the four crosses.

Six F_2 crosses of groundnut genotypes were evaluated for character association among yield attributing and physiological traits by Vinutha *et al.* (2015) and revealed high association of pod and kernel yield with number of pods per plant and sound mature kernel at phenotypic level. The physiological traits SLA and SCMR showed significant negative correlation with each other in all the crosses except in cross GKVK- 5 X GPBD-4.

Sandhya *et al.* (2016) experimented 20 elite groundnut genotypes and noticed strong positive association between pod yield per plant and kernel yield per plant, oil yield per plant and significant and negative association with late leaf spot severity and rust incidence irrespective of the environments. Inter correlation estimates for yield components revealed that plant height, 100-kernel weight, kernel yield per plant, oil yield per plant, late leaf spot severity, number of matured pods per plant, harvest index and plant height were significantly associated with one another and also with pod yield per plant which indicated that these characters were important components for improvement of pod yield in groundnut.

Correlation analysis by Surbhi *et al.* (2016) for pod yield and its component characters in 24 genotypes of groundnut revealed that the dry pod yield per plant was positively and significantly correlated at both genotypic and phenotypic level with kernel yield per plant, number of pods per plant and plant height.

Anusha and Savithramma (2017) studied 230 RILs of cross NRCG 12568 X NRCG 12326 along with two checks TMV-2 and KCG-2 and recorded that pod yield per plant was significantly and positively associated with primary branches per plant, SCMR, pods per plant and kernel yield per plant whereas it was significantly negatively associated with SLA and sound mature kernel percent.

Ten genotypes of Virginia bunch groundnut were evaluated for correlation studies by Bhargavi *et al.* (2017) and observed relatively high magnitude of genotypic correlation coefficients than the corresponding phenotypic correlation coefficients, indicating strong inherent association between the characters. They have also observed significant positive association of pod yield per plant with number of mature pods per plant, biological yield per plant, biological yield per hectare, 100 kernel weight, oil yield per hectare, kernel yield per plant, kernel yield per hectare and pod yield per hectare both at phenotypic and genotypic levels. On contrary, negative significant association of pod yield with SCMR at 60 DAS, SCMR at 70 DAS and SCMR at maturity was observed by them at genotypic level.

Bhavya *et al.* (2017) evaluated F_4 and F_5 populations generated from a cross GKVK-16 X KCG-2 and recorded significant positive correlation of pod yield per plant with SCMR, pods per plant, kernel yield per plant and sound mature kernel per cent in both F_4 and F_5 generation and for days to first flowering and plant height in F_5 generation indicating that improvement in these characters will lead to improvement in yield. They have also reported that specific leaf area had negative non-significant association with pods per plant and sound mature kernel per cent and pod yield per plant in F_4 generation and significant negative association with pods per plant in F_5 generation.

Field experiments carried out by Htin *et al.* (2017) indicated that hundred pod weight, hundred seed weight, shelling percent, specific chlorophyll meter reading, days to maturity, plant height and number of pods per plant had significant positive association on yield per plant. Specific leaf area showed negative genotypic correlation with yield per plant.

Mukesh and Lal (2017) conducted correlation coefficient analysis for yield and its contributing traits in groundnut germplasm and observed that plant height at 40 DAS and hundred kernel weight was significantly and positively correlated with pod yield (q/ha).

Studies on character association for kernel yield and its component characters in six parents and their 15 F_1 crosses in groundnut by Trivikrama *et al.* (2017) revealed higher genotypic correlations than the phenotypic correlations indicating strong inherent association between the two corresponding characters and selection for these characters might be rewarding. They also observed that the characters pod yield per plant, mature pods per plant, 100-kernel weight, pods per plant, pegs per plant, harvest index and shelling percentage had highly significant and positive association with kernel yield per plant and also exhibited significant positive inter-correlations among themselves.

Association analysis of 90 genotypes along with three check varieties were evaluated by Tulsiram *et al.* (2017a) and revealed that dry pod yield per plant showed positive and significant correlation at both genotypic and phenotypic levels with kernel yield per plant, 100-kernel weight, sound mature kernels and biological yield per plant.

Character association studies by Yusuf *et al.* (2017b) in 16 groundnut genotypes for 12 characters revealed that the grain yield/ha showed positive and significant genetic correlation with pod weight per plant, seed weight per plant and 100 seed weight. They have also reported that grain yield was negatively correlated with number of seeds per pod at all genotypic, environmental and phenotypic levels.

Mahesh *et al.* (2018b) conducted correlation studies on 144 groundnut genotypes and observed that kernel yield per plant, mature pods per plant, sound mature kernel and haulm yield per plant had significant positive correlation with dry pod yield at both phenotypic and genotypic level but hundred kernel weight showed the significant positive correlation with pod yield only at genotypic level. They also observed that the traits like days to 50% flowering, days to maturity, number of immature pods per plant and shelling percentage had negative correlation with dry pod yield per plant at both phenotypic and genotypic level where as shelling percentage had significant positive correlation at phenotypic level.

2.5 STUDIES ON PATH COEFFICIENT ANALYSIS

Path co-efficient analysis is a statistical device developed by Wright (1921) which helps in partitioning of the correlation coefficients into direct and indirect effects of independent variable on dependent variable. The correlation coefficients 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 these direct and indirect effects. Hence, path co-efficient analysis is of much importance in any plant breeding program.

A brief review of literature available on path co-efficient analysis is presented hereunder.

Maximum positive direct effect of kernel yield on pod yield was recorded by Reddi *et al.* (1986) whereas Durgarani *et al.* (1987) reported that number of primaries, secondaries, number of pods, shelling percentage and 100-kernel weight exhibited positive direct effect on yield.

Prasanthi *et al.* (1990) analysed 40 crosses in advanced segregating generations of groundnut and recorded high positive direct effect of kernel weight on pod yield whereas its indirect effect was observed through number of primary branches while pods per plant showed moderate negative direct effect on pod yield.

From path analysis in F_2 population of an intersubspecific cross Robut 33-1 X chico, Manoharan *et al.* (1993) noticed that both pod number and pod weight had high positive direct effect on yield. The indirect influence of dry matter production and harvest index via pod number was also positive and high.

Path coefficient analysis by Francies and Ramalingam (1997) in 55 groundnut genotypes in the F_2 generation revealed that nodes on main axis, nodes on primary branch and number of kernels were the main characters influencing pod yield directly as well as indirectly.

Johar and Mohinder (2001) evaluated 15 Spanish bunch groundnut genotypes in 12 environments and found maximum positive direct effect of number of primary branches on pod yield followed by 100-kernel weight, sound mature kernel percentage, harvest index and number of fruiting nodes. On contrary, maximum negative direct effect by main shoot height was observed by them on pod yield. They also reported that number of secondary branches had highest indirect effect via number of primary branches, 100 kernel weight, sound mature kernel percentage and harvest index.

Roy *et al.* (2003) analysed 95 groundnut genotypes and reported positive direct effect of podding index, 100-kernel weight and number of pods per plant on kernel yield per plant whereas days to 75% flowering and shelling percentage showed negative direct effect on kernel yield.

Lakshmidevamma *et al.* (2004) noticed that kernel yield per plant exerted the highest positive direct effect on pod yield and indirect effects of the components characters *i.e.*, days to 50 per cent flowering, plant height, number of branches per plant, number of mature pods per plant and test weight were found to be high through kernel yield on pod yield.

Regina and Angela (2005) analysed three cultivars and six lines of groundnut and revealed that number of pods per plot showed high positive direct effect on kernel yield followed by weight of 100 seeds and number of seeds per pod.

Path analysis of 13 genotypes along with four checks (JL-24, GPBD-4, Dh-86 and Dh-3-3-30) at six different locations by Patil *et al.* (2006) indicated that the traits number of pods per plant, shelling percentage and sound mature kernel per cent had maximum direct effect on pod yield per plant at minimum three locations indicating that increase in pod number per plant, shelling per cent and sound mature kernel per cent would improve the pod yield of groundnut.

Path analysis by Venkateswarlu *et al.* (2007) on 28 F_1's derived from 8 X 8 diallel revealed high positive direct effects of kernel yield per plant followed by specific leaf nitrogen, root length, shelling percent and number of well filled and mature pods per plant on pod yield indicating that these characters should be given greater emphasis while making selections for higher pod yield.

Parameshwarappa *et al.* (2008) investigated 10 quantitative traits and their contributions towards pod yield in segregating populations of two crosses TKG19A X J11 and J11 X TGLPS3 of groundnut and observed that the number of well filled pods had highest positive direct effects towards pod yield followed by SMK% and 100 kernel weight in the cross TKG19A X J11, whereas total number of pods had major direct effect towards pod yield followed by 100 kernel weight and SMK % in cross J11 X TGLPS3.

Giri (2009) evaluated 20 genotypes of groundnut for path analysis and revealed high positive direct effect of kernel yield on pod yield as well as indirect effect of oil content, sound mature kernel, days to 50 per cent flowering, test weight, days to maturity, and non-reducing sugar through kernel yield on pod yield. Shelling percentage exerted high but negative direct effect on pod yield.

Path analysis in 80 bunch groundnut genotypes by Korat *et al.* (2010) indicated that biological yield per plant and harvest index exhibited high and positive direct effects on pod yield per plant. Moreover days to 50 % flowering and days to maturity showed indirect effects through harvest index on pod yield per plant.

Vekariya *et al.* (2011b) studied path analysis of different characters in 50 diverse genotypes of bunch groundnut and revealed that kernel yield per plant, biological yield per plant and harvest index had high and positive direct effects on pod yield per plant. Plant height and 100-kernel weight exhibited moderate and positive direct effects towards pod yield.

In an experiment involving 34 groundnut genotypes Zaman *et al.* (2011) observed that number of mature nuts per plant had high positive direct effect on seed yield per hectare followed by nut size, shelling percentage, days to 50% flowering and days to maturity. Therefore, branches per plant, plant height, nuts per plant, nut size, kernel size, days to 50% flowering, shelling percentage and days to maturity were identified to be the important characters which could be used in selection for yield.

Seyyed and Seyyed (2012) evaluated 23 groundnut genotypes under drought stress and irrigated conditions and reported that total number of kernels per plant, 100-kernel weight under irrigated condition and total number of pods per plant and 100-kernel weight, total number of kernels per plant, total number of pods per plant and biomass under drought condition exerted high positive direct effects on seed yield. They have also noticed that high indirect contribution was observed via 100-kernel weight and total number of kernels per plant.

Path analysis studies conducted by Shoba *et al.* (2012) in F_3 generation for three crosses (TMV 2 X COG 0437, TMV 2 X COG 0438 and TMV2 X ICGV 97150) of groundnut indicated that pod yield per plant exerted maximum positive direct effect on kernel yield per plant followed by shelling percentage and hundred kernel weight in all the three crosses.

The traits *viz.*, plant height (for the cross TMV 2 X ICGV 97150), number of branches per plant (all the three crosses), number of pods per plant (for the cross TMV 2 X ICGV 97150), rust score (for the crosses TMV 2 X COG 0437 and TMV 2 X ICGV 97150) and LLS score (for the cross TMV 2 X COG 0438) indicated negative direct effect on kernel yield per plant.

Pavan *et al.* (2013) evaluated 66 groundnut genotypes for path analysis studies and revealed high positive direct effect of pod yield per plant and shelling percentage on kernel yield. They have also reported that pod yield per plant also had positive indirect effects through number of mature pods per plant, harvest index, shelling percent and sound mature kernel percentage whereas shelling percent had positive indirect effects through sound mature kernel percentage.

In a study comprising of 36 groundnut genotypes Yohanna (2013) observed that the number of pods per plant had the highest direct contribution to the kernel yield followed by 100 kernel weight and lowest direct effect by haulm yield.

Rao *et al*. (2014) analysed 50 groundnut genotypes and concluded that kernel yield, days to maturity, number of pods per plant and hundred kernel weight had highest direct effects on pod yield.

John and Reddy (2015) evaluated 28 F_2s and found maximum positive direct effect on pod yield per plant was contributed from kernel yield per plant days to 50 per cent flowering and 100-kernel weight indicating that these traits were the important yield contributing characters.

Rathod *et al.* (2015) conducted path analysis on 18 characters in eighteen groundnut genotypes including three checks *viz.*, JL-24, LGN- 1 and LGN -123 and recorded that total sugar, kernel yield, stomata length, LLS severity, test weight, SCMR, days to maturity and oil content exerted the positive direct effect on pod yield. Negative direct effects on pod yield were also exhibited by non-reducing sugars, stomatal frequency, shelling percentage, harvest index and reducing sugars.

Path analysis studies in F_2 segregating generations of three groundnut crosses *viz.*, KCG-6 X ICGV-91114, KCG-6 X TG-69 and TMV 2 X ICGV-00350 by Shashikumara *et al.* (2015) revealed highest direct effects of kernel yield per plant, matured pods per plant and sound mature kernel per cent on pod yield. This indicates that more emphasis can be given for these traits for the improvement of pod yield of groundnut.

Vinutha *et al.* (2015) studied six F_2 crosses of groundnut genotypes and revealed direct effect of kernel yield per plant on pod yield per plant in all the six crosses.

In a study involving 24 groundnut genotypes, Surbhi *et al.* (2016) recorded high direct effects of kernel yield per plant, plant height and matured pods per plant on pod yield per plant. It was also recorded that number of pods per plant had high indirect effect on dry pod yield via kernel yield per plant.

Anusha and Savithramma (2017) carried out path analysis involving 230 RILs of cross NRCG 12568 X NRCG 12326 and two checks TMV-2 and KCG-2 and recorded positive direct effect of pods per plant, kernel yield and primary branches per plant on pod yield per plant.

Bhargavi *et al.* (2017) conducted path analysis on 10 Virginia bunch groundnut genotypes and recorded maximum positive direct effect of kernel yield per plant and 100 kernel weight on pod yield per plant indicating that direct selection for these traits would be effective.

A study on path analysis of 40 genotypes of groundnut by Mukesh and Lal (2017) revealed that the highest positive direct effect on pod yield per plant was exerted by kernel yield (q ha^{-1}) and kernel uniformity. In contrast days to 50% flowering and sound mature kernel percent contributed considerable negative direct effect on pod yield per plant.

Trivikrama *et al.* (2017) carried out path analysis for kernel yield and its component characters in six parents and their 15 F_1 crosses in groundnut and inferred that pod yield exerted the highest positive direct effect on kernel yield followed by shelling percentage and pegs per plant. They have also observed the positive indirect effects of pod yield on kernel yield through days to maturity, plant height, pegs per plant, pods per plant, mature pods per plant, harvest index and 100-kernel weight.

Tulsiram *et al.* (2017a) conducted path analysis of 90 genotypes along with three checks of groundnut and recorded highest positive direct effect on dry pod yield by kernel yield per plant followed by days to maturity, oil content and days to 50% flowering. While, high indirect effect on dry pod yield was exhibited by number of mature pods per plant, oil content, number of branches per plant and protein content. Therefore, these are the important characters which could be used in selection for higher yield of groundnut.

Mahesh *et al.* (2018b) evaluated 144 groundnut genotypes for path analysis and revealed that kernel yield per plant had highest direct effect on dry pod yield. The traits like number of mature pods per plant, sound mature kernels and haulm yield had the high and positive indirect effect on dry pod yield via kernel yield.

Chapter ~ III

Material and Methods

Chapter III

MATERIAL AND METHODS

The experimental materials used and methods followed pertaining to the present investigation entitled "Genetic analysis of yield, yield components and water use efficiency traits under organic and inorganic fertilizer managements in groundnut (*Arachis hypogaea* L.)" were briefly described here under.

3.1 LOCATION OF THE EXPERIMENTAL SITE

The field experiments were conducted at dry land farm of Sri Venkateswara Agricultural College, Tirupati during *Kharif* 2017, located at an altitude of 182.9 m above mean sea level, 13°N latitude and 79°E longitude and situated in southern agroclimatic zone of Andhra Pradesh.

3.2 MATERIAL

The material used in the present study consisted of 27 genotypes and three checks of groundnut obtained from ICRISAT, Patancheru and Principal Scientist (groundnut breeding), RARS, Tirupati, Andhra Pradesh. The list of genotypes is presented in Table 3.1.

3.3 METHOD

3.3.1 Field Layout

The above genetic materials were evaluated in two contiguous trials that differ only in fertilizer managements using Randomized Block Design with three replications during *kharif* 2017 (plate 1a – Inorganic plot, plate 1b – organic plot). The crop was sown on 13th July 2017. Each genotype was accomodated in two rows of 2.5m length with a spacing of 30 cm between the rows and 10 cm between the plants within the row.

Table 3.1. List of 30 genotypes of groundnut and their origin/pedigree

S No.	Genotype	Origin/pedigree
1	Dharani	VRI 2 X TCGP 6
2	ICG-10185	USA
3	ICG-10384	Nigeria
4	ICG-111	Unknown
5	ICG-11322	India
6	ICG-11651	China
7	ICG-11687	India
8	ICG-13099	Unknown
9	ICG-13723	Niger
10	ICG-13787	Niger
11	ICG-15309	Brazil
12	ICG-2738	India
13	ICG-3992	India
14	ICG-434	USA
15	ICG-5236	Chile
16	ICG-7153	India
17	K-1789	(ICGV92069 X ICGV93184) X[(ICGV87121 X ICGV87853) X ICGV92093]
18	TCGS-1631	Tirupati 1 X ICG (FDRS) 79
19	K-1805	(ICGV92069 X ICGV93184) X (ICGS44 X ICGS76)
20	K-6	JL 24 X Ah 316/s
21	K-7 Bold	ICGV86522 X (ICG(FDRs)10 X ICGV91172)
22	K-9	Kadiri 4 X Vemana
23	Kalahasti	TCG 1709 X TCG 1518
24	Narayani	JL 24 X Ah-316/s
25	TCGS-1157	TAG 24 X Jyothi
26	TCGS-1653	TLG 45 X TCGS 876
27	TCGS-1696	ICG (FDRs) 79 X Tirupati 4
28	TCGS-1678	TCGS 876 X GPBD 4
29	TCGS-1330	K 1340 X TG 37 A
30	TCGS-1630	Tirupati 1 X ICG (FDRs) 79

Plate 1a. Inorganic field experiment

Plate 1b. Organic field experiment

3.3.2 Crop Husbandry

In organic management practice, FYM @ 5 t/acre at the time of field preparation was applied. Seed treatment was done with 3% panchagavya, *Trichoderma viride* and *Rhizobium* before one day of sowing. Jeevamruth was applied at 15 days interval. *Pseudomonas* spraying @ 3 ml/lit was done against *Aspergillus* collar rot on 27th DAS and Bramhastram was sprayed against sucking pests. The details of preparation of jeevamrutha, panchagavya and bramhasthram are given in Appendix A, B and C respectively.

In inorganic fertilizer management practice FYM was applied @ 5t/ acre and recommended dose of chemical fertilizers @ of 20 kg N, 40 kg P_2O_5 and 50 kg K_2O per hectare in the form of urea, single super phosphate and Murate of potash were broadcasted before sowing. Seed treatment was done with Carbendazim, *Trichoderma viride* and *Rhizobium*. Larvin @ 1g lit^{-1} was used to control insect pests.

Other cultural practices like weeding, gypsum application @ 500 kg ha^{-1} (40 DAS) and irrigation were followed in common for both practices to maintain good crop growth.

3.3.3 Data Recording

Five plants were randomly chosen from each genotype in both organic and inorganic fertilizer management practices for recording the observations. For the characters days to 50 percent flowering, days to maturity and quality parameters like oil, protein, total carbohydrates and total free amino acids observations were recorded on plot basis. The data were recorded as follows.

3.3.3.1 Days to 50% flowering

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

3.3.3.2 Days to maturity

The total number of days were recorded from sowing to complete maturity of the crop.

3.3.3.3 Plant height (cm)

Plant height was measured in centimeters from the ground level to the tip of main axis at the time of maturity.

3.3.3.4 Number of primary branches per plant

The number of branches produced on the main stem were counted and recorded at the time of harvest

3.3.3.5 Number of pegs per plant

Total number of pegs per plant were recorded by counting all pegs at the time of harvest.

3.3.3.6 Number of pods per plant.

Total number of pods in each plant were counted manually and recorded as total number of pods at harvest.

3.3.3.7 Number of mature pods per plant

The number of fully developed seed bearing mature pods were counted from randomly selected five plants at the time of harvest.

3.3.3.8 Number of immature pods per plant

Number of immature pods per plant was counted at the time of harvest and recorded

3.3.3.9 Hundred seed weight (g)

The weight of randomly selected hundred kernels from each genotype was recorded as 100-seed weight using Electronic top pan balance (precision of 0.001 g)

3.3.3.10 Pod yield per plant (g)

The weight of all the pods from each individual plant was recorded in grams using Electronic top pan balance (precision of 0.001 g).

3.3.3.11 Kernel yield per plant (g)

The kernels obtained by deshelling of pods of individual plants were weighed in grams using Electronic top pan balance (precision of 0.001 g)

3.3.3.12 Shelling percentage

The shelling percentage was recorded based on the weight of the kernels recovered from the pods using the following formula

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

3.3.3.13 Harvest index (%)

The ratio of economic yield (pod yield) to biological yield (total dry matter with pods) was taken as harvest index and expressed in percentage. It was estimated by using the formula:

$$\text{HI} = \frac{\text{Economic yield per plant (g)}}{\text{Biological yield per plant (g)}} \text{ x } 100$$

3.3.3.14. Specific Leaf Area (SLA) (cm^2 g^{-1})

The third leaf from the terminal bud of main stem was taken and used for estimating specific leaf area at 40 and 60 DAS. Leaves were collected from five randomly selected plants from each genotype in each replication and leaf area was estimated using Leaf area meter (LICOR model -3100). Dry weight was recorded by keeping the samples in hot air oven and used for estimation of SLA using the following formula

$$\text{SLA} = \frac{\text{Leaf area (cm}^2\text{)}}{\text{Leaf dry weight (g)}} \times 100$$

3.3.3.15. SPAD chlorophyll meter reading (SCMR)

SPAD chlorophyll meter reading (SCMR) was measured on five randomly selected plants from each genotype in each replication at 40 and 60 DAS using Minolta SPAD-502 chlorophyll meter. Measurements were taken on third leaf from the terminal bud of main axis.

3.3.3.16. Relative water content (RWC) (%)

Leaf discs were collected from randomly selected five plants in each genotype and fresh weight was recorded using electronic top pan balance (precision of 0.001 g) and allowed to float in distilled water for 3 hours. Leaf discs were taken out and weighed and referred as turgid weight. Samples were dried in hot air oven at 80^{o}C for two days and dry weight was recorded. RWC was calculated using the following formula

$$\text{RWC (\%)} = \frac{\text{Fresh weight (g)} - \text{Dry weight (g)}}{\text{Turgid weight (g)} - \text{Dry weight (g)}} \times 100$$

3.3.3.17 Oil content (%)

The percentage of oil content in the seed was estimated using Grain analyzer (INFRATEE 1241). Nearly 100g of dried seed sample was fed into the analyzer and the oil percentage was recorded.

3.3.3.18 Protein content (%)

About 100g of dried seed sample was taken and fed into the grain analyzer (INFRATEE 1241) and the protein content was recorded directly as percentage of protein.

3.3.3.19 Total carbohydrates

Total Carbohydrates was estimated by adopting the method suggested by Sadasivam and Manickam (1961). Basic principle used in carbohydrate estimation is that first they are hydrolysed into simple sugars using dilute hydrochloric acid. In hot acidic medium, glucose is dehydrated to hydroxymethyl furfural which condenses with anthrone and form blue green colored product measured at 630nm.

For extraction of carbohydrates 100mg of sample was taken in a test tube and 5 ml of 2.5 N HCl was added and kept in hot water bath(100^{o}C) for 3 hours. After 3 hours solid sodium carbonate was added and volume was made upto 25 ml with distilled water. Samples were centrifuged for 20 min and supernatant was collected. For 1 ml of aliquot 4 ml of ice cold anthrone reagent was added and kept in hot water bath for 8 min. Samples were cooled rapidly and intensity of green colour was read against a reagent blank at 630nm using spectrophotometer. A standard curve was prepared using glucose and it was linear within the range ($R^2 = 0.987$). The total carbohydrates of the seed sample was then calculated by substituting the sample OD values in the formula derived from the graph ($Y = 0.006X - 0.023$), where Y = OD value of the sample and X = concentration (μgml^{-1}) of carbohydrate. Then the concentration of carbohydrates was converted to concentration of carbohydrates in percent for different entries.

3.3.3.20 Total free amino acids

Total free amino acids was estimated by adopting the method suggested by Sadasivam and Manickam (1961). The basic principle of estimation of total free amino acids is a powerful oxidizing agent (Ninhydrin), decarboxylates the alpha amino acids and carboxylates to give an intensely coloured bluish purple product which is calorimetrically measured at 570 nm.

For extraction, 500 mg of the seed sample is weighed and grinded it in a pestle and mortar with 5 ml of 80 % ethanol. The samples are centrifuged at 6000 rpm for 30 minutes and the supernatant is collected. For estimation, 0.1 ml of extract is taken and 1ml of Ninhydrin solution is added and mixed thoroughly and then the volume is made up to 2 ml with distilled water. The tubes are heated in boiling water bath for 20 min and thereafter cooled to room temperature. Simultaneously, 5 ml of the diluents are added and mixed. After 15 minutes, the intensity of purple color is read against a reagent blank in a spectrophotometer using photometric method at 570 nm. A standard curve was prepared using leucine and it was linear within the range (R^2 =0.984). The total free amino acids of the seed sample was then calculated by substituting the sample OD values in the formula derived from the graph ($Y = 0.012X – 0.202$), where Y = OD value of the sample and X = concentration ($\mu g\ ml^{-1}$) of free amino acids. Then the concentration of free amino acids in $\mu g\ ml^{-1}$ was converted to concentration of free amino acids in mg/g for different entries.

3.4 STATISTICAL ANALYSIS

The treatment means for all the characters for each experiment i.e. organic and inorganic fertilizer managements were subjected to the following statistical analysis. The statistical package used was INDOSTAT.

3.4.1 Analysis of Variance

The data collected on individual characters were subjected to method of analysis of variance commonly applicable to randomized block design as per mathematical 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 ith genotype

γ_j = Effect of jth replication

e_{ij} = Random error associated with ith genotype in jth replication.

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

Source of variation	**Degrees of freedom**	**Sum of squares**	**Mean sum of squares**	**Expected Mean sum of squares**	**F ratio**
Replications	(r-1)	RSS	Mr	-	Mr/Me
Genotypes	(t-1)	VSS	Mt	$\sigma_e^2 + r\sigma_g^2$	Mt/Me
Error	(r-1) (t-1)	ESS	Me	σ_e^2	-
Total	(rt-1)	TSS			

Where,

r = Number of replications

t = Number of genotypes

Mr = Mean sum of squares due to replications

Mt = Mean sum of squares due to genotypes

Me= 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).

3.4.2 Estimation of genetic parameters

3.4.2.1 Variance

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

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

$$\text{Phenotypic variance } \left(\sigma_p^2\right) = \sigma_g^2 + \sigma_e^2$$

σ_g^2 = Genotypic variance

σ_e^2 = Error variance

3.4.2.2 Genotypic and phenotypic coefficient of variation

The genotypic (GCV) and phenotypic (PCV) coefficient of variation were computed 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 $\overline{X}$ were 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

3.4.2.3 Broad sense Heritability

The proportion of genotypic variance to the total variance of the population is referred to as heritability in broad sense [$h^2_{(b)}$] and was calculated by the formula given by Lush (1940).

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

Where,

$h^2_{(b)}$ = Heritability in broad sense

σ^2_g = Genotypic variance

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

σ^2_e = Environmental variance

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

Less than 30% - Low
30 – 60 % - Moderate
More than 60% - High

3.4.2.4 Genetic advance

Genetic advance refers to the expected genetic gain or improvement 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.* (1955a).

$$GA = \sigma_p Hk$$

Where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

H = Heritability (broad sense)

k = Selection differential at 5% selection intensity (2.06)

3.4.2.5 Genetic advance as per cent of mean (GA as per cent mean)

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

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

Where,

GA = Genetic advance

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

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

Less than 10% - Low

10 – 20 % - Moderate

More than 20% - High

3.4.3. Genetic divergence analysis:

3.4.3.1 Mahalanobis' D^2 analysis

The data collected on different characters was analyzed using Mahalanobis's D^2 analysis to determine the genetic divergence among the genotypes.

3.4.3.1.1 Test of significance

Variances were calculated for all the characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1961). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using ‘V’ statistic, which in turn utilizes Wilk’s criterion. The sum of squares and sum of products of error and error + variety, variance – covariance matrix were used for this purpose.

The estimation of Wilk’s criterion was done using the following relationship.

$$‘\Lambda’ = \frac{(E)}{(E+V)}$$

Where,

Λ = Wilk’s criterion
(E) = Determinant of error matrix and
(E+V) = Determinant of error + variety matrix

The significance of ‘Λ’ was tested by

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

Where,

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

n = Degrees of freedom of error + varieties

p = Number of characters

q = Number of genotypes – 1

$\log_e \Lambda = 2.3407 \log_{10} \Lambda$

V (Stat) is distributed as χ^2 with pq degrees of freedom.

3.4.3.1.2 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 computation of D^2 values was reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e., Σdi^2.

3.4.3.1.3 Computation of D^2 values

The D^2 value between 'ith' and 'jth' genotypes for 'p' characters was calculated as

$$D_{ij}^2 = p\Sigma_{t=1} (\overline{Y_{it}} - \overline{Y_{jt}})^2$$

Where,

$\overline{Y_{it}}$ *is* uncorrelated mean value of *i*th genotype for character ‘t’

$\overline{Y_{jt}}$ is uncorrelated mean value of *j*th genotype for character ‘t’

D_{ij}^2 is D^2 between *i*th and *j*th genotype.

3.4.3.1.4 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of χ^2 and is tested against the tabulated value of χ^2 for p degrees of freedom where ‘p’ is the number of characters considered.

3.4.3.1.5 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher’s method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Choudhary (1977).

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2, that population was not considered for including in that cluster. The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued till all the genotypes were included into one or other cluster.

3.4.3.1.6 Average intra cluster distance

For the measurement of intra cluster distances, the formula used was

$$\Sigma D^2_i/n$$

Where,

$\Sigma D^2 i$ = the sum of distances between all possible combinations (n) of populations included in a cluster.

3.4.3.1.7 Average inter cluster distance

Clusters were taken one by one and the distances from other clusters were calculated. The distance between two clusters was the sum of D^2 values between the members of one cluster to each of the members of the other clusters divided by the product of number of genotypes in both the clusters under consideration.

$$\text{Average inter cluster distance} = \frac{D^2}{(n_1 \text{ X } n_2)}$$

Where, n_1 and n_2 are number of genotypes of two clusters.

3.3.3.1.8 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, had been used to denote the distance.

3.4.3.1.9 Contribution of individual characters towards divergence

In all combinations, each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$). Rank 1 is given to the highest mean difference and the rank P to the lowest difference, where, P is the total number of characters. Percentage contribution of each character (X) towards genetic divergence was calculated using the following formula.

$$\text{Percentage contribution of the character X} = \frac{(\mathrm{N \, x \, 100})}{M}$$

Where,

N = Number of genotype combinations where the character was ranked first

M = All possible combinations of number of genotypic pairs

3.4.4. Character Association Analysis

Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955b) to determine the degree of association of the characters with yield and also among the yield components.

3.4.4.1 Genotypic correlation coefficient (r_g)

$$r_g\,(x_i x_j) = \frac{\mathrm{CoV_g}\ (x_i x_j)}{\sqrt{V_g(x_i)\,V_g(x_j)}}$$

where,

$r_g\,(x_i x_j)$ = Genotypic correlation between ‘i^th^’ and ‘j^th^’ characters

$V_g\,(x_i)$ = Genotypic variance of ‘i^th^’ character

$V_g\,(x_j)$ = Genotypic variance of ‘j^th^’ character

$\mathrm{Cov}_{(g)}\,(x_i x_j)$ = Genotypic covariance between ‘i^th^’ and ‘j^th^’ characters.

3.4.4.2 Phenotypic correlation coefficient (r_p)

$$r_p\,(x_i x_j) = \frac{\mathrm{CoV_p}\ (x_i x_j)}{\sqrt{V_p(x_i).V_p(x_j)}}$$

Where,

$V_p\,(x_i)$ = Phenotypic variance of ‘i^th^’ character

V_p (x_j) = Phenotypic variance of ‘j^{th}’ character

Cov_p (x_ix_j)=Phenotypic covariance between ‘i^{th}’ and ‘j^{th}’ 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% and 1% level where, ‘n’ denotes the number of treatments used in the calculations

3.4.5 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.

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

where,

r_{1y} to r_{iy} = Coefficient of correlation between causal factors 1 to I and dependent character 1

r_{12} to r_{i1} = 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:

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

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:

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 & Discussion

Chapter IV

RESULTS AND DISCUSSION

Thirty genotypes of groundnut were evaluated for variability, genetic parameters, genetic divergence, character association and path analysis for 22 characters. The data collected from these characters were subjected to statistical analysis and the results were furnished here under.

4.1 ANALYSIS OF VARIANCE

The data recorded on twenty two characters was subjected to analysis of variance and the results for organic and inorganic fertilizer managements were presented in Tables 4.1 and 4.2 respectively. Under both organic and inorganic fertilizer managements highly significant differences were observed among the genotypes for all the characters *viz.,* days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, total number of pods per plant, hundred kernel weight, shelling percentage, harvest index, kernel yield per plant, SLA at 40 DAS, SLA at 60 DAS, SCMR at 40 DAS, SCMR at 60 DAS, relative water content, oil content, protein content, carbohydrate content, total free amino acids and pod yield per plant. These differences among the genotypes was mainly due to the presence of considerable amount of genetic variation.

4.2 MEAN PERFORMANCE

The mean performance of 30 genotypes for all the 22 characters under organic and inorganic fertilizer managements was furnished in Table 4.3

Table 4.1 Analysis of variance for 22 characters in 30 genotypes of groundnut under organic fertilizer management

S. No	Character	Mean sum of squares		
		Replications (df:2)	Treatments (df:29)	Error (df:58)
1	Days to 50 % flowering	0.678	23.666**	3.333
2	Days to maturity	0.544	53.013**	1.533
3	Plant height	11.982	130.809**	31.796
4	Number of primary branches per plant	0.075	1.333**	0.379
5	Number of pegs per plant	1.097	70.984**	25.806
6	Number of mature pods per plant	3.612	21.755**	7.983
7	Number of immature pods per plant	1.141	1.230**	0.421
8	Number of pods per plant	0.624	26.972**	9.228
9	Hundred kernel weight	1.073	159.729**	11.272
10	Shelling percentage	7.818	32.684**	5.561
11	Harvest index	8.918	47.444**	10.520
12	Kernel yield per plant	12.502	20.220**	4.869
13	SLA at 40 DAS	615.588	1282.921*	676.233
14	SLA at 60 DAS	206.576	2002.123**	133.160
15	SCMR at 40 DAS	15.141	19.482**	5.501
16	SCMR at 60 DAS	12.947	30.559**	6.339
17	Relative water content	33.453	34.989*	17.860
18	Oil content	0.225	3.313**	0.086
19	Protein content	0.00007	0.008**	0.0007
20	Carbohydrate content	0.062	36.888**	1.336
21	Total free amino acids	0.000008	0.181**	0.007
22	Pod yield per plant	21.484	39.356**	11.542

*, ** significance at 5 % and 1 % level respectively

Table 4.2 Analysis of variance for 22 characters in 30 genotypes of groundnut under inorganic fertilizer management

S. No	Character	Mean sum of squares		
		Replications (df:2)	Treatments (df:29)	Error (df:58)
1	Days to 50 % flowering	1.078	20.431**	0.572
2	Days to maturity	26.144	39.579**	8.489
3	Plant height	4.259	153.885**	1.392
4	Number of primary branches per plant	0.546	1.535**	0.604
5	Number of pegs per plant	12.994	122.418**	15.307
6	Number of mature pods per plant	14.872	46.739**	5.545
7	Number of immature pods per plant	0.152	1.467*	0.372
8	Number of pods per plant	12.076	53.401**	8.104
9	Hundred kernel weight	37.753	65.933**	14.149
10	Shelling percentage	22.218	27.401*	12.692
11	Harvest index	19.849	51.985**	11.718
12	Kernel yield per plant	8.350	19.939**	3.571
13	SLA at 40 DAS	416.208	1064.781**	505.163
14	SLA at 60 DAS	682.021	2601.710**	569.080
15	SCMR at 40 DAS	7.095	18.442**	2.328
16	SCMR at 60 DAS	6.065	29.441**	2.027
17	Relative water content	16.004	60.700**	15.304
18	Oil content	0.001	3.069**	0.072
19	Protein content	0.0006	0.008**	0.001
20	Carbohydrate content	0.021	0.850**	0.070
21	Total free amino acids	0.006	0.139**	0.012
22	Pod yield per plant	11.979	38.988**	9.307

*, ** significance at 5 % and 1 % level respectively

Table 4.3. Mean performance of 30 groundnut genotypes for 22 characters under organic and inorganic fertilizer managements

	DF		DM		PH		NPB		NPEGP		NMP		NIMP		NPP		100 KW		SP		HI	
GENOTYPE	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN
Dharani	25.67	30.67	97.00	99.33	50.87	63.74	4.20	4.07	20.53	25.33	11.73	15.33	1.13	1.00	12.87	16.33	50.97	47.38	77.03	67.10	44.56	44.01
ICG-10185	30.00	35.33	100.33	100.33	58.20	41.40	5.87	5.27	25.80	20.73	11.00	10.27	2.47	1.80	13.47	12.07	52.87	46.63	66.24	58.77	24.46	25.24
ICG-10384	30.00	35.33	100.33	94.33	39.40	43.27	5.27	4.07	27.33	23.33	14.87	11.00	1.13	1.67	16.00	12.67	51.77	44.75	65.40	60.89	40.46	43.83
ICG-111	31.33	35.00	100.33	93.00	51.53	34.82	5.33	4.47	24.73	27.80	10.47	11.20	1.93	0.93	12.40	12.13	36.17	44.75	65.17	54.40	23.79	35.97
ICG-11322	30.00	35.67	97.00	100.00	47.33	46.59	5.33	5.87	23.53	29.47	15.07	16.40	1.13	2.07	16.20	18.47	45.56	42.86	69.67	56.85	40.49	36.44
ICG-11651	26.33	27.33	97.00	99.00	37.67	35.27	3.93	3.87	25.40	27.27	11.73	14.80	2.33	1.80	14.06	16.27	46.81	45.07	67.42	64.98	45.80	47.42
ICG-11687	26.67	30.00	100.33	100.00	53.27	58.63	3.80	4.07	30.13	25.07	12.73	12.47	2.73	2.93	15.47	15.40	37.20	39.07	65.51	59.16	33.90	32.59
ICG-13099	31.00	35.33	93.00	94.33	44.67	46.27	4.60	4.07	17.07	16.73	8.60	10.80	0.80	0.93	9.40	11.73	51.37	47.38	67.57	62.75	39.33	38.71
ICG-13723	32.33	35.33	100.33	100.00	44.27	36.27	3.73	3.80	13.20	23.00	6.13	13.00	0.73	1.00	6.87	14.00	48.69	46.74	72.12	68.39	33.95	53.65
ICG-13787	33.67	35.67	100.33	100.00	39.00	42.27	4.40	4.47	23.73	24.80	12.93	13.60	0.80	1.20	13.73	14.80	54.85	43.53	70.47	63.18	38.84	34.16
ICG-15309	27.00	30.00	100.33	93.00	46.67	49.40	4.33	3.80	21.53	15.27	11.60	7.93	1.27	1.00	12.87	8.93	45.87	40.87	65.98	53.30	34.51	38.49
ICG-2738	26.00	34.33	93.00	93.00	53.00	46.80	4.00	3.87	22.73	21.40	8.07	9.53	1.28	2.20	9.40	11.73	53.15	34.19	70.25	55.53	39.47	28.96
ICG-3992	36.00	37.33	101.00	100.00	41.27	41.99	4.87	5.20	21.27	21.20	11.87	8.60	2.73	3.07	14.60	10.87	42.90	42.13	64.99	64.29	27.94	18.72
ICG-434	26.67	30.00	93.00	93.00	40.33	45.27	4.00	4.13	19.53	21.40	8.93	12.60	1.93	2.13	10.87	14.73	42.55	36.02	66.76	49.14	31.20	37.84
ICG-5236	29.00	35.00	97.00	93.00	43.67	36.93	4.73	5.93	25.33	18.87	11.47	10.73	1.20	1.13	12.67	11.87	52.58	48.75	71.45	53.76	43.60	37.24
ICG-7153	31.00	35.00	101.00	100.33	46.07	46.45	4.87	4.87	35.80	41.53	19.47	26.00	3.00	2.60	22.47	27.87	46.34	42.01	65.43	62.99	35.28	42.11
K-1789	28.67	32.67	98.67	98.00	47.80	44.40	4.60	5.27	28.33	23.47	12.20	13.40	2.80	2.40	15.00	15.80	30.32	38.05	52.02	50.88	31.00	32.47
TCGS-1631	29.33	32.00	96.00	96.00	49.60	52.02	4.00	4.27	18.33	22.67	9.07	12.20	1.60	1.13	10.67	13.33	44.89	40.55	60.02	55.91	35.84	34.16
K-1805	26.67	31.33	104.00	104.00	39.33	45.13	5.53	4.93	25.47	20.20	11.27	10.47	1.87	1.73	13.13	12.20	48.44	44.85	68.28	51.27	29.90	42.92
K-6	26.33	34.33	93.00	93.00	43.73	51.05	3.87	5.07	17.53	22.33	8.27	12.60	1.93	2.07	10.20	14.67	46.34	43.18	71.26	60.73	38.31	40.64
K-7 bold	26.67	30.00	104.00	92.67	37.13	38.91	5.13	5.87	20.93	22.13	10.93	13.87	1.33	0.93	12.27	14.80	53.69	50.21	67.66	59.55	42.21	41.58
K-9	26.00	30.33	101.33	96.00	42.53	51.27	4.53	4.87	26.87	45.73	12.00	24.87	2.20	3.53	14.20	28.40	41.56	39.48	73.65	65.66	41.57	49.90
Kalahasti	27.33	31.33	87.00	89.33	35.07	34.40	4.87	4.80	17.67	23.53	9.40	14.93	1.60	1.60	11.00	16.53	42.56	32.77	58.23	55.54	39.69	33.69
Narayani	26.33	32.00	93.00	93.00	52.40	51.60	3.40	4.00	17.20	20.07	8.33	9.67	1.53	1.73	9.87	11.40	47.69	51.84	62.78	58.27	34.48	37.85
TCGS-1157	34.33	35.00	101.00	93.00	38.40	36.47	4.93	5.80	26.93	17.67	14.40	10.07	1.53	1.27	15.93	11.33	58.63	41.14	66.89	52.35	44.54	36.46
TCGS-1653	28.33	31.33	96.00	98.67	51.27	48.00	6.07	4.87	25.33	29.07	10.87	14.33	1.80	2.73	12.67	17.07	28.86	34.63	63.34	52.93	27.60	37.94
TCGS-1696	28.33	31.33	104.00	96.00	60.87	52.68	4.00	3.93	14.40	21.93	7.13	13.60	0.93	2.00	8.07	15.60	45.41	42.59	64.87	59.35	26.24	37.52
TCGS-1678	26.67	29.33	104.00	101.33	49.47	43.67	4.27	4.53	20.53	21.13	10.40	12.00	1.80	1.47	12.20	13.47	34.20	40.43	54.86	54.81	28.13	39.88
TCGS-1330	33.00	36.33	101.00	98.00	40.93	35.67	5.27	6.07	21.60	19.93	13.47	12.53	1.13	1.73	14.60	13.93	55.72	47.13	63.82	61.71	34.39	37.06
TCGS-1630	29.67	30.67	104.00	92.67	54.33	43.47	4.80	4.80	20.00	19.00	11.07	10.93	1.27	2.07	12.33	12.67	46.58	40.77	56.72	54.78	26.09	33.94
Mean	29.01	32.84	98.61	96.48	46.00	44.80	4.62	4.70	22.63	23.74	11.18	12.99	1.67	1.80	12.86	14.71	46.15	42.66	65.86	58.31	35.30	37.71
S. E. (m)	1.05	0.44	0.71	1.68	3.26	0.68	0.36	0.45	2.93	2.26	1.63	1.36	0.37	0.35	1.75	1.64	1.94	2.17	1.36	2.06	1.87	1.98
C. D. at 5%	2.98	1.24	2.02	4.76	9.22	1.93	1.01	1.27	8.30	6.40	4.62	3.85	1.06	1.00	4.96	4.65	5.49	6.15	3.85	5.82	5.30	5.59
C.V. (%)	6.29	2.30	1.26	3.02	12.26	2.63	13.32	16.55	22.45	16.48	25.27	18.13	38.99	33.96	23.62	19.35	7.27	8.82	4.34	7.15	8.94	9.06

O : organic Fertilizer Management , I : Inorganic Fertilizer Management

Cont…

Table 4.3 Contd…

	KYPP		SLA 40		SLA 60		SCMR 40		SCMR 60		RWC		OIL		PRO		CAR		TFA		PYPP	
GENOTYPE	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN	O	IN
Dharani	11.04	11.12	166.73	167.88	161.81	155.85	37.53	36.27	37.43	35.70	83.39	73.83	47.45	47.50	25.65	25.85	24.00	14.00	0.93	0.85	14.36	16.68
ICG-10185	9.58	7.26	213.56	167.71	158.95	149.55	37.27	40.27	37.50	35.00	80.72	68.80	45.10	45.85	24.80	25.45	21.50	21.00	0.95	0.92	14.38	12.26
ICG-10384	11.97	8.54	193.56	208.42	172.86	176.85	36.93	37.17	34.00	38.70	76.02	77.93	46.55	47.45	26.10	25.65	21.00	15.00	0.70	0.71	18.29	13.85
ICG-111	8.31	7.41	182.72	173.26	167.37	155.11	39.33	39.47	36.47	41.40	75.28	71.57	45.85	46.85	25.50	26.60	25.00	24.50	0.74	0.97	12.53	13.59
ICG-11322	12.24	11.05	162.55	166.50	162.24	150.87	35.60	41.50	33.50	36.17	76.41	70.80	47.65	46.45	25.25	25.60	26.00	21.50	0.66	0.71	17.53	19.30
ICG-11651	9.74	8.98	170.37	195.13	166.59	149.73	38.00	39.93	38.67	38.47	85.62	87.73	48.35	49.05	26.10	25.70	13.00	7.00	0.92	1.04	14.42	14.04
ICG-11687	7.08	7.87	194.51	181.74	174.29	169.85	35.27	36.30	35.93	33.00	79.89	76.00	47.80	47.30	25.00	25.70	23.00	17.00	0.75	0.92	10.80	13.26
ICG-13099	6.81	7.80	194.67	190.47	201.41	158.55	37.70	39.63	32.67	36.93	70.92	74.16	46.55	46.00	26.25	25.65	19.00	20.00	0.74	0.77	10.17	12.42
ICG-13723	4.73	10.58	178.28	224.30	161.74	157.42	37.83	41.33	35.77	39.70	80.67	73.00	46.55	46.05	26.30	25.60	22.50	17.50	0.58	0.84	6.57	15.57
ICG-13787	10.30	9.58	186.11	174.26	155.57	166.63	37.00	39.83	37.63	37.50	77.14	71.67	46.75	46.45	26.15	25.90	23.00	15.50	0.67	0.77	14.67	15.33
ICG-15309	9.40	5.95	213.88	223.03	186.59	225.04	34.67	38.93	35.70	34.03	75.89	77.13	46.90	47.05	26.45	26.35	24.00	15.50	0.98	0.98	14.33	11.14
ICG-2738	6.38	5.19	181.44	198.10	181.26	195.43	35.30	38.13	33.87	36.70	82.83	77.90	47.65	47.45	26.40	25.20	23.50	20.00	1.05	1.05	9.08	9.14
ICG-3992	7.49	5.56	173.78	174.27	162.13	150.38	36.17	38.63	35.27	36.70	78.83	68.17	47.45	47.30	25.50	24.10	15.00	15.50	1.45	0.96	11.69	8.94
ICG-434	5.86	7.54	212.47	179.14	175.32	160.30	31.67	37.83	35.63	36.37	73.53	75.20	48.75	48.70	25.95	24.85	16.00	15.00	0.90	0.68	8.78	15.24
ICG-5236	8.58	8.16	193.61	182.82	163.54	172.69	37.73	40.93	35.17	38.23	79.93	74.10	47.15	46.35	25.90	25.95	15.50	16.00	0.54	0.98	11.99	15.25
ICG-7153	10.97	15.38	174.67	176.88	182.17	161.29	40.87	41.93	39.13	39.17	76.91	78.97	46.50	46.50	25.70	24.95	17.00	15.50	0.88	0.75	16.76	24.49
K-1789	4.65	5.80	174.52	172.56	274.35	225.49	32.37	34.80	34.80	38.90	78.88	70.43	48.65	48.50	24.95	25.40	31.50	22.00	0.86	0.61	8.94	11.17
TCGS-1631	4.98	6.75	149.77	174.47	185.09	205.82	35.17	35.23	35.57	43.47	89.27	74.83	49.15	48.50	24.60	26.35	13.00	13.50	0.71	0.79	8.32	12.10
K-1805	6.59	6.76	159.48	182.40	228.63	197.72	36.73	36.73	40.93	43.07	85.14	71.37	47.40	47.70	25.50	25.45	17.00	10.50	0.87	0.91	9.67	13.18
K-6	6.67	10.00	206.27	213.28	195.84	156.40	34.63	38.90	32.77	36.00	77.97	88.53	48.15	48.20	25.70	25.55	21.50	13.50	0.72	0.71	9.49	16.58
K-7 bold	9.22	10.66	159.86	223.74	207.98	229.91	39.13	37.53	43.97	42.00	81.02	78.73	46.35	45.15	26.15	26.20	27.00	22.50	1.78	1.73	13.59	17.76
K-9	7.18	15.58	170.13	168.93	172.17	160.96	38.90	39.07	45.17	48.13	85.22	74.93	47.05	46.55	25.80	25.70	19.00	15.50	0.71	1.23	9.74	23.72
Kalahasti	7.12	8.60	220.31	196.04	197.69	218.07	31.17	36.37	36.43	39.63	76.83	80.87	46.70	46.65	25.25	24.60	10.50	17.00	0.96	0.78	12.23	15.57
Narayani	6.07	6.72	223.09	201.79	176.27	178.75	35.33	36.60	35.47	34.70	75.97	80.57	47.95	47.70	25.65	25.70	26.00	19.50	0.79	0.78	9.68	11.55
TCGS-1157	14.90	6.86	148.41	181.96	140.24	171.99	41.10	37.93	43.73	38.70	74.41	68.93	46.10	46.70	26.35	25.55	20.50	24.00	0.63	0.71	22.25	13.06
TCGS-1653	5.59	6.59	173.82	208.14	186.12	237.85	34.67	33.23	37.73	40.07	77.97	78.57	46.55	47.00	25.60	25.70	18.50	22.50	0.94	1.04	8.75	12.45
TCGS-1696	5.12	8.37	198.48	164.46	202.52	205.03	32.80	33.90	37.07	40.03	80.76	75.23	48.50	47.70	25.35	26.10	17.00	10.50	0.77	1.04	8.16	14.41
TCGS-1678	4.99	7.21	174.25	180.41	200.69	220.39	33.80	34.87	37.43	40.10	87.27	92.60	48.40	48.25	25.25	25.55	19.00	11.00	0.94	0.69	8.81	13.16
TCGS-1330	9.89	11.30	172.90	219.66	160.53	159.76	38.97	39.67	40.83	39.07	89.22	68.33	46.15	45.30	26.05	26.05	25.50	16.00	0.83	0.79	15.56	18.35
TCGS-1630	5.75	6.03	161.74	189.60	196.06	226.37	33.87	32.70	34.63	40.46	86.47	73.73	49.50	48.50	24.70	25.40	15.50	12.00	0.83	0.95	10.13	11.04
Mean	7.97	8.51	182.86	188.71	181.93	181.66	36.25	37.85	37.03	38.60	80.01	75.82	47.32	47.16	25.67	25.61	20.35	16.68	0.86	0.89	12.05	14.49
S. E. (m)	1.27	1.09	15.01	12.98	6.66	13.77	1.35	0.88	1.45	0.82	2.44	2.26	0.17	0.15	0.02	0.02	0.67	0.15	0.05	0.06	1.96	1.76
C. D. at 5%	3.61	3.09	42.50	36.73	18.86	38.99	3.83	2.49	4.11	2.33	6.91	6.4	0.48	0.44	0.04	0.05	1.89	0.44	0.14	0.18	5.55	4.99
C.V. (%)	27.67	22.21	14.22	11.91	6.34	13.13	6.47	4.03	6.80	3.69	6.71	6.42	0.62	0.57	0.52	0.61	4.34	6.52	9.81	12.14	28.18	21.06

O : organic Fertilizer Management, I : Inorganic Fertilizer Management

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height
NPB : Number of primary branches per plant
NPEGP: Number of pegs per plant
NMP : Number of mature pods per plant

NIMP : Number of immature pods per plant
NPP : Number of pods per plant
100 KW : Hundred kernel weight
SP : Shelling percentage
HI : Harvest index
KYPP : Kernel yield per plant

SLA 40 : Specific leaf area at 40 DAS
SLA 60 : Specific leaf area at 60 DAS
SCMR 40 : SCMR at 40 DAS
SCMR 60 : SCMR at 60 DAS
RWC : Relative water content

OIL : Oil content
PRO : Protein content
CAR : Carbohydrate content
TFA : Total free amino acids
PYPP : Pod yield per plant

4.2.1 Days to 50% flowering

Under organic fertilizer management the mean of the genotypes for days to 50% flowering ranged from 25.67 days (Dharani) to 36 days (ICG-3992). Seventeen genotypes were earlier when compared to general mean for days to 50% flowering (29.01 days). In inorganic fertilizer management the mean of genotypes for days to 50% flowering ranged from 27.33 days (ICG-11651) to 37.33 days (ICG-3992). Sixteen genotypes were earlier than the general mean for days to 50% flowering (32.84 days) in inorganic fertilizer management.

4.2.2 Days to maturity

Days to maturity varied from 87 days to 104 days under organic fertilizer management whereas in inorganic fertilizer management it ranged from 89.33 days to 104 days. Among all the genotypes Kalahasti showed early maturity in both organic (87days) and inorganic (89.33days) management practices. In organic and inorganic fertilizer managements twelve and fifteen genotypes matured early than their general means 98.61days (organic) and 96.48 days (inorganic) respectively.

4.2.3 Plant height

For plant height under organic fertilizer management the mean values are ranged from 35.07cm (Kalahasti) to 60.87cm (TCGS-1696) with the general mean of 46cm whereas in inorganic fertilizer management it ranged from 34.4cm (Kalahasti) to 63.74cm (Dharani) with the general mean of 44.8cm. In each fertilizer managements fifteen genotypes were taller than their respective general means.

4.2.4 Number of primary branches per plant

The number of primary branches ranged from 3.4 (Narayani) to 6.07 (TCGS-1653) in organic and 3.8 (ICG-13723 and ICG-15309) to 6.07

(TCGS-1330) in inorganic fertilizer managements. Fourteen genotypes in organic and fifteen genotypes in inorganic were having more number of primary branches than their general means 4.62 (organic) and 4.7 (inorganic).

4.2.5 Number of pegs per plant

Number of pegs per plant varied from 13.20 (ICG-13723) to 35.80 (ICG-7153) in organic and from 15.27 (ICG-15309) to 45.73 (K-9) in inorganic fertilizer managements. Fifteen genotypes in organic and nine genotypes in inorganic have more number of pegs per plant than their general means 22.63 and 23.74 respectively.

4.2.6 Number of mature pods per plant

Fifteen genotypes from organic and twelve genotypes from inorganic recorded more number of mature pods than their general means 11.18 and 12.99 respectively. Under organic management the number of mature pods ranged from 6.13 (ICG-13723) to 19.47 (ICG-7153) whereas in inorganic management it varied from 7.93 (ICG-15309) to 26 (ICG-7153).

4.2.7 Number of immature pods per plant

The mean values for number of immature pods in organic management ranged from 0.73 (ICG-13723) to 3.00 (ICG-7153) and in inorganic management ranged from 0.93 (ICG-111, ICG-13099 and K-7 bold) to 3.53 (K-9) with the general means 1.67 and 1.8 respectively. Seventeen genotypes in organic and sixteen genotypes in inorganic recorded less number of immature pods than their general means.

4.2.8 Number of pods per plant

Number of pods per plant ranged from 6.87 (ICG-13723) to 22.47 (ICG-7153) in organic with the general mean of 12.86 and from 8.93

(ICG-15309) to 28.4 (K-9) in inorganic management with the general mean of 14.71. Fifteen genotypes in organic and thirteen genotypes in inorganic recorded more number of pods per plant than their general means 12.86 (organic) and 14.71 (inorganic).

4.2.9 Hundred kernel weight

For hundred kernel weight the mean values are varied from 28.86 g (TCGS-1653) to 58.63 g (TGCS-1157) in organic with general mean of 46.15 g whereas in inorganic management system it ranged from 32.77 g (Kalahasti) to 51.84 g (Narayani) with the general mean of 42.66 g. Seventeen genotypes in organic and fifteen genotypes in inorganic registered higher hundred kernel weight than their general means.

4.2.10 Shelling percentage

The means for the shelling percentage under organic management ranged from 52.02% (K-1789) to 77.03% (Dharani) and in inorganic management it varied from 49.14% (ICG-434) to 68.39% (ICG-13723). Sixteen genotypes in organic and fifteen genotypes in inorganic have higher shelling percentage than their general means 65.86% and 58.31% respectively.

4.2.11 Harvest Index

Fourteen genotypes in organic and sixteen genotypes in inorganic registered higher harvest index than their general means 35.3% (organic) and 37.71% (inorganic). The means of genotypes ranged from 23.79% (ICG-111) to 45.8% (ICG-11651) in organic and 18.72% (ICG-3992) to 53.65% (ICG-13723) in inorganic management system.

4.2.12 Kernel yield per plant

Highest kernel yield per plant than the general means was recorded by thirteen genotypes in organic and twelve genotypes in inorganic. The mean values of genotypes varied from 4.65 g (K-1789) to 14.9 g (TCGS-1157) in organic with a general mean of 7.97 g whereas in inorganic it ranged from 5.19 g (ICG-2738) to 15.58 g (K-9) with a general mean of 8.51 g

4.2.13 SLA at 40 DAS

Eighteen genotypes in organic and seventeen genotypes in inorganic registered SLA at 40 DAS less than their general means 182.86 cm^2 g^{-1} and 188.71 cm^2 g^{-1} respectively. The means of SLA at 40 DAS ranged from 148.41 cm^2 g^{-1} (TCGS-1157) and 223.09 cm^2 g^{-1} (Narayani) in organic and 164.46 cm^2 g^{-1} (TCGS-1696) and 224.3 cm^2 g^{-1} (ICG-13723) in inorganic management system.

4.2.14 SLA at 60 DAS

Means of genotypes for SLA at 60 DAS varied from 140.24 cm^2 g^{-1} (TCGS-1157) to 274.35 cm^2 g^{-1} (K-1789) in organic and 149.55 cm^2 g^{-1} (ICG-10185) to 237.85 cm^2 g^{-1} (TCGS-1653) in inorganic. Seventeen genotypes in organic and nineteen genotypes in inorganic recorded less values than their general means 181.93 cm^2 g^{-1} (organic) and 181.66 cm^2 g^{-1} (inorganic).

4.2.15 SCMR at 40 DAS

Under organic management system the means of SCMR at 40 DAS ranged from 31.17 (Kalahasti) to 41.1 (TCGS-1157) with the general mean of 36.25 whereas in inorganic it varied from 32.7 (TCGS-1630) to 41.93 (ICG-7153) with a general mean of 37.85. Fifteen genotypes in organic and sixteen genotypes in inorganic recorded higher SCMR at 40 DAS than their general means.

4.2.16 SCMR at 60 DAS

The means of SCMR at 60 DAS ranged from 32.67 (ICG-13099) to 45.17 (K-9) in organic and from 33 (ICG-11687) to 48.13 (K-9) in inorganic. Thirteen genotypes in organic and sixteen genotypes in inorganic showed higher SCMR at 60 DAS than their general means 37.03 and 38.6 respectively.

SLA and SCMR are important physiological traits associated with water use efficiency. It was reported that water use efficiency has negative correlation with SLA and positive correlation with SCMR. It was also reported that SLA and SCMR are negatively correlated. Selection for low SLA and high SCMR will lead to improvement in water use efficiency of genotypes.

4.2.17 Relative water content (RWC)

Thirteen genotypes in organic and twelve genotypes in inorganic registered higher values of RWC then their general means 80.01 % and 75.82 % respectively. In organic management system the means of RWC ranged from 70.92 % (ICG-13099) to 89.27 % (TGCS-1631) and in inorganic management system it varied from 68.17 % (ICG-3992) to 92.6 % (TCGS-1678).

4.2.18 Oil content

For oil content fifteen genotypes from each organic and inorganic recorded higher values than their general means 47.32 % (organic) and 47.16 % (inorganic). The mean values are varied from 45.1 % (ICG-10185) to 49.5 % (TCGS-1630) in organic and from 45.15 % (K-7 bold) to 49.05 % (ICG-11651) in inorganic systems.

Over 60% of global groundnut production is crushed for extraction of oil for edible and industrial uses. Enhancing seed oil content with desirable fatty acid composition is one of the most important objectives of groundnut breeding programmes globally. Hence selection for genotypes having high oil content is needed.

4.2.19 Protein content

The protein content in organic management system ranged from 24.6 % (TCGS-1631) to 26.45 % (ICG-15309) with a general mean of 25.67 % whereas in inorganic system it varied from 24.1 % (ICG-3992) to 26.6 % (ICG-111) with a general mean of 25.61 %. Fifteen genotypes in organic and sixteen genotypes in inorganic recorded higher protein content than their general means.

Protein in groundnut kernels is increasingly becoming important as food and feed sources, especially in developing countries. It contains high quality protein than meat, eggs, and most of other vegetables and becoming important food in reducing malnutrition. Hence selection for genotypes having high protein content is needed.

4.2.20 Total carbohydrate

Sixteen genotypes in organic and thirteen genotypes in inorganic registered higher carbohydrate content than their general means 20.35 % and 16.68 % respectively. The means of genotypes ranged from 10.5 % (Kalahasti) to 31.5 % (K-1789) in organic and 7 % (ICG-11651) to 24.5 % (ICG-111) in inorganic management systems.

4.2.21 Total free amino acids

Under organic fertilizer management the means of total free amino acids varied from 0.54 mg g^{-1} (ICG-5236) to 1.78 mg g^{-1} (K-7 bold) with a general mean of 0.86 mg g^{-1} whereas in inorganic system it ranged from 0.61

mg g^{-1} (K-1789) to 1.73 mg g^{-1} (K-7 bold) with a general mean of 0.89 mg g^{-1}. Twelve genotypes from organic and fourteen genotypes in inorganic recorded higher values of total free amino acids than their general means.

Drought conditions in groundnut leads to accumulation of low molecular weight solutes such as sugars, free amino acids etc. Hence studies for variation of these biomolecules will help to screen the genotypes for water stress.

4.2.22 Pod yield per plant

For pod yield per plant the mean values ranged from 6.57 g (ICG-13723) to 22.25 g (TCGS-1157) in organic and 8.94 g (ICG-3992) to 24.49 g (ICG-7153) in inorganic management systems. Thirteen genotypes in organic and twelve genotypes in inorganic recorded higher pod yield per plant than their general means 12.05 (organic) and 14.49 (inorganic).

The top five genotypes for each character based on mean performance under organic and inorganic fertilizer managements were presented in Table 4.4. These genotypes are worthy of utilization for improvement of characters under respective fertilizer managements.

The genotypes TCGS-1157, ICG-11322, ICG-10384, ICG-7153 showed higher performance for both pod yield per plant and kernel yield per plant, under organic fertilizer managements. TCGS-1157 also showed better performance for characters like number of pods per plant, hundred kernel weight, harvest index, SLA at 40 DAS, SLA at 60 DAS, SCMR at 40 DAS, SCMR at 60 DAS and protein content. ICG-10384 performed better for number of pegs per plant, number of mature pods per plant and number of pods per plant. The genotypes ICG-11322 recorded higher values for number of primary branches per plant and number of mature pods per plant, kernel yield per plant and carbohydrate content while ICG-7153 registered more number of pegs per plant, number of pods per plant, kernel yield per

Table 4.4 Summary of top five groundnut genotypes based on mean performance of 22 characters under organic and inorganic fertilizer managements

Character	Organic	Inorganic	Both
DF	Dharani, ICG-2738, K-9, ICG-11651, K-6, Narayani	ICG-11651, TCGS-1678, K-7, ICG-434, ICG-15309, ICG- 11687	ICG-11651
DM	Kalahasti, Narayani, K-6, ICG-434, ICG-2738, ICG-13099	Kalahasti, TCGS-1630, K-7, TCGS-1157, Narayani, K-6, ICG-5236, ICG-434, ICG-2738, ICG-15309, ICG-111	Kalahasti, Narayani, K-6, ICG-434, ICG-2738
PH	TCGS-1696, ICG-10185, TCGS-1630, ICG-11687, ICG-2738	Dharani, ICG-11687, TCGS-1696, TCGS-1631, Narayani	TCGS-1696, ICG-11687
NPB	TCGS-1653, ICG-10185, K-1805, ICG-111, ICG-11322	TCGS-1330, ICG-5236, K-7, ICG-11322, TCGS-1157	ICG-11322
NPEGP	ICG-7153, ICG-11687, K-1789, ICG-10384, TCGS-1157	K-9, ICG-7153, ICG-11322, TCGS-1653, ICG-111	ICG-7153
NMP	ICG-7153, ICG-11322, ICG-10384, TCGS-1157, TCGS-1330	ICG-7153, K-9, ICG-11322, Dharani, Kalahasti	ICG-7153, ICG-11322
NIMP	ICG-13723, ICG-13099, ICG-13787, TCGS-1696, Dharani, ICG-10384, ICG-11322, TCGS-1330	ICG-111, ICG-13099, K-7, Dharani, ICG-13723, ICG-15309	ICG-13723, ICG-13099, Dharani
NPP	ICG-7153, ICG-11322, ICG-10384, TCGS-1157, ICG-11687	K-9, ICG-7153, ICG-11322, TCGS-1653, Kalahasti	ICG-7153, ICG-11322
100KW	TCGS-1157, TCGS-1330, ICG-13787, K-7, ICG-2738	Narayani, K-7, ICG-5236, ICG-13099, Dharani	K-7
SP	Dharani, k-9, ICG- 13723, K-6, ICG-13787	ICG-13723, Dharani, K-9, ICG-11651, ICG-3992	Dharani, k-9, ICG- 13723,
HI	ICG-11651, Dharani, TCGS-1157, ICG-5236, K-7	ICG-13723, K-9, ICG-11651, Dharani, ICG-10384	ICG-11651, Dharani
KYPP	TCGS-1157, ICG-11322, ICG-10384, Dharani, ICG-7153	K-9, ICG-7153, TCGS-1330, Dharani, ICG-11322	ICG-11322, Dharani, ICG-7153

Cont..

Table 4.4 Contd..

SLA40	TCGS-1157, TCGS-1631, K-1805, K-7, TCGS-1630	TCGS-1696, ICG-11322, ICG-10185, Dharani, K-9	--
SLA60	TCGS-1157, ICG-13787, ICG-10185, TCGS-1330, ICG-13723	ICG-10185, ICG-11651, ICG-3992, ICG-11322, ICG-111	ICG-10185
SCMR 40	TCGS-1157, ICG-7153, ICG-111, K-7, TGCS-1330	ICG-7153, ICG-11322, ICG-13723, ICG-5236, ICG-10185	ICG-7153
SCMR 60	K-9, K-7, TCGS-1157, K-1805, TCGS-1330	K-9, TCGS-1631, K-1805, K-7, ICG-111	K-9, K-7, K-1805
RWC	TCGS-1631, TCGS-1330, TCGS-1678, TCGS-1630, ICG-11651	TCGS-1678, K-6, ICG-11651, Kalahasti, Narayani	TCGS-1678, ICG-11651
OIL	TCGS-1630, TCGS-1631, ICG-434, K-1789, TCGS-1696	ICG-11651, ICG-434, K-1789, TCGS-1631, TCGS-1630	TCGS-1630, TCGS-1631, ICG-434, K-1789
PRO	ICG-15309, ICG-2738, TCGS-1157, ICG-13723, ICG-13099	ICG-111, ICG-15309, TCGS-1631, K-7, TCGS-1696	ICG-15309
CAR	K-1789, K-7, ICG-11322, Narayani, TCGS-1330	ICG-111, TCGS-1157, K-7, TCGS-1653, K-1789	K-1789, K-7
TFA	K-7, ICG-3992, ICG-2738, ICG-15309, Kalahasti	K-7, K-9, ICG-2738, ICG-11651, TCGS-1653, TCGS-1696	K-7, ICG-2738
PYPP	TCGS-1157, ICG-10384, ICG-11322, ICG-7153, TCGS-1330	ICG-7153, K-9, ICG-11322, TCGS-1330, K-7	ICG-11322, ICG-7153, TCGS-1330

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height
NPB : Number of primary branches per plant
NPEGP: Number of pegs per plant
NMP : Number of mature pods per plant

NIMP : Number of immature pods per plant
NPP : Number of pods per plant
100 KW : Hundred kernel weight
SP : Shelling percentage
HI : Harvest index
KYPP : Kernel yield per plant

SLA 40 : Specific leaf area at 40 DAS
SLA 60 : Specific leaf area at 60 DAS
SCMR 40 : SCMR at 40 DAS
SCMR 60 : SCMR at 60 DAS
RWC : Relative water content

OIL : Oil content
PRO : Protein content
CAR : Carbohydrate content
TFA : Total free amino acids
PYPP : Pod yield per plant

plant and high SCMR at 40 DAS. The genotype TCGS-1330 showed better performance for pod yield per plant, number of mature pods per plant, hundred kernel weight, SLA at 60 DAS, SCMR at 40 DAS, SCMR at 60 DAS, relative water content and carbohydrate content. Dharani showed early days to 50% flowering, high shelling percentage, harvest index and kernel yield per plant. Hence it was observed that under organic fertilizer management the genotypes TCGS-1157, ICG-10384, ICG-11322, ICG-7153, TCGS-1330 and Dharani will be promising donors for improvement of yield and yield attributing characters.

Under inorganic fertilizer management ICG-7153, K-9, ICG-11322 and TCGS-1330 showed better performance for both kernel yield and pod yield per plant. ICG-7153 also showed better performance for number of pegs per plant, number of mature pods per plant, number of pods per plant and SCMR at 40 DAS whereas K-9 showed better performance for number of pegs per plant, number of mature pods per plant, number of pods per plant, shelling percentage, harvest index, number of pods per plant, SLA at 40 DAS, SLA at 60 DAS and total free amino acids. ICG-11322 recorded more number of primary branches per plant, number of pegs per plant, number of mature pods per plant, low SLA at 40 DAS and SLA at 60 DAS. K-7 bold recorded early days to 50% flowering, days to maturity, more number of primary branches per plant, hundred kernel weight, protein content, carbohydrate content and total free amino acids. Dharani showed better performance for plant height, number of mature pods per plant, hundred kernel weight, shelling percentage and harvest index, kernel yield per plant and SLA at 40 DAS. Hence under inorganic conditions the genotypes ICG-7153, K-9, ICG-11322, TCGS-1330, K-7 bold, Dharani can be used for improvement of yield and other respective characters for which these genotypes were better performed.

t-test was conducted for 22 characters in 30 groundnut genotypes under organic and inorganic fertilizer managements and results were furnished in Table 4.5. Differential ranking was observed among the genotypes between two fertilizer management systems. Some genotypes performed better in organic conditions than in inorganic conditions for various characters. The characters days to 50% flowering, days to maturity, number of mature pods per plant, hundred kernel weight, shelling percentage, SCMR at 40 DAS, relative water content, carbohydrate content and pod yield per plant showed significant differences between organic and inorganic conditions whereas other characters *viz.*, plant height, number of primary branches per plant, number of pegs per plant, number of immature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SLA at 40 DAS, SLA at 60 DAS, SCMR at 60 DAS, oil content, protein content and total free amino acids exhibited non-significant difference between organic and inorganic fertilizer managements. Though there was a significant difference for pod yield per plant in organic and inorganic conditions kernel yield per plant showed non-significant difference between two fertilizer managements.

4.3 VARIABILITY AND GENETIC PARAMETERS

In breeding programmes the genetic variability present in the population helps in selection of desirable genotypes. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the genotypes. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. Hence the variability for 22 characters among 30 genotypes were studied in both organic and inorganic conditions and the results were presented here under.

Table 4.5 Test of significance for 22 characters in 30 groundnut genotypes under organic and inorganic fertilizer managements

Character	p-value
Days to 50 % flowering	**0.000****
Days to maturity	**0.04***
Plant height	**0.5**
Number of primary branches per plant	**0.66**
Number of pegs per plant	**0.45**
Number of mature pods per plant	**0.04***
Number of immature pods per plant	**0.45**
Number of pods per plant	**0.06**
100 kernel weight	**0.03***
Shelling percentage	**0.000****
Harvest index	**0.16**
Kernel yield per plant	**0.43**
SLA at 40 DAS	**0.26**
SLA at 60 DAS	**0.97**
SCMR at 40 DAS	**0.02***
SCMR at 60 DAS	**0.06**
Relative water content	**0.004****
Oil content	**0.54**
Protein content	**0.71**
Carbohydrate content	**0.003****
Total free amino acids	**0.62**
Pod yield per plant	**0.01****

*,** significance at 5% and 1% level respectively

4.3.1 Estimation of Variability and Genetic Parameters under Organic Management

The variability and genetic parameters like phenotypic and genotypic coefficients of variation, heritability in broad sense, genetic advance and genetic advance as per cent of mean for 22 characters involving 30 genotypes under organic fertilizer management were presented in Table 4.6

4.3.1.1 Variability studies

For all the characters phenotypic co-efficient of variation was more than the genotypic co-efficient of variation indicating the influence of environment in all these traits. Similar kind of results were obtained by Manjubhargavi *et al.* (2016b) and Aparna (2017a).

The characters number of immature pods per plant (GCV : 31.18%; PCV : 49.92%), kernel yield per plant (GCV : 28.37% ; PCV : 39.63%), pod yield per plant (GCV : 25.26% ; PCV : 37.84%) and total free amino acid content (GCV : 27.96% ; PCV : 29.63%) recorded higher estimates of variability indicating the presence of ample variation for these traits among the genotypes and selection could be effective for further improvement of these characters. Higher estimates of GCV and PCV for kernel yield per plant and pod yield per plant was reported by Manjubhargavi *et al.* (2016b) and Aparna (2017a). Aparna (2017a) also reported high GCV and PCV for number of immature pods per plant.

Moderate estimates of GCV and high PCV were exhibited by number of pegs per plant (GCV : 17.15 ; PCV : 28.25), number of mature pods per plant (GCV : 19.16% ; PCV : 31.71%) and number of pods per plant (GCV : 18.91% ; PCV : 30.26%). Similar kind of results for number of mature pods per plant was reported by Manjubhargavi *et al.* (2016b).

Table 4.6 Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as per cent of mean for 22 characters in 30 groundnut genotypes under organic fertilizer management

S. 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	29.01	25.67	36.00	6.78	10.11	8.97	10.96	67.00	4.39	15.14
2	Days to maturity	98.61	87.00	104.00	17.16	18.69	4.20	4.38	91.80	8.18	8.29
3	Plant height (cm)	46.00	35.07	60.87	33.00	64.80	12.49	17.50	50.90	8.45	18.36
4	Number of primary branches per plant	4.62	3.40	6.07	0.32	0.70	12.22	18.08	45.70	0.79	17.00
5	Number of pegs per plant	22.63	13.20	35.80	15.06	40.87	17.15	28.25	36.80	4.85	21.45
6	Number of mature pods per plant	11.18	6.13	19.47	4.59	12.57	19.16	31.71	36.50	2.67	23.85
7	Number of immature pods per plant	1.67	0.73	3.00	0.27	0.69	31.18	49.92	39.00	0.67	40.11
8	Number of pods per plant	12.86	6.87	22.47	5.92	15.14	18.91	30.26	39.10	3.13	24.35
9	Hundred kernel weight (g)	46.15	28.86	58.63	49.49	60.76	15.24	16.89	81.40	13.08	28.34
10	Shelling percentage	65.86	52.02	77.03	9.04	14.60	5.53	7.03	61.90	4.87	8.97
11	Harvest index (%)	35.30	23.80	45.80	12.31	22.83	9.67	13.17	53.90	5.31	14.62
12	Kernel yield per plant (g)	7.97	4.65	14.90	5.12	9.99	28.37	39.63	51.20	3.34	41.84
13	SLA at 40 DAS (cm^2 g^{-1})	182.86	148.41	223.09	202.23	878.46	7.78	16.21	23.00	14.06	7.69
14	SLA at 60 DAS (cm^2 g^{-1})	181.93	140.24	274.35	622.99	756.15	13.72	15.11	82.40	46.67	25.65
15	SCMR at 40 DAS	36.25	31.17	41.10	4.66	10.16	5.96	8.79	45.90	3.01	8.31
16	SCMR at 60 DAS	37.03	32.67	45.17	8.07	14.41	7.67	10.25	56.00	4.38	11.83
17	Relative water content (%)	80.01	70.92	89.27	5.71	23.57	3.79	7.70	24.20	2.42	3.84
18	Oil content (%)	47.32	45.10	49.50	1.08	1.16	2.19	2.28	92.60	2.06	4.34
19	Protein content (%)	25.67	24.60	26.45	0.003	0.003	0.98	1.11	78.00	0.09	1.78
20	Carbohydrate content (%)	20.35	10.50	31.50	11.85	13.19	12.92	13.63	89.90	6.72	25.23
21	Total free amino acids (mg g^{-1})	0.86	0.54	1.78	0.06	0.07	27.96	29.63	89.00	0.47	54.36
22	Pod yield per plant (g)	12.05	6.57	22.25	9.27	20.81	25.26	37.84	44.5	4.19	34.73

Moderate estimates of GCV and PCV were observed for the characters plant height (GCV : 12.49 %; PCV : 17.5%), number of primary branches per plant (GCV : 12.22% ; PCV : 18.08%), hundred kernel weight (GCV : 15.24% ; PCV : 16.89%), SLA at 60 DAS (GCV : 13.72 %; PCV : 15.11%) and carbohydrate content (GCV : 12.92% ; PCV : 13.63%). Moderate estimates of GCV and PCV for plant height was also reported by Manjubhargavi *et al*. (2016b).

Low GCV and moderate PCV were recorded for the characters days to 50% flowering (GCV : 8.97% ; PCV : 10.96%), harvest index (GCV : 9.67% ; PCV : 13.17%), SLA at 40 DAS (GCV : 7.78% ; PCV : 16.21%) and SCMR at 60 DAS (GCV : 7.67% ; PCV : 10.25%). Low GCV and moderate PCV for days to 50% flowering was observed by Manjubhargavi *et al*. (2016b)

The characters days to maturity (GCV : 4.20% ; PCV : 4.38%), shelling percentage (GCV : 5.53% ; PCV 7.03%), SCMR at 40 DAS (GCV : 5.96% ; PCV : 8.79%), relative water content (GCV : 3.79% ; PCV : 7.7%), oil content (GCV : 2.19% ; PCV : 2.28%), protein content (GCV : 0.98% ; PCV : 1.11%) recorded lower estimates of GCV and PCV indicating the limited scope of selection for these traits in organic fertilizer management. Majubhargavi *et al*. (2016b) also observed lower estimates of GCV and PCV for oil content and protein content. Lower estimates of GCV and PCV for days to maturity was reported by Aparna (2017a).

4.3.1.2 Heritability

High heritability estimates were observed for the characters oil content (92.6%), days to maturity (91.8%), carbohydrate content (89.9%) total free amino acids (89%), SLA at 60 DAS (82.4), hundred kernel weight (81.4%), protein content (78%), days to 50 % flowering (67%), and shelling percentage (61.9%) indicating that the effect of environment is least on these characters. Similar kind of results for days to 50 % flowering, days to maturity, hundred kernel weight was reported by Aparna (2017a). High heritability for oil content and protein content was in accordance with the results of Manjubhargavi *et al.* (2016b)

The characters SCMR at 60 DAS (56%), harvest index (53.9%), kernel yield per plant (51.20%), plant height (50.9%), SCMR at 40 DAS (45.9%), number of primary branches per plant (45.70%), pod yield per plant (44.5%), number of pods per plant (39.1%), number of immature pods per plant (39%), number of pegs per plant (36.8%), number of mature pods per plant (36.5%) exhibited moderate heritability. Moderate heritability for number of primary branches per plant, number of pods per plant, number of mature pods per plant, kernel yield per plant, harvest index was in accordance with the results of Manjubhargavi *et al.* (2016b). Aparna (2017a) also reported moderate heritability for kernel yield per plant, number of pegs per plant, number of primary branches per plant and harvest index.

Low heritability estimates were recorded for the characters relative water content (24.2%), SLA at 40 DAS (23%) indicating that these traits are highly influenced by the environment.

4.3.1.3 Genetic advance

High genetic advance was recorded for the character SLA at 60 DAS (46.67%) and moderate genetic advance for the characters SLA at 40 DAS (14.06%) and hundred kernel weight (13.08%).

Low genetic advance was observed for the characters plant height (8.45%), days to maturity (8.18%), carbohydrate content (6.72%), harvest index (5.31%), shelling percentage (4.87%), number of pegs per plant (4.85%), days to 50 % flowering (4.39%), SCMR at 60 DAS (4.38%), pod yield per plant (4.19%), kernel yield per plant (3.34%), number of pods per plant (3.13%), SCMR at 40 DAS (3.01%), number of mature pods per plant

(2.67%), relative water content (2.42%), oil content (2.06%), number of primary branches (0.79%), number of immature pods per plant (0.67%), total free amino acids (0.47%) and protein content (0.09%).

4.3.1.4 Genetic advance as per cent of mean

High genetic advance as per cent of mean was observed for total free amino acids (54.36%) followed by kernel yield per plant (41.84%), number of immature pods per plant (40.11%), pod yield per plant (34.73%), hundred kernel weight (28.34%), SLA at 60 DAS (25.65%), carbohydrate content (25.23%), number of pods per plant (24.35%), number of mature pods per plant (23.85%) and number of pegs per plant (21.45%).

The characters plant height (18.36%), number of primary branches (17%), days to 50% flowering (15.14%), harvest index (14.62%) and SCMR at 60 DAS (11.83%) exhibited moderate genetic advance as per cent of mean whereas the characters shelling percentage (8.97%), SCMR at 40 DAS (8.31%), days to maturity (8.29%), SLA at 40 DAS (7.69), oil content (4.34%), relative water content (3.84%) and protein content (1.78%) exhibited low genetic advance as per cent of mean.

High heritability coupled with high genetic advance as per cent of mean were reported for the characters total free amino acids (h^2_{bs} = 89%, GAM = 54.36%), carbohydrate content (h^2_{bs} = 89.9%, GAM = 25.23%), SLA at 60 DAS (h^2_{bs} = 82.4%, GAM = 25.65%) and hundred kernel weight (h^2_{bs} = 81.4%, GAM = 28.34%) indicating that the influence of additive gene action and hence the selection for these traits would be very effective under organic fertilizer management. Similar kind of results for hundred kernel weight was reported by Aparna (2017a)

The character days to 50% flowering exhibited high heritability coupled with moderate genetic advance (h^2_{bs} = 67%, GAM = 15.14%) indicating the presence of both additive and non-additive gene action with preponderance of additive genetic variance and selection would be effective to some extent.

Moderate heritability with high genetic advance was exhibited by the characters kernel yield per plant (h^2_{bs} = 51.2%, GAM = 41.84%), number of pegs per plant (h^2_{bs} = 36.8%, GAM = 21.45%), number of pods per plant (h^2_{bs} = 39.1%, GAM = 24.35%), number of immature pods per plant (h^2_{bs} = 39%, GAM = 40.11%), number of mature pods per plant (h^2_{bs} = 36.5%, GAM = 23.85%) and pod yield per plant (h^2_{bs} = 44.5%, GAM = 34.73%) which indicated that pedigree method of breeding and phenotypic selection would be effective for improvement of these traits. Moderate heritability coupled with high genetic advance for kernel yield per plant, number of pegs per plant was earlier reported by Aparna (2017a). Manjubharagvi *et al*. (2016b) reported moderate heritability coupled with high genetic advance for number of pods per plant, number of mature pods per plant, kernel yield per plant and pod yield per plant.

Moderate heritability and moderate genetic advance as per cent of mean was recorded for the characters plant height (h^2_{bs} = 50.9%, GAM = 18.36%), number of primary branches (h^2_{bs} = 45.7%, GAM = 17%), harvest index (h^2_{bs} = 53.9, GAM = 14.62%) and SCMR at 60 DAS (h^2_{bs} = 56%, GAM = 11.83%) indicating that both additive and non-additive gene actions have a role in their inheritance and phenotypic selection would be effective to some extent. Similar kind of results for number of primary branches per plant and harvest index were earlier reported by Aparna (2017a)

The characters days to maturity (h^2_{bs} = 91.8%, GAM = 8.29), shelling percentage (h^2_{bs} = 61.9, GAM = 8.97%), oil content (h^2_{bs} = 92.6%, GAM = 4.34%) and protein content (h^2_{bs} = 78%, GAM = 1.78%) exhibited high heritability coupled with low genetic advance as per cent of mean indicating the presence of non-additive gene action and high heritability may be due to favorable environment rather than the inherent performance of the genotype and hence selection may not be effective. High heritability coupled with low genetic advance for oil content and protein content was in accordance with the results of Manjubhargavi *et al*. (2016b).

The character SCMR at 40 DAS (h^2_{bs} = 45.9%, GAM = 8.31%) showed moderate heritability coupled with low genetic advance as per cent of mean. The characters SLA at 40 DAS (h^2_{bs} = 23%, GAM = 7.69%) and relative water content (h^2_{bs} = 24.2%, GAM = 3.84%) exhibited low heritability coupled with low genetic advance as per cent of mean indicating that high influence of environment on these traits and selection would be ineffective.

4.3.2 Estimation of Variability and Genetic Parameters under Inorganic Fertilizer Management

Phenotypic and genotypic coefficients of variation, heritability in broad sense, genetic advance and genetic advance as per cent of mean for 22 characters involving 30 genotypes under inorganic fertilizer management were presented in Table 4.7

4.3.2.1 Variability studies

For all the characters studied phenotypic coefficient of variation is greater than genotypic coefficient of variation indicating the effect of environment on these traits. These results are in accordance with the results obtained by Narasimhulu *et al.* (2012), Yusuf *et al*. (2017a), Aparna *et al*. (2018) and Mahesh *et al*. (2018b).

The characters number of immature pods per plant (GCV : 33.65% ; PCV : 47.80%), number of mature pods per plant (GCV : 28.52% ; PCV : 33.80%), kernel yield per plant (GCV : 27.46% ; PCV : 35.32%), number of pods per plant (GCV : 26.41% ; PCV : 32.74%), number of pegs per plant

Table 4.7 Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as per cent of mean for 22 characters in 30 groundnut genotypes under inorganic fertilizer management

S 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	32.84	27.33	37.33	6.62	7.19	7.83	8.17	92.00	5.09	15.48
2	Days to maturity	96.48	89.33	104.00	10.36	18.85	3.34	4.50	55.00	4.92	5.10
3	Plant height (cm)	44.80	34.40	63.74	50.83	52.22	15.91	16.13	97.30	14.49	32.34
4	Number of primary branches per plant	4.70	3.80	6.07	0.31	0.92	11.87	20.37	33.90	0.67	14.24
5	Number of pegs per plant	23.74	15.27	45.73	35.70	51.01	25.17	30.09	70.00	10.30	43.39
6	Number of mature pods per plant	12.99	7.93	26.00	13.73	19.28	28.52	33.80	71.20	6.44	49.59
7	Number of immature pods per plant	1.80	0.93	3.53	0.365	0.74	33.65	47.80	49.50	0.88	48.78
8	Number of pods per plant	14.71	8.93	28.40	15.09	23.20	26.41	32.74	65.10	6.46	43.89
9	Hundred kernel weight (g)	42.66	32.77	51.84	17.26	31.41	9.74	13.14	55.00	6.35	14.87
10	Shelling percentage	58.31	49.14	68.39	4.90	17.59	4.45	8.42	27.90	2.41	4.83
11	Harvest index (%)	37.71	18.72	53.65	13.42	25.14	9.70	13.28	53.40	5.51	14.60
12	Kernel yield / plant (g)	8.51	5.19	15.59	5.46	9.03	27.46	35.32	60.40	3.74	43.98
13	SLA at 40 DAS (cm^2 g^{-1})	188.71	164.46	224.30	186.54	691.70	7.24	13.94	27.00	14.61	7.74
14	SLA at 60 DAS (cm^2 g^{-1})	181.66	149.55	237.85	677.54	1246.62	14.33	19.43	54.40	39.53	21.76
15	SCMR at 40 DAS	37.85	32.70	41.93	5.37	7.70	6.12	7.33	69.80	0.70	5.11
16	SCMR at 60 DAS	38.60	33.00	48.13	9.14	11.17	7.83	8.66	81.80	5.63	14.59
17	Relative water content (%)	75.82	68.17	92.60	15.13	30.44	6.39	9.06	49.70	5.65	9.28
18	Oil content (%)	47.16	45.15	49.05	0.99	1.07	2.12	2.20	93.30	1.99	4.22
19	Protein content (%)	25.61	24.10	26.60	0.002	0.003	0.95	1.12	71.00	0.08	1.64
20	Carbohydrate content (%)	16.68	7.00	24.50	0.27	0.34	12.62	14.21	78.90	0.95	23.11
21	Total free amino acids (mg g^{-1})	0.89	0.61	1.73	0.04	0.05	23.15	26.14	78.4	0.37	42.24
22	Pod yield/ plant (g)	14.49	8.94	24.49	9.89	19.20	21.71	30.25	51.5	4.65	32.11

(GCV : 25.17% ; PCV : 30.09%), total free amino acids (GCV : 23.15 ; PCV : 26.14) and pod yield per plant (GCV : 21.71% ; PCV : 30.25%) exhibited high GCV and PCV indicating ample amount of variation among the genotypes and selection would be effective for further improvement of these characters.

The results of Mahesh *et al.* (2018b) is similar to the present report of high GCV and PCV for number of immature pods per plant, number of mature pods per plant and kernel yield per plant. High estimates of GCV and PCV for kernel yield per plant was also reported by Mukesh and Lal (2017), Chavadhari *et al.* (2017) and Hussein *et al.* (2018). High GCV and PCV for number of pods per plant and pod yield per plant were in accordance with the results obtained by Hussein *et al.* (2018). High GCV and PCV for kernel yield per plant and pod yield per plant was also reported by Nandini *et al.* (2011) and Venkataramana *et al.* (2015).

Moderate GCV and high PCV was exhibited by number of primary branches per plant (GCV: 11.87% ; PCV : 20.37%). Moderate GCV and moderate PCV was exhibited by plant height (GCV : 15.91% ; PCV : 16.13%), SLA at 60 DAS (GCV : 14.33% PCV : 19.43%) and carbohydrate content (GCV : 12.62% ; PCV : 14.21%) whereas low GCV and moderate PCV was exhibited by 100 kernel weight (GCV : 9.74% ; PCV : 13.14%), harvest index (GCV : 9.7% ; PCV : 13.28%) and SLA at 40 DAS (GCV : 7.24% ; PCV : 13.94%).

Moderate estimates of GCV and PCV for plant height is similar with the results of Nandini *et al.* (2011), Chavadhari *et al.* (2017), Yusuf *et al.* (2017a) and Hussein *et al.* (2018).

The characters days to 50% flowering (GCV : 7.83% ; PCV : 8.17%), days to maturity (GCV : 3.34% ; PCV : 4.5%), shelling percentage (GCV : 4.45% ; PCV : 8.42%), SCMR at 40 DAS (GCV : 6.12% ; PCV : 7.33%), SCMR at 60 DAS (GCV : 7.83% ; PCV : 8.66%), relative water content (GCV : 6.39% ; PCV : 9.06%), oil content (GCV : 2.12% ; PCV : 2.20%) and protein content (GCV : 0.95% ; PCV : 1.12%) recorded low GCV and PCV.

Lower estimates of GCV and PCV for days to 50% flowering was in accordance with the results of Chavadhari *et al.* (2017), Mukesh and Lal (2017), Hussein *et al.* (2018) and Mahesh *et al.* (2018b). Chavadhari *et al.* (2017), Mukesh and Lal (2017) also reported low estimates of GCV and PCV for days to maturity. Results of low GCV and PCV for shelling percentage, protein content and oil content were similar to the reports of Omprakash and Nadaf (2017). Lower estimates of GCV and PCV for oil content and shelling percentage were also recorded by Mahesh *et al.* (2018b).

4.3.2.2 Heritability

In inorganic fertilizer management the characters plant height (97.3%) exhibited high heritability followed by oil content (93.3%), days to 50% flowering (92%), SCMR at 60 DAS (81.8%), carbohydrate content (78.9%), total free amino acids (78.4%), number of mature pods per plant (71.2%), protein content (71%), number of pegs per plant (70.00%), SCMR at 40 DAS (69.8%), number of pods per plant (65.1%) and kernel yield per plant (60.4%) indicating that the effect of environment is least in expression of these characters.

Moderate heritability was registered for the characters days to maturity (55%), hundred kernel weight (55%), SLA at 60 DAS (54.4%), harvest index (53.4%), pod yield per plant (51.5%), relative water content (49.7%), number of immature pods per plant (49.5%) and number of primary branches per plant (33.9%).

The characters shelling percentage (27.9%) and SLA at 40 DAS (27%) exhibited low heritability indicating that these characters are highly influenced by the environment

4.3.2.3 Genetic advance

SLA at 60 DAS (39.53%) exhibited high genetic advance whereas SLA at 40 DAS (14.61%) and plant height (14.49%), number of pegs per plant (10.30%), recorded moderate genetic advance. The other characters *viz.*, days to 50% flowering (5.09%), days to maturity (4.92%), number of primary branches per plant (0.67%), number of mature pods per plant (6.44%), number of immature pods per plant (0.88%), number of pods per plant (6.46%), hundred kernel weight (6.35%), shelling percentage (2.41%), harvest index (5.51%), kernel yield per plant (3.74%), pod yield per plant (4.65%), SCMR at 40 DAS (0.7%), SCMR at 60 DAS (5.63%), relative water content (5.65%), oil content (1.99%), protein content (0.08%), carbohydrate content (0.95%) and total free amino acids (0.37%) recorded low genetic advance.

4.3.2.4 Genetic advance as per cent of mean

Higher genetic advance as per cent of mean was recorded for, number of mature pods per plant (49.59%), number of immature pods per plant (48.78%), kernel yield per plant (43.98%), number of pods per plant (43.89%), number of pegs per plant (43.39%), total free amino acids (42.24%), plant height (32.34%), pod yield per plant (32.11%), carbohydrate content (23.11%) and SLA at 60 DAS (21.76) indicating that these characters were governed by additive genes and the selection for these characters will be rewarding in crop improvement.

Moderate genetic advance as per cent of mean was exhibited by the characters days to 50% flowering (15.48%), hundred kernel weight (14.87%), harvest index (14.6%), SCMR at 60 DAS (14.59%) and number of primary branches per plant (14.24%). The characters days to maturity (5.1%), shelling percentage (4.83%), SLA at 40 DAS (7.74%), SCMR at 40 DAS (5.11%), relative water content (9.28%), oil content (4.22%) and protein content (1.64%) exhibited low genetic advance as per cent of mean.

High heritability coupled with high genetic advance as per cent of mean were recorded for the characters plant height (h^2_{bs} = 97.3%, GAM = 32.34%), number of pegs per plant (h^2_{bs} = 70.00%, GAM = 43.39%), number of mature pods per plant (h^2_{bs}= 71.2%, GAM = 49.59), number of pods per plant (h^2_{bs} = 65.1%, GAM = 43.89%), kernel yield per plant (h^2_{bs} = 60.4%, GAM = 43.98%), carbohydrate content (h^2_{bs} = 78.9%, GAM = 23.11%) and total free amino acids (h^2_{bs} = 78.4% GAM = 42.24%) indicating the preponderance of additive gene action in expression of these characters and selection would be effective for improvement of these characters.

High heritability coupled with high genetic advance as per cent of mean for number of mature pods per plant and kernel yield per plant were also reported by Bhargavi *et al.* (2016), Chavadhari *et al.* (2017), Yusuf *et al.* (2017a) and Mahesh *et al.* (2018b). Bhavya *et al*. (2017), Yusuf *et al.* (2017a) and Mahesh *et al.* (2018b) also reported high heritability coupled with high genetic advance as per cent of mean for plant height. Bhavya *et al*. (2017) reported similar kind of results for number of pods per plant. Nandini *et al.* (2011) also reported high heritability coupled with high genetic advance as per cent of mean for plant height and number of pods per plant.

High heritability with moderate genetic advance as per cent of mean was exhibited by the characters days to 50 % flowering (h^2_{bs} = 92%, GAM = 15.48%) and SCMR at 60 DAS (h^2_{bs} = 81.8%, GAM = 14.59%). High heritability with moderate genetic advance as per cent of mean for days to 50% flowering was also reported by Balaraju *et al.* (2016)

The characters SCMR at 40 DAS (h^2_{bs} = 69.8%, GAM = 5.11%), oil content (h^2_{bs} = 93.3%, GAM = 4.22%) and protein content (h^2_{bs} =71%, GAM = 1.64%) recorded high heritability coupled with low genetic advance as per cent of mean. Silimilar kind of results for oil content was obtained by Bhargavi *et al.* (2016)

The characters number of primary branches per plant (h^2_{bs} = 33.9%, GAM = 14.24%), hundred kernel weight (h^2_{bs} = 55%, GAM = 14.87%) and harvest index (h^2_{bs} = 53.4%, GAM = 14.60%) showed moderate heritability coupled with moderate genetic advance as per cent of mean. Venkataramana *et al.* (2015) recorded similar kind of results for hundred kernel weight.

Moderate heritability coupled with high genetic advance as per cent of mean was exhibited by the characters number of immature pods per plant (h^2_{bs} = 49.5%, GAM = 48.78%), pod yield per plant (h^2_{bs} = 51.5%, GAM = 32.11%) and SLA at 60 DAS (h^2_{bs} = 54.4%, GAM = 21.76%) suggesting that pedigree method of breeding and phenotypic selection can be used for improvement of these characters. Moderate heritability coupled with high genetic advance as per cent of mean was also reported by Venkataramana *et al.* (2015) for pod yield per plant

Moderate heritability and low genetic advance as per cent of mean were recorded for the characters days to maturity (h^2_{bs} = 55%, GAM = 5.11%) and relative water content (h^2_{bs} = 49.7%, GAM = 9.28%). Moderate heritability and low genetic advance as per cent of mean for relative water content was in conformity with the findings of Srivalli *et al.* (2016).

The characters shelling percentage (h^2_{bs} = 27.9%, GAM = 4.83%) and SLA at 40 DAS (h^2_{bs} = 27%, GAM = 7.74%) showed low heritability coupled with low genetic advance as per cent of mean indicating that these characters are highly influenced by the environment and the selection would be ineffective.

Comparison of variability and genetic parameters in 30 groundnut genotypes for 22 characters were presented in Table 4.8. The character total free amino acids exhibited high heritability, high genetic advance as per cent of mean and high GCV in both organic and inorganic fertilizer managements whereas number of pegs per plant, number of mature pods per plant, number of pods per plant and total kernel yield per plant showed high heritability, high genetic advance and high GCV in inorganic management indicating that these characters are showing additive gene action and the selection would be effective under respective fertilizer managements. The traits SLA at 40 DAS exhibited low heritability, low genetic advance as per cent of mean and low GCV under both managements whereas relative water content in organic and shelling percentage in inorganic conditions also showed low heritability, low genetic advance as per cent of mean and low GCV indicating the significant role of environment in the expression of these characters.

4.4 GENETIC DIVERGENCE

In self-pollinated crops like groundnut genetic divergence plays an important role in improvement of the crop. Knowledge on genetic diversity is needed for the selection of better parents that can be utilized in hybridization programmes. Greater the genetic diversity in crop species, better is the chance of evolving promising and desired types. Hence 30 genotypes of groundnut were quantitatively assessed by Mahalanobis D^2 statistic under organic and inorganic fertilizer managements.

4.4.1 Genetic Divergence under Organic Fertilizer Management

Under organic fertilizer management 30 genotypes of groundnut were grouped into seven clusters. The distribution of genotypes into clusters was

Table 4.8 Comparison of genetic parameters of 22 characters between organic and inorganic fertilizer managements in groundnut

		Organic			Inorganic			
		Heritability			Heritability			
		High	**Moderate**	**Low**	**High**	**Moderate**	**Low**	
Genetic advance as per centof mean	**High**	TFA	NIMP, KYPP,PYPP	--	NPEGP, NMPP,NPP, KYPP, TFA	NIMP, PYPP,	--	**High GCV**
	Moderate	--	NPEGP	--	--	--	--	
	Low	--	--	--	--	--	--	
Genetic advance as per centof mean	**High**	SLA 60, 100 KW, CAR	NMPP, NPP	--	PH, CAR,	SLA 60	--	**Moderate GCV**
	Moderate	--	PH, NPB	--	--	NPB	--	
	Low	--	--	--	--	--	--	
Genetic advance as per centof mean	**High**	--	--	--	--	--	--	**Low GCV**
	Moderate	DF	HI, SCMR 60	--	DF, SCMR 60	100 KW, HI	--	
	Low	DM, SP, OIL, PRO	SCMR 40	SLA 40, RWC	SCMR 40, OIL, PRO	DM, RWC	SP, SLA 40	

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height
NPB : Number of primary branches per plant
NPEGP: Number of pegs per plant
NMP : Number of mature pods per plant
NIMP : Number of immature pods per plant
NPP : Number of pods per plant
100 KW : Hundred kernel weight
SP : Shelling percentage
HI : Harvest index
KYPP : Kernel yield per plant
SLA 40 : Specific leaf area at 40 DAS
SLA 60 : Specific leaf area at 60 DAS
SCMR 40 : SCMR at 40 DAS
SCMR 60 : SCMR at 60 DAS
RWC : Relative water content
OIL : Oil content
PRO : Protein content
CAR : Carbohydrate content
TFA : Total free amino acids
PYPP : Pod yield per plant

presented in Table 4.9 and Fig 1. Cluster I was the largest with 24 genotypes while all other clusters are monogenotypic.

4.4.1.1 Intra and inter cluster distances

The average intra and inter-cluster D^2 and D values of various clusters were furnished in Table 4.10 and cluster diagram was presented in Fig 2. The maximum inter cluster distance is observed between cluster III and VII (318.24) followed by cluster IV and VII (282.60), II and VII (250.60). Hence the genotypes from these combinations of clusters can be utilized for hybridization programmes.

The intra cluster distance for cluster I is 56.76 and for other clusters i.e., II, III, IV, V, VI and VII intra cluster distance is 0 as they were monogenotypic clusters.

4.4.1.2 Cluster means

The cluster means for each of 22 characters in 30 genotypes of groundnut were presented Table 4.11

The cluster means for days to 50 % flowering ranged from 26.67 days (VII) to 36.00 days (V) with a general mean of 29.50 days. Lower values than the general mean were observed in four clusters I, IV, VI and VII.

Days to maturity has their cluster means ranged from 87 days (IV) to 104 days (II, VII). Two clusters III, IV, have their cluster means less than its general mean (98.47 days).

Cluster means for plant height varied from 35.07 cm (IV) to 54.33 cm (II). The clusters I, II, III, VI were having superior values than its general mean (44.52).

Table 4.9 Clustering of 30 groundnut genotypes under organic fertilizer management

Cluster	Number of Genotypes	Genotypes
I	24	K-6, Narayani, ICG-11322, Dharani, ICG-13099, ICG-13787, ICG-10384, ICG-15309, ICG-13723, TCGS-1330, ICG-11687, ICG-7153, K-9, ICG-5236, TCGS-1157, ICG-2738, ICG-434, TCGS-1696, K-1805, ICG-111, TCGS-1653, TCGS-1678, ICG-10185, ICG-11651
II	1	TCGS-1630
III	1	TCGS-1631
IV	1	Kalahasti
V	1	ICG-3992
VI	1	K-1789
VII	1	K-7 bold

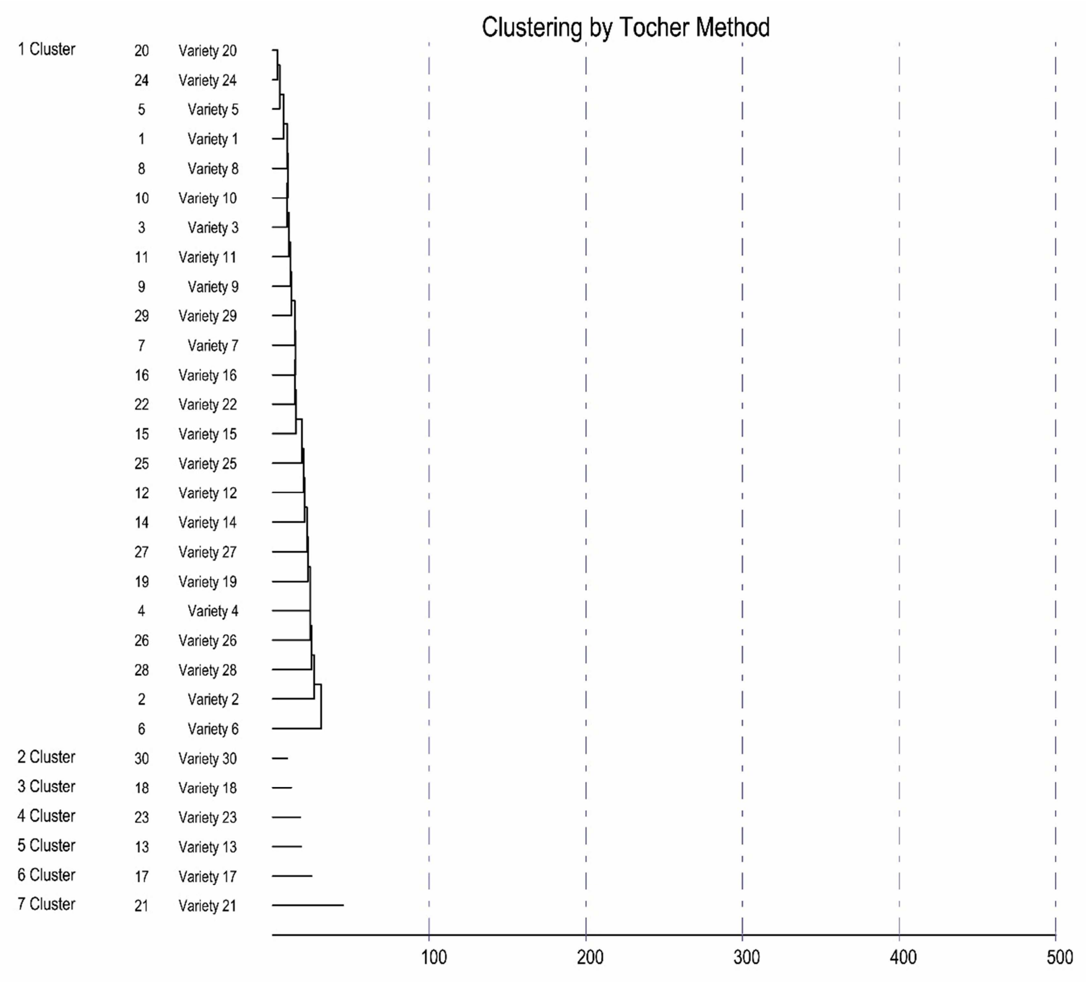

Fig. 4.1 Grouping of genotypes into clusters using Tocher's method under organic fertilizer management.

Variety 1	: Dharani	Variety 11	: ICG-15309	Variety 21	: K-7 bold
Variety 2	: ICG-10185	Variety 12	: ICG-2738	Variety 22	: K-9
Variety 3	: ICG-10384	Variety 13	: ICG-3992	Variety 23	: Kalahasti
Variety 4	: ICG-111	Variety 14	: ICG-434	Variety 24	: Narayani
Variety 5	: ICG-11322	Variety 15	: ICG-5236	Variety 25	: TCGS-1157
Variety 6	: ICG-11651	Variety 16	: ICG-7153	Variety 26	: TCGS-1653
Variety 7	: ICG-11687	Variety 17	: K-1789	Variety 27	: TCGS-1696
Variety 8	: ICG-13099	Variety 18	: TCGS-1631	Variety 28	: TCGS-1678
Variety 9	: ICG-13723	Variety 19	: K-1805	Variety 29	: TCGS-1330
Variety 10	: ICG-13787	Variety 20	: K-6	Variety 30	: TCGS-1630

Table 4.10 Inter and Intra cluster (diagonal) average of D^2 and D values (in parentheses) of 30 groundnut genotypes under organic fertilizer management

Cluster	I	II	III	IV	V	VI	VII
I	**56.76** **(7.53)**	97.92 (9.90)	92.73 (9.63)	95.68 (9.78)	87.30 (9.34)	146.45 (12.10)	198.85 (14.10)
II		**0.00** **(0.00)**	33.17 (5.76)	155.98 (12.49)	65.05 (8.07)	141.28 (11.89)	250.60 (15.83)
III			**0.00** **(0.00)**	83.49 (9.14)	77.51 (8.80)	202.63 (14.23)	318.24 (17.84)
IV				**0.00** **(0.00)**	119.73 (10.94)	234.12 (15.30)	282.60 (16.81)
V					**0.00** **(0.00)**	151.85 (12.32)	134.24 (11.59)
VI						**0.00** **(0.00)**	178.62 (13.36)
VII							**0.00** **(0.00)**

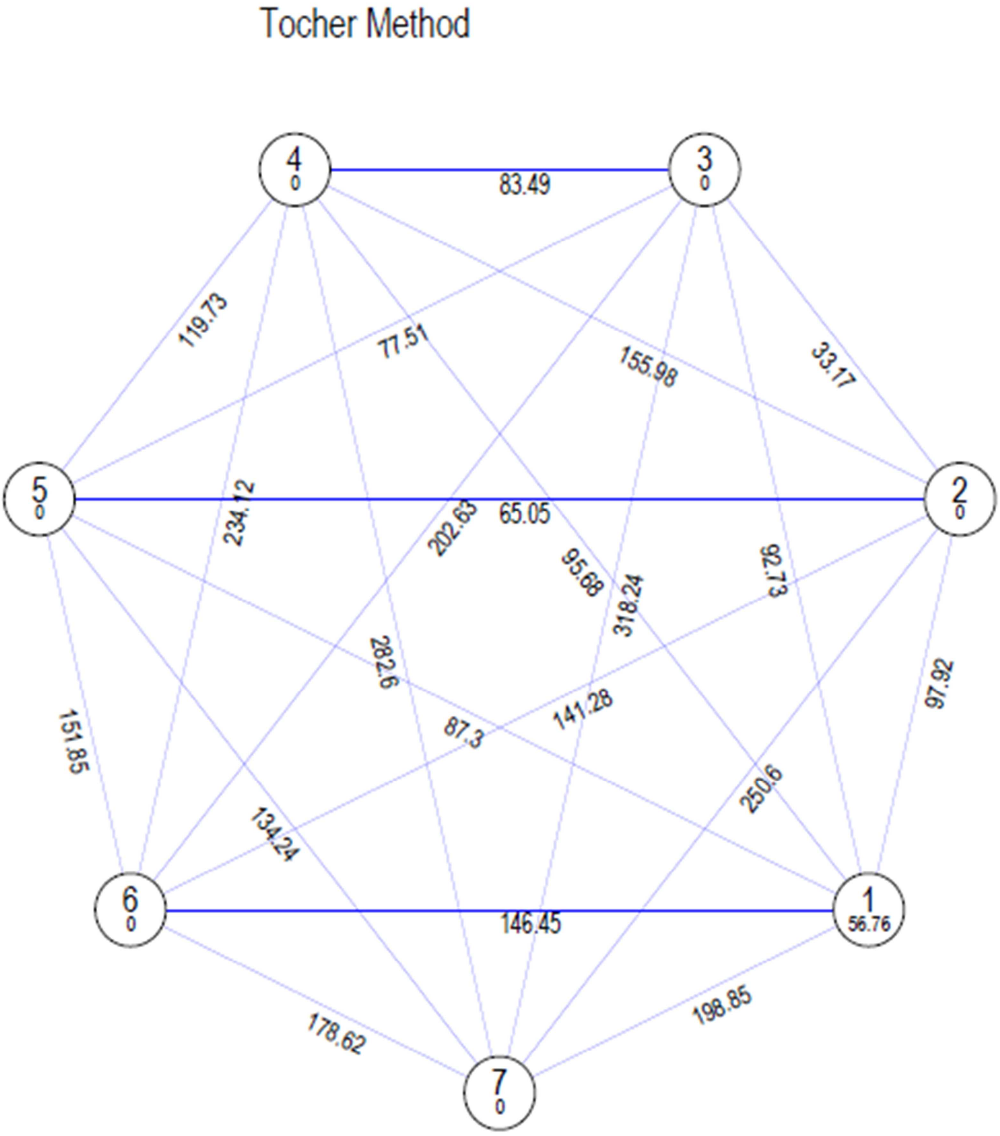

Fig. 4.2 Average inter and intra cluster distances under organic fertilizer management.

Table 4.11 Cluster means for 22 characters in groundnut under organic fertilizer management

Cluster No.	DF	DM	PH	NPB	NPEGP	NMP	NIMP	NPP	100KW	SP	HI	KYPP	SLA 40	SLA 60	SCMR 40	SCMR 60	RWC	OIL	PRO	CAR	TFA	PYPP
I	28.86	98.65	46.45	4.59	23.01	11.29	1.61	12.93	46.82	67.34	35.62	8.33	185.25	176.45	36.65	37.09	79.55	47.16	25.78	20.75	0.80	12.37
II	29.67	104.00	54.33	4.80	20.00	11.07	1.27	12.33	46.58	56.72	26.09	5.75	161.74	196.06	33.87	34.63	86.47	49.50	24.70	15.50	0.83	10.13
III	29.33	96.00	49.60	4.00	18.33	9.07	1.60	10.33	44.89	60.02	35.84	4.98	149.77	185.09	35.17	35.57	89.27	49.15	24.60	13.00	0.71	8.32
IV	27.33	87.00	35.07	4.87	17.67	9.40	1.60	11.00	42.56	58.23	39.69	7.12	220.31	197.69	31.17	36.43	76.83	46.70	25.25	10.50	0.96	12.23
V	36.00	101.00	41.27	4.87	21.27	11.87	2.73	14.60	42.90	64.99	27.94	7.49	173.78	162.13	36.17	35.27	78.83	47.45	25.50	15.00	1.45	11.69
VI	28.67	98.67	47.80	4.60	28.33	12.20	2.80	15.00	30.32	52.02	31.00	4.65	174.52	274.35	32.37	34.80	78.88	48.65	24.95	31.50	0.86	8.94
VII	26.67	104.00	37.13	5.13	20.93	10.93	1.33	12.27	53.69	67.66	42.21	9.22	159.86	207.98	39.13	43.97	81.02	46.35	26.15	27.00	1.78	13.59
	29.50	98.47	44.52	4.69	21.36	10.83	1.85	12.64	43.97	61.00	34.06	6.79	175.03	199.96	34.93	36.82	81.55	47.85	25.28	19.04	1.06	11.04

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height
NPB : Number of primary branches per plant
NPEGP : Number of pegs per plant
NMP : Number of mature pods per plant

NIMP : Number of immature pods per plant
NPP : Number of pods per plant
100 KW : Hundred kernel weight
SP : Shelling percentage
HI : Harvest index
KYPP : Kernel yield per plant

SLA 40 : Specific leaf area at 40 DAS
SLA 60 : Specific leaf area at 60 DAS
SCMR 40 : SCMR at 40 DAS
SCMR 60 : SCMR at 60 DAS
RWC : Relative water content

OIL : Oil content
PRO : Protein content
CAR : Carbohydrate content
TFA : Total free amino acids
PYPP : Pod yield per plant

Number of primary branches exhibited an overall mean of 4.69 with cluster means ranging from 4.00 (III) to 5.13 (VII). Four clusters (II, IV, V, VII) showed higher cluster means than their general mean.

Number of pegs per plant showed the cluster means ranged from 17.67 (IV) to 28.33 (VI) with a general mean of 21.36. Cluster I and VI recorded more cluster mean than the general mean.

Cluster means for number of mature pods varied from 9.07 (III) to 12.20 (VI). Clusters I, II, V, VI and VII recorded higher values than their general mean 10.83.

Number of immature pods were highest in cluster VI (2.80) and lowest in cluster II (1.27). Clusters I, II, III, IV, and VII showed lesser values than their general mean 1.85.

The cluster means for number of pods per plant ranged from 10.33 (III) to 15 (VI) with the general mean (12.64). Higher values than the general mean were observed in clusters I, V and VI.

The cluster means for hundred kernel weight varied from 30.32 g (VI) to 53.69 g (VII). The clusters I, II, III, and VII have their cluster means more than their general mean (43.97 g).

Shelling percentage exhibited the range of cluster means from 52.02% (VI) to 67.66% (VII) with the general mean of 61.00%. Higher cluster means than the average was recorded in clusters I, V and VII.

Three clusters I, III, IV and VII showed cluster means higher than the general mean (34.06%) for harvest index. Cluster means are varied from 26.09% (II) to 42.21% (VII).

Cluster means for kernel yield per plant ranged from 4.65 g (VI) to 9.22 g (VII) with a general mean of 6.79 g. Cluster I, IV, V and VII showed higher means than the general mean.

SLA at 40 DAS has cluster means ranged from 149.77 cm^2 g^{-1} (III) to 220.31 cm^2 g^{-1} (IV) with a general mean of 175.03 cm^2 g^{-1}. Clusters II, III, V, VI and VII are desirable clusters with lower cluster means than the general mean.

Cluster means for SLA at 60 DAS varied from 162.13 cm^2 g^{-1} (V) to 274.35 cm^2 g^{-1} (VI). Clusters I, II, III, IV, V have cluster means less than the general mean (199.96 cm^2 g^{-1}).

Cluster means for SCMR at 40 DAS ranged from 31.17 (IV) to 39.13 (VII) with a general mean of 34.93. Higher SCMR at 40 DAS than the general mean was observed with clusters I, III, V and VII.

SCMR at 60 DAS exhibited highest cluster mean in cluster VII (43.97) and lowest cluster mean in cluster II (34.63). Clusters I and VII showed higher cluster means than the general mean 36.82.

Cluster means for relative water content ranged from 76.83% (IV) to 89.27 (III) with a general mean of 81.55%. Clusters II, III exhibited higher cluster means than the general mean.

Oil content showed the range of cluster means from 46.35% (VII) to 49.50% (II) with a general mean of 47.85%. Clusters II, III, and VI showed higher cluster means than the general mean.

For protein content clusters I, V and VII showed higher cluster means than the general mean (25.28%). Cluster means are varied from 24.60% (III) 26.15% (VII).

Carbohydrate content recorded the cluster means from 10.5% (IV) to 31.5 (VI) with a general mean of 19.04%. Clusters I, VI and VII had higher cluster means than the general mean.

Cluster means for total free amino acids varied from 0.71 (III) to 1.78 (VII) with a general mean of 1.06. Cluster V and VII showed higher cluster mean than the general mean

Cluster means for pod yield per plant varied from 8.32 g (III) to 13.59 (VII) with a general mean of 11.04 g. Clusters I, IV, V and VII higher pod yield per plant than the general mean.

4.4.1.3 Relative contribution of individual character towards divergence

The per cent contribution of 22 characters were presented in Table 4.12. The character oil content contributed maximum (21.15%) towards genetic divergence by taking first rank 92 times followed by carbohydrate content (17.93%), total free amino acids (17.93%), days to maturity (14.94%), SLA at 60 DAS (13.79%), hundred kernel weight (5.52%), protein content (3.22%), pod yield per plant (2.76%), kernel yield per plant (1.15%), SCMR at 60 DAS (0.92%), days to 50% flowering (0.23%), number of pegs per plant (0.23%) and number of mature pods per plant (0.23%).

The other character like plant height, number of primary branches per plant, number of immature pods per plant, number of pods per plant, shelling percentage, harvest index, SLA at 40 DAS, SCMR at 40 DAS and relative water content did not contribute to the divergence.

Considering the genetic divergence between clusters and the mean performance of genotypes, the crosses TCGS-1157 X K-7 bold, TCGS-1157 X K-1789, TCGS-1330 X K-7 bold and Dharani X K-7 bold can be utilized

Table 4.12 Relative contribution of 22 characters to genetic diversity under organic fertilizer management

S. No.	Character	No. of times ranked first	% contribution
1	Days to 50 % flowering	1	0.23
2	Days to maturity	65	14.94
3	Plant height	0	0.00
4	Number of primary branches per plant	0	0.00
5	Number of pegs per plant	1	0.23
6	Number of mature pods per plant	1	0.23
7	Number of immature pods per plant	0	0.00
8	Number of pods per plant	0	0.00
9	Hundred kernel weight	24	5.52
10	Shelling percent	0	0.00
11	Harvest index	0	0.00
12	Kernel yield per plant	5	1.15
13	SLA at 40 DAS	0	0.00
14	SLA at 60 DAS	60	13.79
15	SCMR at 40 DAS	0	0.00
16	SCMR at 60 DAS	4	0.92
17	Relative water content	0	0.00
18	Oil content	92	21.15
19	Protein content	14	3.22
20	Carbohydrate content	78	17.93
21	Total free amino acids	78	17.93
22	Pod yield per plant	12	2.76

to get transgressive segregants for yield, water use efficiency and quality traits under organic fertilizer management.

4.4.2 Genetic Divergence under Inorganic Fertilizer Management

Under inorganic fertilizer management 30 genotypes of groundnut were grouped into five clusters. The distribution of genotypes into various clusters were presented in Table 4.13 and Fig 3. Cluster I is the largest cluster with 23 genotypes. Cluster II contain 4 genotypes and remaining clusters (III, IV, V) are monogenotypic clusters.

4.4.2.1 Intra and inter cluster distances

The average inter and intra cluster D^2 and D values were furnished in Table 4.14 and cluster diagram was presented in Fig 4. Highest inter-cluster distance was observed between cluster II and III (307.58) followed by cluster II and V (289.54), cluster II and IV (257.50).

Intra cluster distance is maximum in cluster II (69.96) followed by cluster I (69.69). Intra-cluster distance for other clusters i.e., III, IV and Vis 0 as they are monogenotypic clusters.

Based on inter cluster distances the clusters II and III, II and V, II and IV were found to be more divergent. Hence the genotypes from these clusters can be utilized as potential parents and crossing among them would be suggested to generate a wide range of variability for effective selection for improvement of various characters.

4.4.2.2 Cluster means

Cluster means for 22 characters of 30 groundnut genotypes under inorganic fertilizer management were presented in Table 4.15

Table 4.13 Clustering of 30 groundnut genotypes under inorganic fertilizer management

Cluster	Number of Genotypes	Genotypes
I	23	ICG-10185, ICG-13787, ICG-13099, ICG-11322, ICG-10384, TCGS-1157, ICG-5236, ICG-13723, ICG-111, Kalahasti, K-1805, ICG-2738, ICG-7153, ICG-3992, TCGS-1630, ICG-15309, TCGS-1653, K-1789, TCGS-1678, ICG-434, K-6, Narayani, TCGS-1696
II	4	Dharani, ICG-11687, TCGS-1631, K-9
III	1	TCGS-1330
IV	1	K-7 bold
V	1	ICG-11651

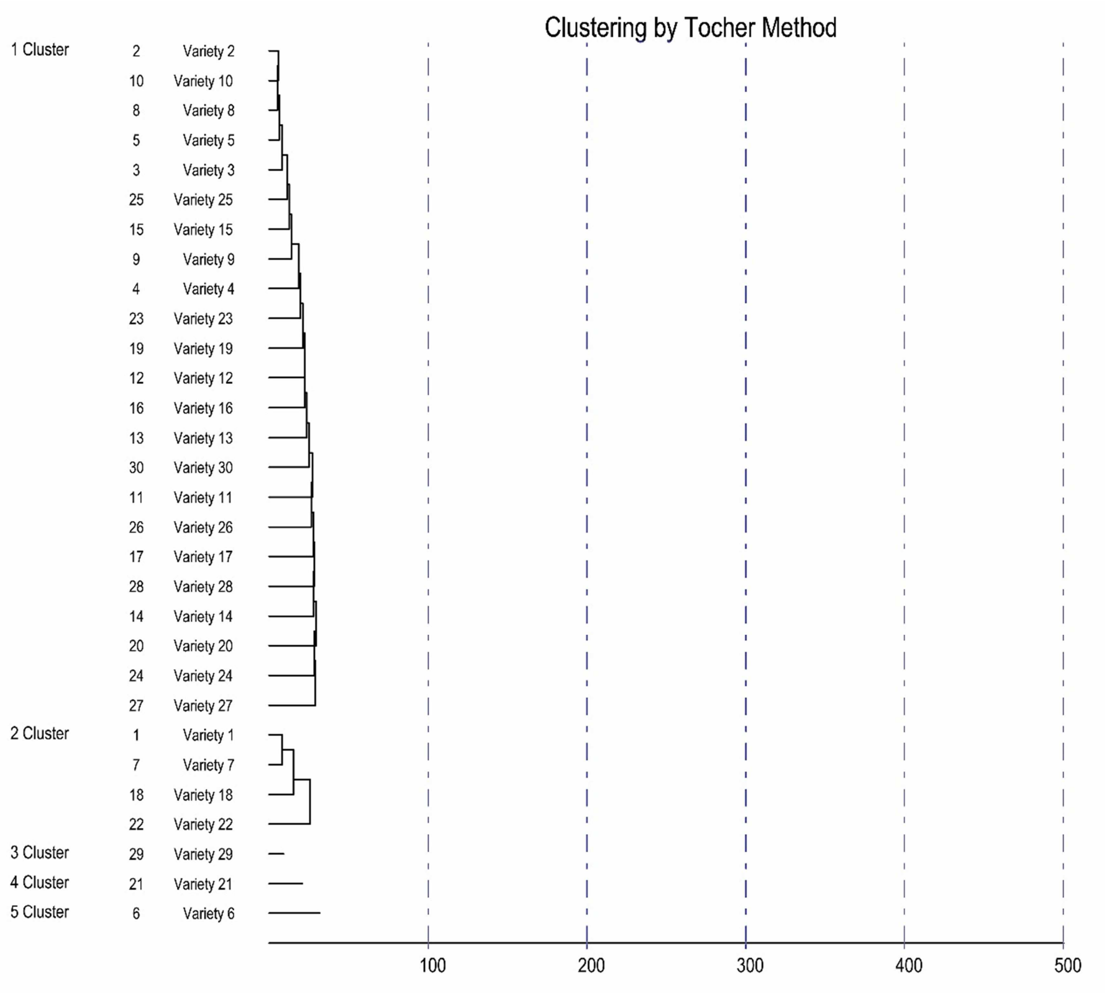

Fig. 4.3 Grouping of genotypes into clusters using Tocher's method under inorganic fertilizer management.

Variety 1	: Dharani	Variety 11	: ICG-15309	Variety 21	: K-7 bold
Variety 2	: ICG-10185	Variety 12	: ICG-2738	Variety 22	: K-9
Variety 3	: ICG-10384	Variety 13	: ICG-3992	Variety 23	: Kalahasti
Variety 4	: ICG-111	Variety 14	: ICG-434	Variety 24	: Narayani
Variety 5	: ICG-11322	Variety 15	: ICG-5236	Variety 25	: TCGS-1157
Variety 6	: ICG-11651	Variety 16	: ICG-7153	Variety 26	: TCGS-1653
Variety 7	: ICG-11687	Variety 17	: K-1789	Variety 27	: TCGS-1696
Variety 8	: ICG-13099	Variety 18	: TCGS-1631	Variety 28	: TCGS-1678
Variety 9	: ICG-13723	Variety 19	: K-1805	Variety 29	: TCGS-1330
Variety 10	: ICG-13787	Variety 20	: K-6	Variety 30	: TCGS-1630

Table 4.14 Inter and Intra cluster (diagonal) average of D^2 and D values (in parentheses) of 30 groundnut genotypes under inorganic fertilizer management

Cluster	I	II	III	IV	V
I	**69.69** **(8.35)**	129.45 (11.38)	130.88 (11.44)	141.06 (11.88)	164.92 (12.84)
II		**69.96** **(8.36)**	307.58 (17.54)	257.50 (16.05)	289.54 (17.02)
III			**0.00** **(0.00)**	89.54 (9.46)	244.80 (15.65)
IV				**0.00** **(0.00)**	179.84 (13.41)
V					**0.00** **(0.00)**

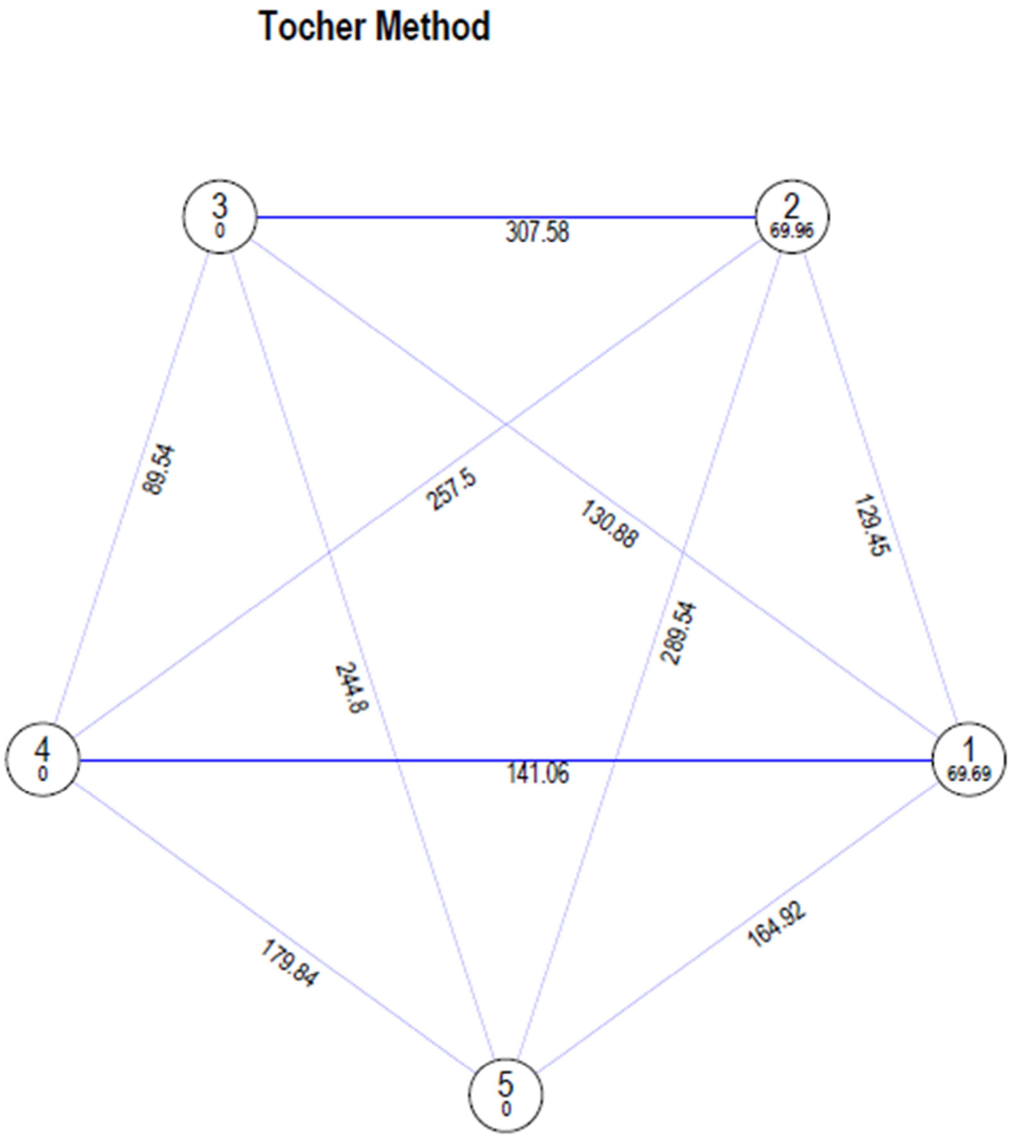

Fig. 4.4 Average inter and intra cluster distances under inorganic fertilizer management.

Table 4.15 Cluster means for 22 characters in groundnut under inorganic fertilizer management

Cluster No.	DF	DM	PH	NPB	NPEGP	NMP	NIMP	NPP	100KW	SP	HI	KYPP	SLA 40	SLA 60	SCMR 40	SCMR 60	RWC	OIL	PRO	CAR	TFA	PYPP
I	33.42	96.23	43.85	4.69	22.78	12.33	1.77	14.06	42.21	57.18	36.72	7.95	188.25	183.40	37.90	38.19	75.66	47.19	25.52	17.17	0.84	13.86
II	30.75	97.83	56.42	4.32	29.70	16.22	2.15	18.28	41.62	61.96	40.17	10.33	173.26	173.12	36.72	40.08	74.89	47.46	25.90	15.00	0.95	16.44
III	36.33	98.00	35.67	6.07	19.93	12.53	1.73	13.93	47.13	61.71	37.06	11.30	219.66	159.76	39.67	39.07	68.33	45.30	26.05	16.00	0.79	18.35
IV	30.00	92.67	38.91	5.87	22.13	13.87	0.93	14.80	50.21	59.55	41.58	10.66	223.74	229.91	37.53	42.00	78.73	45.15	26.20	22.50	1.73	17.76
V	27.33	99.00	35.27	3.87	27.27	14.80	1.80	16.27	45.07	64.98	41.42	8.98	195.13	149.73	39.93	38.47	87.73	49.05	25.70	7.00	1.04	14.04
General mean	31.57	96.75	42.02	4.96	24.36	13.95	1.68	15.47	45.25	61.08	39.39	9.84	200.01	179.18	38.35	39.56	77.07	46.83	25.87	15.53	1.07	16.09

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height
NPB : Number of primary branches per plant
NPEGP: Number of pegs per plant
NMP : Number of mature pods per plant

NIMP : Number of immature pods per plant
NPP : Number of pods per plant
100 KW : Hundred kernel weight
SP : Shelling percentage
HI : Harvest index
KYPP : Kernel yield per plant

SLA 40 : Specific leaf area at 40 DAS
SLA 60 : Specific leaf area at 60 DAS
SCMR 40 : SCMR at 40 DAS
SCMR 60 : SCMR at 60 DAS
RWC : Relative water content

OIL : Oil content
PRO : Protein content
CAR : Carbohydrate content
TFA : Total free amino acids
PYPP : Pod yield per plant

Cluster means for days to 50% flowering ranged from 27.33 days (V) to 36.33 days (III) with a general mean of 31.57 days. Clusters II, IV and V showed lower cluster means than the general mean.

Cluster means for days to maturity ranged from 92.67 days (IV) to 99 days (V) with a general mean 96.75 days. Clusters I and IV showed early maturity than the general mean.

Plant height exhibited general cluster mean of 42.02 cm. It varied from 35.27 cm (V) to 56.42 cm (II). Clusters I and II had higher cluster means than the general mean.

Number of primary branches recorded cluster means from 3.87 (V) to 6.07 (III) with a general mean of 4.96. More number of primary branches than the general mean were exhibited by the clusters III and IV.

Cluster means for number of pegs per plant ranged from 19.93 (III) to 29.70 (II). Cluster II and V exhibited higher cluster mean than the general mean (24.36).

Number of mature pods in clusters varied from 12.33 (I) to 16.22 (II) with a general mean of 13.95. Cluster II and V exhibited more number of mature pods than the general mean.

Number of immature pods recorded a general cluster mean of 1.68 which ranged from 0.93 (IV) to 2.15 (II). Clusters IV showed lower number of immature pods than the general mean

Cluster means for number of pods per plant varied from 13.93 (III) to 18.28 (II) with a general mean of 15.47. Cluster II and V recorded more number of pods per plant then the general mean.

Hundred kernel weight recorded highest cluster mean in cluster IV (50.21 g) and lowest in cluster II (41.62 g) with a general mean of 45.25 g. Higher values than the general mean were recorded in clusters III and IV

Shelling percentage exhibited the general cluster mean of 61.08% which ranged from 57.18% (I) to 64.18% (V). Clusters II, III and V showed higher shelling percentage than the general cluster mean.

Cluster means for harvest index varied from 36.72% (I) to 41.58 (IV). Clusters II, IV and V exhibited higher values of cluster means than the general cluster mean (39.39%).

Cluster means for kernel yield per plant varied from 7.95 g (I) to 11.30 g (III) with a general mean of 9.84. Clusters II, III and IV recorded higher kernel yield per plant than the general cluster mean.

SLA at 40 DAS recorded cluster means from 173.26 (II) to 223.74 (IV) with a general mean of 200.01. Clusters I, II and V have desirable genotypes with low SLA at 40 DAS than the general cluster mean.

Clusters II, III and V exhibited lower values of cluster means than the general cluster mean (179.18) for SLA at 60 DAS. The cluster means are varied from 149.73 (V) to 229.91 (IV).

Cluster means for SCMR at 40 DAS varied from 36.72 (II) to 39.93 (V) with a general mean of 38.35. Higher values than the general cluster means were recorded in clusters III, V.

SCMR at 60 DAS showed cluster means from 38.19 (I) to 42 (IV) with a general mean of 39.56. Clusters II and IV recorded higher values of cluster means than the general cluster mean.

Relative water content exhibited a general cluster mean of 77.07% which ranged from 68.33% (III) to 87.73% (V). Clusters IV and V showed higher relative water content than the general cluster mean.

Cluster means for oil content varied from 45.15% (IV) to 49.05% (V) with a general mean of 46.83%. Higher oil content than the general cluster mean was recorded for the clusters I, II and V.

Cluster means for protein content ranged from 25.52% (I) to 26.2% (IV). Clusters II, III and IV exhibited higher protein content than the general cluster mean (25.87%).

Carbohydrate content was highest in cluster IV (22.50%) and lowest in cluster V (7%) with a general mean of 15.53%. Clusters I, III and IV showed higher carbohydrate content than the general cluster mean.

Total free amino acids exhibited the cluster means from 0.79 (III) to 1.73 (IV) with a general mean of 1.07. Higher values of total free amino acids than the general cluster mean was recorded for clusters IV.

Cluster means for pod yield per plant was varied from 13.86 g (I) to 18.35 g (III) with a general mean of 16.09 g. Clusters II, III and IV recorded higher pod yield per plant than the general cluster mean.

4.4.2.3 Relative contribution of individual character towards divergence

The contribution of various characters towards genetic divergence under inorganic fertilizer managements were presented in Table 4.16. The character plant height was ranked first for 192 times and contributed more towards genetic divergence (44.14%) followed by oil content (21.61%), days to 50% flowering (8.51%), SCMR at 60 DAS (6.44%), carbohydrate content (5.06%), total free amino acids (4.60%), protein content (2.76%), hundred kernel weight (1.15%), number of pegs per plant (0.92%), number of pods per plant (0.92%), SCMR at 40 DAS (0.92%), relative water content

Table 4.16 Relative contribution of 22 characters to genetic diversity under inorganic fertilizer management

S. No.	Character	No. of times ranked first	% contribution
1	Days to 50 % flowering	37	8.51
2	Days to maturity	1	0.23
3	Plant height	192	44.14
4	Number of primary branches per plant	0	0.00
5	Number of pegs per plant	4	0.92
6	Number of mature pods per plant	2	0.46
7	Number of immature pods per plant	1	0.23
8	Number of pods per plant	4	0.92
9	Hundred kernel weight	5	1.15
10	Shelling percent	1	0.23
11	Harvest index	1	0.23
12	Kernel yield per plant	0	0.00
13	SLA at 40 DAS	0	0.00
14	SLA at 60 DAS	3	0.69
15	SCMR at 40 DAS	4	0.92
16	SCMR at 60 DAS	28	6.44
17	Relative water content	4	0.92
18	Oil content	94	21.61
19	Protein content	12	2.76
20	Carbohydrate content	22	5.06
21	Total free amino acids	20	4.60
22	Pod yield per plant	0	0.00

(0.92%), SLA at 60 DAS (0.69), number of mature pods per plant (0.46), days to maturity (0.23%), number of immature pods per plant (0.23%) and harvest index (0.23%).

The characters number of primary branches, kernel yield per plant, SLA at 40 DAS and pod yield per plant showed no contribution towards genetic divergence.

Based on cluster distance and cluster means the crosses K-9 X ICG-11651, Dharani X ICG-11651, K-9 X K-7 bold, Dharani X K-7 bold and TCGS-1330 X ICG-11651 can be recommended for the development of transgressive segregants for yield and water use efficiency traits under inorganic fertilizer management.

4.5 CHARACTER ASSOCIATION ANALYSIS

Yield is a complex character which depends on various component characters hence direct selection for yield would not be a reliable approach. Correlation coefficient is one of the statistical measure which reveals the degree and direction of relationship among the characters. Hence in order to assess the direction and magnitude of association existing between pod yield and other component characters phenotypic correlation coefficients were calculated under both organic and inorganic fertilizer managements.

4.5.1 Correlation between Pod Yield and its Component Traits under Organic Fertilizer Management

The phenotypic correlation coefficient of pod yield per plant with days to 50% flowering, days to maturity, number of primary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, number of pods per plant, hundred kernel weight, shelling percentage, harvest index, kernel yield per plant, SLA at 40 DAS, SLA at 60 DAS, SCMR at 40 DAS, SCMR at 60 DAS, relative water content, oil content, protein content, carbohydrate content and total free amino acids were presented in Table 4.17

Pod yield per plant showed highly significant positive correlation with kernel yield per plant (r = 0.978) followed by number of mature pods per plant (r = 0.808), number of pods per plant (r = 0.756), number of pegs per plant (r = 0.588), harvest index (r = 0.449), SCMR at 40 DAS (r = 0.405), number of primary branches per plant (r = 0.397), hundred kernel weight (r = 0.353), days to 50% flowering (r = 0.302) and SCMR at 60 DAS (r = 0.231).

This indicates that selection for high kernel yield per plant, more number of mature pods per plant, number of pods per plant, number of pegs per plant, number of primary branches per plant, high harvest index, hundred kernel weight and having high water use efficiency will lead to increase in pod yield per plant.

Significant positive correlation of pod yield per plant with days to 50% flowering, number of pods per plant, number of mature pods per plant, harvest index, hundred kernel weight and kernel yield per plant was earlier reported by Manjubhargavi *et al.* (2016a) and Aparna *et al.* (2017b). Manjubhargavi *et al.* (2016a) also reported significant positive correlation of number of primary branches per plant with pod yield per plant.

Significant negative correlation of pod yield per plant was reported with plant height (r = -0.283), SLA at 60 DAS (r = -0.361) and oil content (r = -0.408). Significant negative correlation of pod yield per plant with oil content was in accordance with the results of Manjubhargavi *et al.* (2016a).

Non-significant positive correlation is recorded between pod yield per plant with days to maturity (r = 0.128), number of immature pods per plant (r = 0.069), shelling percentage (r = 0.097), protein content (r = 0.191) and carbohydrate content (r = 0.128) whereas non-significant negative

Table 4.17. Phenotypic correlation coefficients among pod yield and its components in groundnut under organic fertilizer management

	DM	PH	NPB	NPEGP	NMP	NIMP	NPP	100KW	SP	HI	KYPP	SLA40	SLA60	SCMR 40	SCMR 60	RWC	OIL	PRO	CAR	TFA	PYPP
DF	0.220*	-0.158	0.244*	0.053	0.209*	-0.053	0.174	0.213*	-0.069	-0.090	0.268*	-0.136	-0.308**	0.315**	0.031	-0.126	-0.355**	0.057	-0.000	-0.084	0.302**
DM		0.110	0.194	0.216*	0.251*	0.070	0.243*	0.039	-0.045	-0.260*	0.119	-0.321**	0.005	0.276**	0.387**	0.374**	-0.076	-0.076	0.186	0.136	0.128
PH			-0.113	-0.136	-0.229*	-0.018	-0.222*	-0.201	-0.149	-0.431**	-0.291**	0.092	0.001	-0.251*	-0.228*	-0.021	0.173	-0.342**	0.171	-0.107	-0.283**
NPB				0.375**	0.424**	0.121	0.408**	-0.005	-0.063	-0.194	0.367**	-0.219*	0.005	0.216*	0.165	0.033	-0.426**	-0.109	0.032	0.138	0.397**
NPEGP					0.853**	0.545**	0.900**	-0.071	0.003	0.184	0.561**	-0.078	-0.042	0.259*	0.165	0.090	-0.203	-0.047	0.093	-0.027	0.588**
NMP						0.299**	0.976**	0.067	-0.020	0.299**	0.767**	-0.157	-0.153	0.310**	0.201	0.107	-0.219*	-0.016	0.089	-0.012	0.808**
NIMP							0.494**	-0.341**	-0.181	-0.160	0.026	0.078	0.124	-0.004	0.111	0.063	0.049	-0.306**	-0.094	0.199	0.069
NPP								-0.011	-0.050	0.242*	0.710**	-0.120	-0.116	0.290**	0.209*	0.110	-0.188	-0.069	0.057	0.035	0.756**
100KW									0.458**	0.372**	0.421**	-0.085	-0.385**	0.386**	0.095	-0.100	-0.322**	0.438**	0.012	-0.037	0.353**
SP										0.359**	0.293**	0.002	-0.425**	0.308**	0.084	-0.070	-0.272**	0.475**	0.078	-0.109	0.097
HI											0.505**	-0.017	-0.175	0.254*	0.225*	0.013	-0.048	0.361**	0.028	-0.090	0.449**
KYPP												-0.114	-0.435**	0.457**	0.242*	-0.038	-0.441**	0.270*	0.153	-0.028	0.978**
SLA40													-0.061	-0.412**	-0.182	-0.239*	-0.060	0.051	-0.026	-0.002	-0.101
SLA60														-0.289**	-0.107	0.060	0.368**	-0.290**	0.085	0.193	-0.361**
SCMR 40															0.404**	0.015	-0.505**	0.325**	0.151	-0.019	0.405**
SCMR 60																0.215*	-0.273**	0.160	0.021	0.198	0.231*
RWC																	0.273**	-0.257*	-0.025	-0.035	-0.028
OIL																		-0.367**	-0.221*	-0.082	-0.408**
PRO																			0.167	0.029	0.191
CAR																				0.016	0.128
TFA																					-0.002

*, ** Significance at 5% and 1% level respectively

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height
NPB : Number of primary branches per plant
NPEGP: Number of pegs per plant
NMP : Number of mature pods per plant

NIMP : Number of immature pods per plant
NPP : Number of pods per plant
100 KW : Hundred kernel weight
SP : Shelling percentage
HI : Harvest index
KYPP : Kernel yield per plant

SLA 40 : Specific leaf area at 40 DAS
SLA 60 : Specific leaf area at 60 DAS
SCMR 40 : SCMR at 40 DAS
SCMR 60 : SCMR at 60 DAS
RWC : Relative water content

OIL : Oil content
PRO : Protein content
CAR : Carbohydrate content
TFA : Total free amino acids
PYPP : Pod yield per plant

correlation is observed with SLA at 40 DAS (r = -0.101), relative water content (r = -0.028) and total free amino acids (r = -0.002).

4.5.2 Inter-correlation among Traits under Organic Fertilizer Management

4.5.2.1 Days to 50% flowering

Days to 50% flowering showed highly significant and positive association with SCMR at 40 DAS (r = 0.315) followed by kernel yield per plant (r = 0.268), number of primary branches per plant (r = 0.244), days to maturity (r = 0.220), hundred kernel weight (r = 0.213) and number of mature pods per plant (r = 0.209). It also showed significant negative correlation with SLA at 60 DAS (r = -0.308) and oil content (r = -0.355). This indicates that selection for early flowering genotypes will decrease the duration of crop but it may also reduce the kernel yield per plant, hundred kernel weight and number of mature pods per plant.

Significant positive correlation of days to 50% flowering with number of primary branches per plant, number of mature pods per plant, kernel yield per plant and significant negative correlation with oil content was earlier reported by Manjubhargavi *et al.* (2016a). Aparna *et al.* (2017b) reported significant positive correlation of days to 50% flowering with days to maturity, number of mature pods per plant, hundred kernel weight and kernel yield per plant.

4.5.2.2 Days to maturity

Significant positive correlation of day to maturity is observed with SCMR at 60 DAS (r = 0.387), relative water content (r = 0.374), SCMR at 40 DAS (r = 0.276), number of mature pods per plant (r = 0.251) and number of pods per plant (r = 0.243), number of pegs per plant (r = 0.216) indicating that selection of early maturity genotypes will lead to decrease in number of pegs per plant, number of mature pods per plant and number of pods per plant and water use efficiency of genotypes.

It also exhibited significant negative correlation with harvest index (r = -0.260) and SLA at 40 DAS (r = -0.321) indicating that selection for early maturing genotypes will increase the harvest index.

Significant positive correlation of days to maturity with number of mature pods per plant and number of pods per plant was earlier reported by Aparna *et al.* (2017b).

4.5.2.3 Plant height

Plant height exhibited significant negative correlation with number of pods per plant (r = -0.222), SCMR at 60 DAS (r = -0.228), number of mature pods per plant (r = -0.229), SCMR at 40 DAS (r = -0.251), kernel yield per plant (r = -0.291), protein content (r = -0.342) and harvest index (r = -0.431).

This indicates that selection for taller plants will reduce number of pods per plant, number of mature pods per plant, kernel yield per plant, harvest index and water use efficiency of genotypes.

Aparna *et al.* (2017b) observed significant negative correlation of plant height with harvest index.

4.5.2.4 Number of primary branches per plant

Number of primary branches showed significant positive correlation with number of mature pods per plant (r = 0.424), number of pods per plant (r = 0.408), number of pegs per plant (0.375), kernel yield per plant (r = 0.367) and SCMR at 40 DAS (r = 0.216) and it also showed significant negative correlation with SLA at 40 DAS (r = -0.219) and oil content (r = -0.426).

Selection for more number of primary branches will increase number of pegs per plant, number of mature pods per plant, number of pods per plant, kernel yield per plant.

Significant positive correlation for number of primary branches per plant with number of pegs per plant, number of mature pods per plant, number of pods per plant and kernel yield per plant was recorded by Aparna *et al.* (2017b). Majubhargavi *et al.* (2016a) also reported significant positive correlation of number of primary branches per plant with number of mature pods per plant and kernel yield per plant.

4.5.2.5 Number of pegs per plant

Significant positive correlation is recorded for number of pegs per plant with number of pods per plant (r = 0.900), number of mature pods per plant (r = 0.853), kernel yield per plant (r = 0.561), number of immature pods per plant (r = 0.545) and SCMR at 40 DAS (r = 0.259)

This indicates that selection for more number of pegs per plant will lead to increase in number of pods per plant, number of immature pods per plant, number of mature pods per plant and kernel yield per plant.

Significant positive correlation of number of pegs per plant with number of mature pods per plant, number of immature pods per plant and number of pods per plant was in accordance with the results of Aparna *et al.* (2017b)

4.5.2.6 Number of mature pods per plant

Number of mature pods per plant showed highly significant positive correlation with number of pods per plant (r = 0.976) followed by kernel yield per plant (r = 0.767), SCMR at 40 DAS (r = 0.310), number of immature pods per plant (r = 0.299) and harvest index (r = 0.299). It also showed significant negative correlation with oil content (r = -0.219)

This indicates that selection for more number of mature pods per plant will increase the kernel yield per plant.

Significant positive correlation of number of mature pods per plant with harvest index and kernel yield per plant was earlier reported by Manjubhargavi *et al.* (2016a) and Aparna *et al.* (2017b) while significant negative correlation was observed with oil content by Manjubhargavi *et al.* (2016a).

4.5.2.7 Number of immature pods per plant

Number of immature pods per plant recorded significant positive correlation with number of pods per plant (r = 0.494) whereas it recorded significant negative correlation with hundred kernel weight (r = -0.341) and protein content (r = -0.306) indicating that increase in more number of immature pods per plant will reduce the hundred kernel weight.

Significant positive correlation of number of immature pods per plant with number of pods per plant was reported by Aparna *et al.* (2017b).

4.5.2.8 Number of pods per plant

Highly significant positive correlation is observed for number of pods per plant with kernel yield per plant (r = 0.710) followed by SCMR at 40 DAS (r = 0.290), harvest index (r = 0.242) and SCMR at 60 DAS (r = 0.209). This indicates that selection for more number of pods per plant will increase the kernel yield per plant and harvest index.

Significant positive correlation of number of pods per plant with harvest index and kernel yield per plant was earlier reported by Manjubhargavi *et al.* (2016a) and Aparna *et al.* (2017b).

4.5.2.9 Hundred kernel weight

Significant positive correlation is observed for hundred kernel weight with shelling percentage (r = 0.458), protein content (r = 0.438), kernel yield per plant (r = 0.421), SCMR at 40 DAS (r = 0.386) and harvest index (r =0.372) whereas it showed significant negative correlation with SLA at 60 DAS (r = -0.385) and oil content (r = -0.322).

Selection for high hundred kernel weight will increase the shelling percentage, kernel yield per plant and harvest index.

Manjubhargavi *et al.* (2016a) reported significant positive correlation of hundred kernel weight with protein content and kernel yield per plant. Aparna *et al.* (2017b) also reported significant positive correlation of hundred kernel weight with shelling percentage, harvest index and kernel yield per plant.

4.5.2.10 Shelling percentage

Shelling percentage showed highly positive significant correlation with protein content (r = 0.475) followed by harvest index (r = 0.359), SCMR at 40 DAS (r = 0.308) and kernel yield per plant (r = 0.293). It also showed significant negative correlation with SLA at 60 DAS (r = -0.425) and oil content (r = -0.272). This indicates that increase in shelling percentage will lead to increase in harvest index and kernel yield per plant.

Similar reports of significant positive correlation of shelling percentage with harvest index and kernel yield per plant was earlier reported by Manjubhargavi *et al.* (2016a) and Aparna *et al.* (2017b)

4.5.2.11 Harvest index

Significant positive correlation was observed for harvest index with kernel yield per plant (r = 0.505), protein content (r = 0.361), SCMR at 40

DAS (r = 0.254) and SCMR at 60 DAS (r = 0.225) indicating that selection for high harvest index will increase the kernel yield per plant.

4.5.2.12 Kernel yield per plant

Kernel yield per plant exhibited significant positive correlation with SCMR at 40 DAS (r = 0.457), protein content (r = 0.270) and SCMR at 60 DAS (r = 0.242) whereas it exhibited significant negative correlation with SLA at 60 DAS (r = -0.435) and oil content (r = -0.441).

Significant positive correlation of kernel yield with SCMR and negative correlation with SLA indicates that selection for high water use efficiency i.e., for low SLA and high SCMR will lead to increase in kernel yield per plant.

Significant positive correlation of kernel yield per plant with protein content was in accordance with the results of Manjubhargavi et al. (2016a)

4.5.2.13 SLA at 40 DAS

SLA at 40 DAS recorded significant negative correlation with SCMR at 40 DAS (r = -0.412) and relative water content (r = -0.239)

4.5.2.14 SLA at 60 DAS

SLA at 60 DAS exhibited significant positive correlation with oil content (r = 0.368) and significant negative correlation with SCMR at 40 DAS (r = -0.289) and protein content (r = -0.290)

4.5.2.15 SCMR at 40 DAS

Significant positive correlation was observed for SCMR at 40 DAS with SCMR at 60 DAS (r = 0.404) whereas it showed significant negative correlation with oil content (r = -0.505)

4.5.2.16 SCMR at 60 DAS

SCMR at 60 DAS showed significant positive correlation with relative water content (r = 0.215) and significant negative correlation with oil content (r = -0.273)

4.5.2.17 Relative water content

Significant positive correlation was observed for relative water content with oil content (r = 0.273) and significant negative correlation was observed with protein content (r = -0.257)

4.5.2.18 Oil content

Oil content exhibited significant negative correlation with carbohydrate content (r = -0.221) and protein content (r = -0.367) indicating that selection for genotypes with high oil content may decrease the carbohydrate and protein content.

Plant height showed significant negative correlation with number of mature pod per plant, number of pods per plant, harvest index and kernel yield per plant indicating that selection of taller plants may adversely affect these traits.

Significant positive correlation was observed for number of pegs per plant with number of mature pods per plant, number of immature pods per plant, number of pods per plant and kernel yield per plant suggesting that selection for more number of pegs per plant would lead to increase in these characters.

SCMR at 40 DAS and SCMR at 60 DAS were significantly and positively associated with number of pods per plant, harvest index and kernel yield per plant suggesting that selection of genotypes with high SCMR will lead to improvement in these characters.

SLA at 60 DAS showed significant negative association with pod yield per plant indicating that selection for genotypes with low SLA will result in high yield coupled with high water use efficiency types. The trait oil content also significantly negatively correlated with pod yield per plant suggesting that selection for high oil content may decrease the yield in groundnut.

The traits days to 50% flowering, number of primary branches per plant, number of mature pods per plant, number of pods per plant, hundred kernel weight, harvest index, kernel yield per plant, SLA at 40 DAS, SCMR at 40 DAS and SCMR at 60 DAS exhibited significant positive correlation with pod yield per plant indicating that selection can be carried out for these characters to increase pod yield per plant.

4.5.3 Correlation between Pod Yield and its Component Traits under Inorganic Fertilizer Management

The phenotypic correlation coefficients obtained for all the 22 characters under inorganic fertilizer management are furnished in Table 4.18.

Pod yield per plant exhibited highly significant and positive correlation with kernel yield per plant (r = 0.947) followed by number of mature pods per plant (r = 0.829), number of pods per plant (r = 0.796), number of pegs per plant (r = 0.703), harvest index (r = 0.472), SCMR at 40 DAS (r = 0.359), number of primary branches (r = 0.295) and SCMR at 60 DAS (r = 0.265).

This indicates that selection for the above characters *viz.*, kernel yield per plant, number of mature pods per plant, number of pods per plant, harvest index, SCMR at 40 DAS, number of pegs per plant, number of primary branches and SCMR at 60 DAS leads to simultaneous improvement of pod yield and water use efficiency.

Table 4.18. Phenotypic correlation coefficients among pod yield and its components in groundnut under inorganic fertilizer management

	DM	PH	NPB	NPEGP	NMP	NIMP	NPP	100K	SP	HI	KYPP	SLA40	SLA60	SCMR 40	SCMR 60	RWC	OIL	PRO	CAR	TFA	PYPP
DF	0.046	-0.298^{**}	0.251^{*}	-0.062	-0.116	-0.065	-0.117	0.220^{*}	0.095	-0.282^{**}	0.044	-0.049	-0.396^{**}	0.452^{**}	-0.156	-0.418^{**}	-0.468^{**}	-0.151	0.405^{**}	-0.294^{**}	0.022
DM		0.166	0.027	0.211^{*}	0.141	0.16	0.147	0.06	0.104	0.07	0.119	-0.175	-0.092	0.135	-0.007	-0.063	-0.011	-0.084	-0.204	-0.155	0.089
PH			-0.295^{**}	0.149	0.14	0.213^{*}	0.159	-0.088	0.084	0.044	0.062	-0.2	0.026	-0.310^{**}	-0.225^{*}	0.067	0.300^{**}	0.099	-0.15	-0.054	0.023
NPB				0.059	0.143	0.021	0.138	0.11	-0.081	-0.164	0.226^{*}	-0.088	0.005	0.141	0.141	-0.164	-0.329^{**}	-0.085	0.245^{*}	0.041	0.295^{**}
NPEGP					0.898^{**}	0.540^{**}	0.927^{**}	-0.176	0.166	0.259^{*}	0.702^{**}	-0.250^{*}	-0.215^{*}	0.211^{*}	0.383^{**}	0.067	-0.097	-0.051	-0.018	0.127	0.703^{**}
NMP						0.396^{**}	0.983^{**}	-0.131	0.210^{*}	0.357^{**}	0.820^{**}	-0.198	-0.153	0.167	0.364^{**}	0.103	-0.137	-0.063	-0.088	0.093	0.829^{**}
NIMP							0.523^{**}	-0.326^{**}	-0.098	-0.231^{*}	0.137	-0.198	-0.067	-0.081	0.107	-0.004	0.161	-0.337^{**}	-0.087	0.048	0.177
NPP								-0.185	0.145	0.300^{**}	0.772^{**}	-0.221^{*}	-0.141	0.145	0.356^{**}	0.096	-0.098	-0.094	-0.08	0.094	0.796^{**}
100KW									0.349^{**}	0.17	0.166	0.137	-0.235^{*}	0.237^{*}	-0.021	-0.123	-0.267^{*}	0.289^{**}	-0.002	0.11	0.069
SP										0.191	0.475^{**}	0.021	-0.309^{**}	0.218^{*}	0.025	0.004	-0.199	0.018	-0.141	0.123	0.179
HI											0.496^{**}	0.295^{**}	-0.02	0.127	0.268^{*}	0.299^{**}	-0.002	0.294^{**}	-0.226^{*}	0.029	0.472^{**}
KYPP												-0.044	-0.267^{*}	0.386^{**}	0.257^{*}	0.049	-0.353^{**}	0.069	-0.068	0.131	0.947^{**}
SLA40													0.235^{*}	0.047	-0.062	0.244^{*}	-0.181	0.118	0.073	0.121	-0.056
SLA60														-0.578^{**}	0.210^{*}	0.112	0.163	0.097	0.012	0.2	-0.208^{*}
SCMR 40															-0.156	-0.14	-0.478^{**}	-0.054	0.144	-0.057	0.359^{**}
SCMR 60																-0.021	-0.038	0.177	-0.118	0.315^{**}	0.265^{*}
RWC																	0.321^{**}	-0.037	-0.353^{**}	0.033	0.055
OIL																		-0.152	-0.524^{**}	-0.297^{**}	-0.325^{**}
PRO																			0.062	0.258^{*}	0.062
CAR																				0.071	-0.041
TFA																					0.100

*, ** Significance at 5% and 1% level respectively

DF	: Days to 50% flowering	NIMP	: Number of immature pods per plant	SLA 40	: Specific leaf area at 40 DAS	OIL	: Oil content
DM	: Days to maturity	NPP	: Number of pods per plant	SLA 60	: Specific leaf area at 60 DAS	PRO	: Protein content
PH	: Plant height	100 KW	: Hundred kernel weight	SCMR 40	: SCMR at 40 DAS	CAR	: Carbohydrate content
NPB	: Number of primary branches per plant	SP	: Shelling percentage	SCMR 60	: SCMR at 60 DAS	TFA	: Total free amino acids
NPEGP	: Number of pegs per plant	HI	: Harvest index	RWC	: Relative water content	PYPP	: Pod yield per plant
NMP	: Number of mature pods per plant	KYPP	: Kernel yield per plant				

Similar kind of results *viz.,* significant positive correlation of pod yield per plant with number of mature pods per plant and kernel yield per plant was reported by Shashikumara *et al.* (2015), Trivikrama *et al.* (2017) and Mahesh *et al.* (2018b). Significant positive correlation for kernel yield per plant with pod yield per plant was also recorded by Jayalakshmi and Reddy (2003), Giri (2009), Rao *et al.* (2014), Surbhi *et al.* (2016) and Mukesh and Lal (2017). Significant positive correlation of harvest index with pod yield per plant was reported by Jayalakshmi and Reddy (2003), Shahshikumara *et al.* (2015), Tulsiram *et al.* (2017a). Trivikrama *et al.* (2017) reported significant positive correlation of number of pegs per plant and number of pods per plant with pod yield per plant. Rao *et al.* (2014) and Shashikumara *et al.* (2015) also observed significant positive correlation of pod yield with number of pods per plant. Significant positive correlation with of pod yield per plant with SCMR was observed by Shashikumara *et al.* (2015).

Pod yield per plant also exhibited significant negative correlation with SLA at 60 DAS (r = -0.208) and oil content (r = -0.325). Similar kind of results i.e., significant negative correlation for oil content with pod yield was also reported by Tulsiram *et al*. (2017a) and for SLA was reported by Shashikumara *et al*. (2015).

Non-significant positive correlation of pod yield per plant is observed with shelling percentage (r = 0.179), number of immature pods per plant (r = 0.177), days to maturity (r = 0.089), hundred kernel weight (r = 0.069), protein content (r = 0.062), relative water content (r = 0.055), plant height (r = 0.023), days to 50% flowering (r = 0.022) and total free amino acids (r = 0.100).

The above results for plant height and hundred kernel weight were in accordance with the results of Mahesh *et al.* (2018a). Non-significant positive correlation of days to 50% flowering, days to maturity, plant height and shelling percentage with pod yield was also reported by Trivikram *et al.* (2017).

It also exhibited non-significant negative correlation with SLA at 40 DAS (r = -0.056) and carbohydrate content (r = -0.041).

4.5.4 Inter-correlation among Traits under Inorganic Fertilizer Management

4.5.4.1 Days to 50% flowering

Days to 50% flowering exhibited significant positive correlation with SCMR at 40 DAS (r = 0.452), carbohydrate content (r = 0.405), number of primary braches per plant (r = 0.251) and hundred kernel weight (r = 0.220) whereas significant negative correlation is observed with oil content (r = -0.468), relative water content (r = -0.418), SLA at 60 DAS (r = -0.396), plant height (r = -0.298), total free amino acids (r = -0.294) and harvest index (r = -0.282) indicating that selection for early flowering types will lead to increase in water use efficiency.

Significant positive correlation of days to 50% flowering with hundred kernel weight was recorded by Giri (2009) and Surbhi *et al.* (2017). Significant negative correlation with plant height and oil content was reported by Mahesh et al. (2018b). Parameshwarappa *et al.* (2005) reported significant positive correlation of days to 50% flowering with number of primary branches per plant.

4.5.4.2 Days to maturity

Days to maturity showed significant positive correlation with number of pegs per plant (r = 0.211) indicating that selection for short duration genotypes will lead to decrease in number of pegs per plant.

4.5.4.3 Plant height

Plant height exhibited significant positive correlation with oil content (r = 0.300) and number of immature pods per plant (r = 0.213) whereas it showed significant negative correlation with SCMR at 40 DAS (r = -0.310), number of primary branches (r = -0.295) and SCMR at 60 DAS (r = -0.225) indicating that selection for taller plants leads to decrease in water use efficiency of genotypes.

Significant negative correlation of plant height with oil content was also noticed by Mahesh *et al.* (2018b).

4.5.4.4 Number of primary branches

Number of primary branches recorded significant positive correlation with carbohydrate content (r = 0.245), kernel yield per plant (r = 0.226) and significant negative correlation with oil content (r = -0.329). This indicates that selection for more number of primary branches will lead to increase in kernel yield per plant.

4.5.4.5 Number of pegs per plant

Highly significant positive correlation is observed for number of pegs per plant with number of pods per plant (r = 0.927), number of mature pods per plant (r = 0.898), kernel yield per plant (r = 0.702), number of immature pods per plant (r = 0.540), SCMR at 60 DAS (r = 0.383), harvest index (r = 0.259) and SCMR at 40 DAS (r = 0.211) whereas it showed significant negative correlation with SLA at 60 DAS. This indicates that selection for the genotypes having more number of pegs per plant will lead to increase in number of pods per plant, number of mature pods per plant, number of immature pods per plant harvest index and kernel yield per plant.

Significant positive correlation of number of pegs per plant with number of pods per plant and number of mature pods per plant was recorded by Trivikrama *et al*. (2017).

4.5.4.6 Number of mature pods per plant

Significant positive correlation was observed for number of mature pods per plant with number of pods per plant (r = 0.983), kernel yield per plant (r = 0.820), number of immature pods per plant (r = 0.396), SCMR at 60 DAS (r = 0.364), harvest index (r = 0.357) and shelling percentage (r = 0.210). This indicates that selection for more number of mature pods per plant will lead to increase in number of pods per plant, kernel yield per plant, number of immature pods per plant, harvest index and shelling percentage.

Bhargavi *et al.* (2017), Tulsiram *et al.* (2017a), Yusuf *et al*. (2017b) and Mahesh *et al.* (2018b) also reported significant positive correlation of number of mature pods per plant with kernel yield per plant. Tulsiram *et al.* (2017a) recorded significant positive correlation of number of mature pods per plant with harvest index.

4.5.4.7 Number of immature pods per plant

Number of immature pods per plant recorded significant positive correlation with number of pods per plant (r = 0.523) and significant negative correlation with protein content (r = -0.337), hundred kernel weight (r = -0.326) and harvest index (r = -0.231) indicating that increase in number of immature pods per plant will decrease the hundred kernel weight and harvest index.

Significant negative relationship of number of immature pods per plant with hundred kernel weight was also reported by Mahesh *et al.* (2018b).

4.5.4.8 Number of pods per plant

Significant positive correlation is observed for number of pods per plant with kernel yield per plant (r = 0.772), SCMR at 60 DAS (r = 0.356) and harvest index (r = 0.300) whereas it exhibited significant negative correlation with SLA at 40 DAS (r = -0.221).

This indicates that selection for more number of pods will lead to increase in kernel yield per plant and harvest index.

Significant positive correlation of number of pods per plant with kernel yield per plant was reported by Rao *et al*. (2014), Rathod *et al.* (2015), Surbhi *et al*. (2016).

4.5.4.9 Hundred kernel weight

Under inorganic fertilizer management significant positive correlation was recorded for hundred kernel weight with shelling percentage (r = 0.349), protein content (r = 0.289) and SCMR at 40 DAS (r = 0.237). It also exhibited significant negative correlation with oil content (r = -0.267) and SLA at 60 DAS (r = -0.235).

Similar results of significant negative correlation with oil content was reported by Tulsiram *et al. (*2017a). Significant positive correlation of hundred kernel weight with shelling percentage was recorded by Channayya *et al*. (2011)

4.5.4.10 Shelling percentage

Shelling percentage exhibited significant positive correlation with kernel yield per plant (0.475), SCMR at 40 DAS (r = 0.218) and significant negative correlation with SLA at 60 DAS (r = -0.309) indicating that increase in shelling percentage will lead to increase in kernel yield per plant.

Channayya *et al.* (2011), Rathod *et al.* (2015) and Mahesh *et al.* (2018b) recorded significant positive correlation of shelling percentage with kernel yield per plant.

4.5.4.11 Harvest index

Highly significant positive correlation was recorded for harvest index with kernel yield per plant (r = 0.496) followed by relative water content (r = 0.299), SLA at 40 DAS (r = 0.295), protein content (r = 0.294) and SCMR at 60 DAS (r = 0.268). It also exhibited significant negative correlation with carbohydrate content (r = -0.226). Significant positive correlation of harvest index with kernel yield per plant indicates that selection for genotypes with high harvest index will lead to increase in kernel yield per plant.

Significant positive correlation of harvest index with kernel yield per plant was earlier reported by Jayalaksmi and Reddy (2003).

4.5.4.12 Kernel yield per plant

Kernel yield per plant exhibited significant positive correlation with SCMR at 40 DAS (r = 0.386), SCMR at 60 DAS (r = 0.257) and significant negative correlation with oil content (r = -0.353) and SLA at 60 DAS (r = -0.267) indicating that selection for high water use efficiency genotypes leads to increase in kernel yield per plant.

Significant negative correlation of kernel yield per plant with oil content was also reported by Tulsiram *et al*. (2017a). Significant positive correlation with SCMR at 40 DAS was recorded by Bhargavi *et al.* (2017).

4.5.4.13 SLA at 40 DAS

SLA at 40 DAS recorded significant and positive correlation with SLA at 60 DAS (r = 0.235) and relative water content (r = 0.244)

4.5.4.14 SLA at 60 DAS

Significant negative correlation was registered for SLA at 60 DAS with SCMR at 40 DAS (r = -0.578) and significant positive correlation with SCMR at 60 DAS (r = 0.210)

4.5.4.15 SCMR at 40 DAS

SCMR at 40 DAS exhibited significant negative correlation with oil content (r = -0.478)

4.5.4.16 SCMR at 60 DAS

Significant positive correlation was observed for SCMR at 60 DAS with total free amino acids (r = 0.315)

4.5.4.17 Relative water content

Relative water content recorded significant positive correlation with oil content (r = 0.321) and significant negative correlation with carbohydrate content (r = -0.353)

4.5.4.18 Oil content

Oil content exhibited significant negative correlation with carbohydrate content (r = -0.524) and total free amino acids (r = -0.297) indicating that selection for genotypes with high oil content may decrease the carbohydrate content and total free amino acids.

4.5.4.19 Protein content

Significant positive correlation was recorded for protein content with total free amino acids (r = 0.258)

Number of pegs per plant showed significant positive correlation with number of mature pods per plant, number of immature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SCMR at 40

DAS and SCMR at 60 DAS indicated that selection for more number of pegs per plant will lead to improvement in these characters.

The characters number of mature pods per plant, number of pods per plant and harvest index were significantly positively correlated with each other and also with kernel yield per plant suggesting that increase in these characters will lead to increase in kernel yield per plant.

Pod yield per plant showed significant positive association with number of primary branches, number of pegs per plant, number of mature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SCMR at 40 DAS and SCMR at 60 DAS. These results indicating that improvement of these characters leads to increase in pod yield per plant.

Comparison of correlation between pod yield per plant and its component traits under organic and inorganic fertilizer managements were presented in Table 4.19. The yield traits number of primary branches per plant, number of pegs per plant, number of mature pods per plant, number of pods per plant, harvest index, kernel yield per plant, showed significant positive correlation with pod yield per plant in both organic and inorganic fertilizer managements indicating that selection for these traits improve pod yield per plant in both organic and inorganic fertilizer managements.

Water use efficiency traits like SCMR at 40 DAS and SCMR at 60 DAS exhibited significant positive association with pod yield per plant whereas SLA at 60 DAS showed significant negative correlation with pod yield per plant in both organic and inorganic fertilizer managements indicating that selection of genotypes for high SCMR and low SLA may improve the pod yield per plant along with water use efficiency of genotypes. Pod yield per plant showed significant negative correlation with plant height only under organic fertilizer management indicating that

Table 4.19 Comparison of correlations between pod yield and its component traits under organic and inorganic fertilizer managements

	Organic	Inorganic
Pod yield per plant		
Significant positive	Days to 50% flowering, number of primary branches, number of pegs per plant, number of mature pods per plant, number of pods per plant, hundred kernel weight, harvest index, kernel yield per plant, SCMR at 40 DAS and SCMR at 60 DAS	Number of primary branches per plant, number of pegs per plant, number of mature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SCMR at 40 DAS and SCMR at 60 DAS
Significant negative	Plant height, SLA at 60 DAS and oil content	SLA at 60 DAS and oil content
Days to 50% flowering		
Significant positive	Days to maturity, number of pegs per plant, number of primary branches, number of mature pods per plant, hundred kernel weight, kernel yield per plant and SCMR at 40 DAS	Number of primary branches, hundred kernel weight, SCMR at 40 DAS and carbohydrate content
Significant negative	SLA at 60 DAS and oil content	Plant height, harvest index, SLA at 60 DAS, relative water content, oil content and total free amino acids
Days to maturity		
Significant positive	Number of mature pods per plant, number of pods per plant, SCMR at 40 DAS, SCMR at 60 DAS and relative water content	Number of pegs per plant
Significant negative	Harvest index and SLA at 40 DAS	--
Plant height		
Significant positive	--	Number of immature pods per plant and oil content
Significant negative	Number of mature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SCMR at 40 DAS, SCMR at 60 DAS and protein content	Number of primary branches, SCMR at 40 DAS and SCMR at 60 DAS

Number of primary branches		
Significant positive	Number of pegs per plant, number of mature pods per plant, number of pods per plant, kernel yield per plant and SCMR at 40 DAS	Kernel yield per plant and carbohydrate content
Significant negative	SLA at 40 DAS and oil content	Oil content
Number of pegs per plant		
Significant positive	Number of mature pods per plant, number of immature pods per plant, number of pods per plant, kernel yield per plant and SCMR at 40 DAS	Number of mature pods per plant, number of immature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SCMR at 40 DAS and SCMR at 60 DAS
Significant negative	--	--
Number of mature pods per plant		
Significant positive	Number of immature pods per plant, number of pods per plant, harvest index, kernel yield per plant and SCMR at 40 DAS	Number of immature pods per plant, number of pods per plant, shelling percentage, harvest index, kernel yield per plant and SCMR at 60 DAS
Significant negative	Oil content	--
Number of immature pods per plant		
Significant positive	Number of pods per plant	Number of pods per plant
Significant negative	Hundred kernel weight and protein content	Hundred kernel weight, harvest index and protein content
Number of pods per plant		
Significant positive	Harvest index, kernel yield per plant, SCMR at 40 DAS and SCMR at 60 DAS	Harvest index, kernel yield per plant and SCMR at 60 DAS
Significant negative		SLA at 40 DAS
Hundred kernel weight		
Significant positive	Shelling percentage, harvest index, kernel yield per plant, SCMR at 40 DAS and protein content	Shelling percentage, SCMR at 40 DAS and protein content
Significant negative	SLA at 60 DAS, oil content	SLA at 60 DAS and oil content
Shelling percentage		
Significant positive	Harvest index, kernel yield per plant, SCMR at 40 DAS and protein content	Kernel yield per plant, SCMR at 40 DAS
Significant negative	SLA at 60 DAS, oil content	SLA at 60 DAS

Harvest index		
Significant positive	Kernel yield per plant, SCMR at 40 DAS, SCMR at 60 DAS and protein content	Kernel yield per plant, SLA at 40 DAS, SCMR at 60 DAS, relative water content and protein content
Significant negative	--	Carbohydrate content
Kernel yield per plant		
Significant positive	SCMR at 40 DAS, SCMR at 60 DAS and protein content	SCMR at 40 DAS and SCMR at 60 DAS
Significant negative	SLA at 60 DAS and oil content	SLA At 60 DAS and oil content
SLA at 40 DAS		
Significant positive	--	SLA at 60 DAS and relative water content
Significant negative	SCMR at 40 DAS and relative water content	--
SLA at 60 DAS		
Significant positive	Oil content	--
Significant negative	SCMR at 40 DAS and protein content	SCMR at 40 DAS and SCMR at 60 DAS
SCMR at 40 DAS		
Significant positive	SCMR at 60 DAS	--
Significant negative	Oil content	Oil content
SCMR at 60 DAS		
Significant positive	Relative water content	Total free amino acids
Significant negative	Oil content	--
Relative water content		
Significant positive	Oil content	Oil content
Significant negative	Protein content	Carbohydrate content
Oil content		
Significant positive	--	--
Significant negative	Carbohydrate content and protein content	Carbohydrate content and total free amino acids
Protein content		
Significant positive	--	Total free amino acids
Significant negative	--	--

selection for short genotypes under organic conditions will improve the pod yield per plant.

Plant height showed significant negative association with SCMR at 40 DAS and SCMR at 60 DAS under both organic and inorganic fertilizer managements indicating that selection of short genotypes would increase water use efficiency under both environments. Significant positive association of number of pegs per plant with number of mature pods per plant, number of immature pods per plant, number of pods per plant and kernel yield per plant was observed in both organic and inorganic conditions. Hence selection for more number of pegs would lead to improvement in these characters under both management conditions.

Hundred kernel weight exhibited significant positive correlation with protein content and significant negative correlation with oil content under organic and inorganic fertilizer managements indicating that selection for hundred kernel weight would lead to increase in protein content but oil content would be decreased. Under both organic and inorganic conditions kernel yield per plant showed significant positive association with SCMR at 40 DAS, SCMR at 60 DAS and significant negative association with SLA at 60 DAS and oil content. It indicates that selection for high kernel yield per plant would increase water use efficiency of genotypes but there would be decrease in oil content. It also showed significant positive association with protein content only under organic management indicating that selection for high kernel yield per plant in organic conditions would lead to improvement in protein content.

Oil content showed significant negative association with carbohydrate content, protein content under organic management and with carbohydrate content and total free amino acids under inorganic management. It indicates that selection for high oil content would lead to decrease in carbohydrate content under both fertilizer managements and also decrease in protein content under organic and total free amino acids under inorganic fertilizer managements. Protein content showed significant positive association with total free amino acids under inorganic fertilizer management indicating that selection for high protein content would lead to simultaneous improvement for total free amino acids under inorganic management.

4.6 PATH COEFFICIENT ANALYSIS

Path coefficient analysis splits the correlation coefficient into direct and indirect effects of various yield components on pod yield per plant and helps in effective measurement of direct and indirect causes of association between the characters. The path coefficient analysis was carried out for the characters which showed significant correlations with pod yield per plant under organic and inorganic fertilizer managements.

4.6.1 Direct and Indirect Effects under Organic Fertilizer Management

Using pod yield per plant as dependent variable and twelve characters viz., days to 50% flowering, plant height, number of primary branches, number of pegs per plant, number of mature pods, number of pods per plant, hundred kernel weight, harvest index, kernel yield per plant, SLA at 60 DAS, SCMR at 40 DAS, SCMR at 60 DAS and oil content as independent variables path analysis was carried out and results were presented in Table 4.20 and path diagram was presented in Fig 5.

4.6.1.1 Days to 50% flowering

Days to 50% flowering showed negligible and positive direct effect on pod yield per plant (0.0556). The moderate positive indirect effect through kernel yield per plant (0.2549), and negligible positive indirect effects through number of pods per plant (0.0226), number of mature pods (0.0113), oil content (0.0036), harvest index (0.0026) and SCMR at 60 DAS

Table 4.20 Phenotypic path coefficients for pod yield and its significantly correlated components in groundnut under organic fertilizer management

	DF	PH	NPB	NPEGP	NMP	NPP	100 KW	HI	KYPP	SLA 60	SCMR 40	SCMR 60	OIL	PYPP
DF	**0.0556**	-0.0011	-0.0020	-0.0049	0.0113	0.0226	-0.0027	0.0026	0.2549	-0.0215	-0.0166	0.0004	0.0036	0.3022**
PH	-0.0088	**0.0073**	0.0009	0.0124	-0.0125	-0.0289	0.0026	0.0126	-0.2768	0.0000	0.0132	-0.0028	-0.0017	-0.2826**
NPB	0.0136	-0.0008	**-0.0082**	-0.0341	-0.0230	0.0531	0.0001	0.0057	0.3490	0.0003	-0.0114	0.0021	0.0043	0.3967**
NPEGP	0.0030	-0.0010	-0.0031	**-0.0907**	0.0463	0.1169	0.0009	-0.0054	0.5334	-0.0029	-0.0137	0.0021	0.0020	0.5880**
NMP	0.0116	-0.0017	-0.0035	-0.0774	**0.0543**	0.1268	-0.0009	-0.0087	0.7298	-0.0107	-0.0164	0.0025	0.0022	0.8081**
NPP	0.0096	-0.0016	-0.0033	-0.0816	0.0530	**0.1300**	0.0001	-0.0071	0.6757	-0.0081	-0.0153	0.0026	0.0019	0.7559**
100 KW	0.0118	-0.0015	0.0000	0.0064	0.0037	-0.0014	**-0.0127**	-0.0108	0.4004	-0.0268	-0.0203	0.0012	0.0032	0.3532**
HI	-0.0050	-0.0031	0.0016	-0.0167	0.0163	0.0315	-0.0047	**-0.0292**	0.4807	-0.0122	-0.0134	0.0028	0.0005	0.4490**
KYPP	0.0149	-0.0021	-0.0030	-0.0508	0.0417	0.0923	-0.0054	-0.0147	**0.9517**	-0.0303	-0.0241	0.0030	0.0044	0.9776**
SLA 60	-0.0171	0.0000	0.0000	0.0038	-0.0083	-0.0150	0.0049	0.0051	-0.4139	**0.0697**	0.0152	-0.0013	-0.0037	-0.3607**
SCMR 40	0.0175	-0.0018	-0.0018	-0.0235	0.0169	0.0377	-0.0049	-0.0074	0.4351	-0.0201	**-0.0527**	0.0050	0.0051	0.4050**
SCMR 60	0.0017	-0.0017	-0.0013	-0.0150	0.0109	0.0272	-0.0012	-0.0066	0.2307	-0.0075	-0.0213	**0.0125**	0.0028	0.2313*
OIL	-0.0197	0.0013	0.0035	0.0184	-0.0119	-0.0244	0.0041	0.0014	-0.4199	0.0257	0.0266	-0.0034	**-0.0101**	-0.4085**

*, ** significance at 5 % and 1 % level respectively

Residual effect = 0.1624

DF : Days to 50% flowering
PH : Plant height
NPB : Number of primary branches per plant
NPEGP : Number of pegs per plant
NMP : Number of mature pods per plant
NPP : Number of pods per pod
100 KW : Hundred kernel weight
HI : Harvest index
KYPP : Kernel yield per plant
SLA 60 : Specific leaf area at 60 DAS
SCMR 40 : SCMR at 40 DAS
SCMR 60 : SCMR at 60 DAS
OIL : Oil content

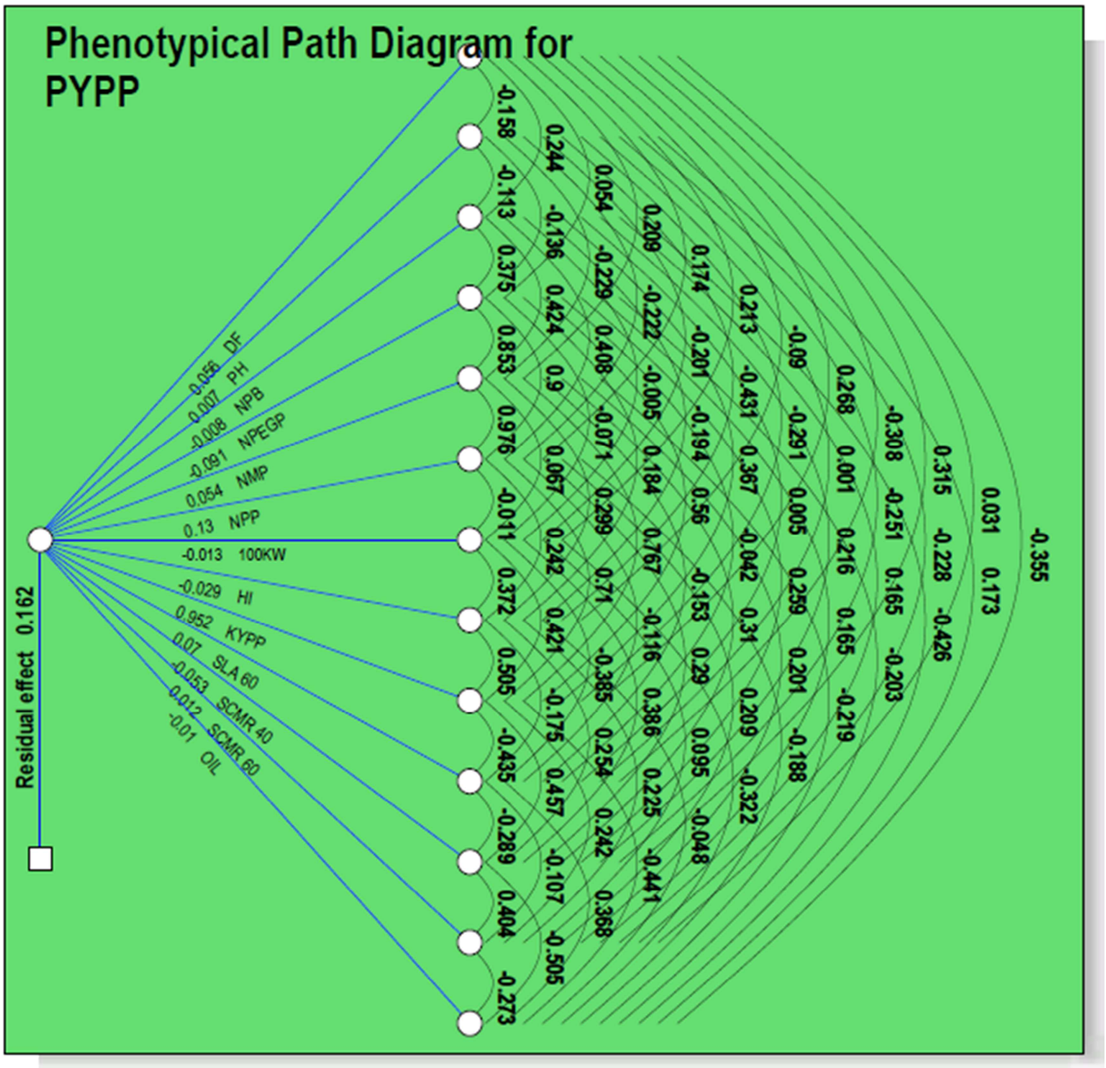

Fig. 4.5 Phenotypic path diagram for pod yield and its significantly correlated component traits under organic fertilizer management.

(0.0004) resulted in significant correlation coefficient (0.3022) higher than its direct effect on pod yield.

4.6.1.2 Plant height

Plant height recorded lowest positive direct effect (0.0073) on pod yield per plant. The significant negative correlation of plant height (-0.2826) on pod yield per plant was through its negative indirect effects via kernel yield per plant (-0.2768), number of pods per plant (-0.0289), number of mature pods per plant (-0.0125), days to 50% flowering (-0.0088), SCMR at 60 DAS (-0.0028) and oil content (-0.0017).

4.6.1.3 Number of primary branches

Number of primary branches per plant exhibited negligible negative direct effect on pod yield per plant (-0.0082). The high positive indirect effect through kernel yield per plant (0.3490) and negligible positive indirect effects through number of pods per plant (0.0531), days to 50% flowering (0.0136), oil content (0.0043), SCMR at 60 DAS (0.0021), SLA at 60 DAS (0.0003), and hundred kernel weight (0.0001) resulted in significant positive correlation (0.3967) of plant height with pod yield per plant.

4.6.1.4 Number of pegs per plant

Number of pegs per plant showed negative direct effect (-0.0907) on pod yield per plant. But its positive correlation (0.5880) on pod yield per plant is due to its negative indirect effects through kernel yield per plant (0.5334), number of pods per plant (0.1169), number of mature pods per plant (0.0463), days to 50% flowering (0.0030), SCMR at 60 DAS (0.0021), oil content (0.0020) and hundred kernel weight (0.0009).

On contrary Aparna *et al*. (2017b) observed positive direct effect of number of pegs per plant on pod yield per plant.

4.6.1.5 Number of mature pods per plant

Number of mature pods per plant recorded negligible positive direct effect (0.0543) on pod yield per plant. But its high positive indirect effect through kernel yield per plant (0.7298) and low positive indirect effects through number of pods per plant (0.1268), days to 50% flowering (0.0116), and SCMR at 60 DAS (0.0025) and oil content (0.0020) resulted in significant positive correlation (0.8081) with pod yield per plant.

Aparna *et al*. (2017b) also observed positive direct effect of number of mature pods per plant on pod yield per plant.

4.6.1.6 Number of pods per plant

Number of pods per plant exhibited positive direct effect (0.1300) on pod yield per plant. The significant positive correlation of number of pods per plant (0.7559) with pod yield per plant was through positive indirect effects via kernel yield per plant (0.6757), number of mature pods per plant (0.0530), SCMR at 60 DAS (0.0026), oil content (0.0019), days to 50% flowering (0.0096), and hundred kernel weight (0.0001).

On contrary Aparna *et al.* (2017b) recorded negative direct effect of number of pods per plant on pod yield per plant.

4.6.1.7 Hundred kernel weight

Hundred kernel weight showed negligible negative direct effect (-0.0127) on pod yield per plant. The positive indirect effects through kernel yield per plant (0.4004), days to 50% flowering (0.0118), number of pegs per plant (0.0064), number of mature pods per plant (0.0037), oil content (0.0032) and SCMR at 60 DAS (0.0012) resulted in significant positive correlation with pod yield per plant (0.3532).

4.6.1.8 Harvest index

Harvest index recorded negative direct effect (-0.0292) on pod yield per plant. The significant positive correlation (0.4490) with pod yield per plant is through positive indirect effects via kernel yield per plant (0.4807), number of pods per plant (0.0315), number of mature pods per plant (0.0163), SCMR at 60 DAS (0.0028), number of primary branches (0.0016) and oil content (0.0005).

Negative direct effect of harvest index on pod yield per plant was also recorded by Aparna *et al.* (2017b).

4.6.1.9 Kernel yield per plant

Kernel yield per plant showed highest positive direct effect (0.9517) on pod yield per plant. Positive indirect effects of kernel yield per plant through number of pods per plant (0.0923), number of mature pods per plant (0.0417), days to 50% flowering (0.0149), oil content (0.0030) and SCMR at 60 DAS (0.0030) also added to the highest significant positive correlation (0.9776) with pod yield per plant.

Similar kind of positive direct effect of kernel yield per plant on pod yield per plant was observed by Aparna *et al.* (2017b).

4.6.1.10 SLA at 60 DAS

SLA at 60 DAS showed low positive direct effect (0.0697) on pod yield per plant but its significant negative correlation (-0.3607) on pod yield per plant is due to negative indirect effects through kernel yield per plant (-0.4139), days to 50% flowering (-0.0171), number of pods per plant (-0.0150), number of mature pods per plant (-0.0083), oil content (-0.0037), SCMR at 60 DAS (-0.0013).

4.6.1.11 SCMR at 40 DAS

SCMR at 40 DAS exhibited negligible negative direct effect (-0.0527) on pod yield per plant. High positive indirect effect through kernel yield plant (0.4351) and negligible positive indirect effects through number of pods per plant (0.0377), days to 50% flowering (0.0175), number of mature pods per plant (0.0169), oil content (0.0051) and SCMR at 60 DAS (0.0050) resulted in significant positive correlation (0.4050) with pod yield per plant.

4.6.1.12 SCMR at 60 DAS

SCMR at 60 DAS recorded negligible positive direct effect (0.0125) with pod yield per plant. Its positive indirect effects through kernel yield per plant (0.2307), number of pods per plant (0.0272), number of mature pods per plant (0.0109), oil content (0.0028) and days to 50% flowering (0.0017) resulted in high significant positive correlation (0.2313) though its direct effect on pod yield per plant was negligible.

4.6.1.13 Oil content

Oil content showed negligible negative direct effect (-0.0101) on pod yield per plant. Its significant negative correlation (-0.4085) with pod yield per plant is due to its negative indirect effects through kernel yield per plant (-0.4199), number of pods per plant (-0.0244), days to 50% flowering (-0.0197), number of mature pods per plant (-0.0119) and SCMR at 60 DAS (-0.0034).

Under organic fertilizer management the residual effect was 0.1624 signifying the consideration of most of the characters in the study.

Under organic fertilizer management kernel yield per plant showed highest direct effect (0.9517) on pod yield per plant whereas other characters days to 50% flowering, plant height, number of primary branches, number of pegs per plant, number of mature pods, number of pods per plant, hundred kernel weight, harvest index, SLA at 60 DAS, SCMR at 40 DAS, SCMR at 60 DAS and oil content exhibited negligible direct effects on pod yield per plant.

The traits number of primary branches per plant, number of pegs per plant, number of mature pods per plant, number of pods per plant, hundred kernel weight, harvest index, SCMR at 40 DAS showed high positive indirect effects through kernel yield per plant on pod yield per plant. Hence under organic fertilizer management kernel yield per plant should be given importance in selection process.

4.6.2 Direct and Indirect Effects under Inorganic Fertilizer Management

Under inorganic fertilizer management path analysis was carried out using pod yield per plant as dependent variable and the traits number of primary branches, number of pegs per plant, number of mature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SLA at 60 DAS, SCMR at 40 DAS, SCMR at 60 DAS and oil content as independent variables and the results were furnished in Table 4.21 and path diagram was presented in Fig 6

4.6.2.1 Number of primary branches per plant

Number of primary branches per plant showed negligible positive direct effect (0.0974) on pod yield per plant but its significant positive correlation (0.2953) with pod yield per plant was due to its positive indirect effects through kernel yield per plant (0.1700), number of pods per plant (0.0691), SCMR at 40 DAS (0.0082) and SLA at 60 DAS (0.0002).

Positive direct effect of number of primary branches per plant on pod yield per plant was also reported by John *et al*. (2015).

Table 4.21 Path coefficients for pod yield and different yield attributes in 30 groundnut genotypes under inorganic fertilizer management

	NPB	NPEGP	NMP	NPP	HI	KYPP	SLA 60	SCMR 40	SCMR 60	OIL	PYPP
NPB	**0.0974**	-0.0080	-0.0277	0.0691	-0.0111	0.1700	0.0002	0.0082	-0.0021	-0.0007	0.2953**
NPEGP	0.0057	**-0.1348**	-0.1732	0.4635	0.0174	0.5272	-0.0089	0.0122	-0.0057	-0.0002	0.7031**
NMP	0.0140	-0.1211	**-0.1929**	0.4915	0.0241	0.6163	-0.0064	0.0097	-0.0055	-0.0003	0.8294**
NPP	0.0135	-0.1250	-0.1897	**0.4999**	0.0202	0.5802	-0.0059	0.0084	-0.0053	-0.0002	0.7960**
HI	-0.0160	-0.0349	-0.0689	0.1499	**0.0673**	0.3725	-0.0008	0.0074	-0.0040	0.0000	0.4723**
KYPP	0.0220	-0.0946	-0.1582	0.3861	0.0334	**0.7513**	-0.0111	0.0223	-0.0039	-0.0007	0.9465**
SLA 60	0.0005	0.0289	0.0296	-0.0703	-0.0014	-0.2006	**0.0416**	-0.0334	-0.0031	0.0003	-0.2080*
SCMR 40	0.0138	-0.0284	-0.0323	0.0723	0.0086	0.2899	-0.0241	**0.0578**	0.0023	-0.0010	0.3589**
SCMR 60	0.0137	-0.0516	-0.0702	0.1778	0.0181	0.1929	0.0087	-0.0090	**-0.0150**	-0.0001	0.2653*
OIL	-0.0321	0.0130	0.0265	-0.0488	-0.0001	-0.2652	0.0068	-0.0277	0.0006	**0.0021**	-0.3250**

*, ** significance at 5 % and 1 % level respectively

Residual effect = 0.2789

NPB : Number of primary branches per plant
NPP : Number of pods per pod
KYPP : Kernel yield per plant
SCMR 60 : SCMR at 60 DAS

NPEGP : Number of pegs per plant
100 KW : Hundred kernel weight
SLA 60 : Specific leaf area at 60 DAS
OIL : Oil content

NMP : Number of mature pods per plant
HI : Harvest index
SCMR 40: SCMR at 40 DAS
PYPP : Pod yield per plant

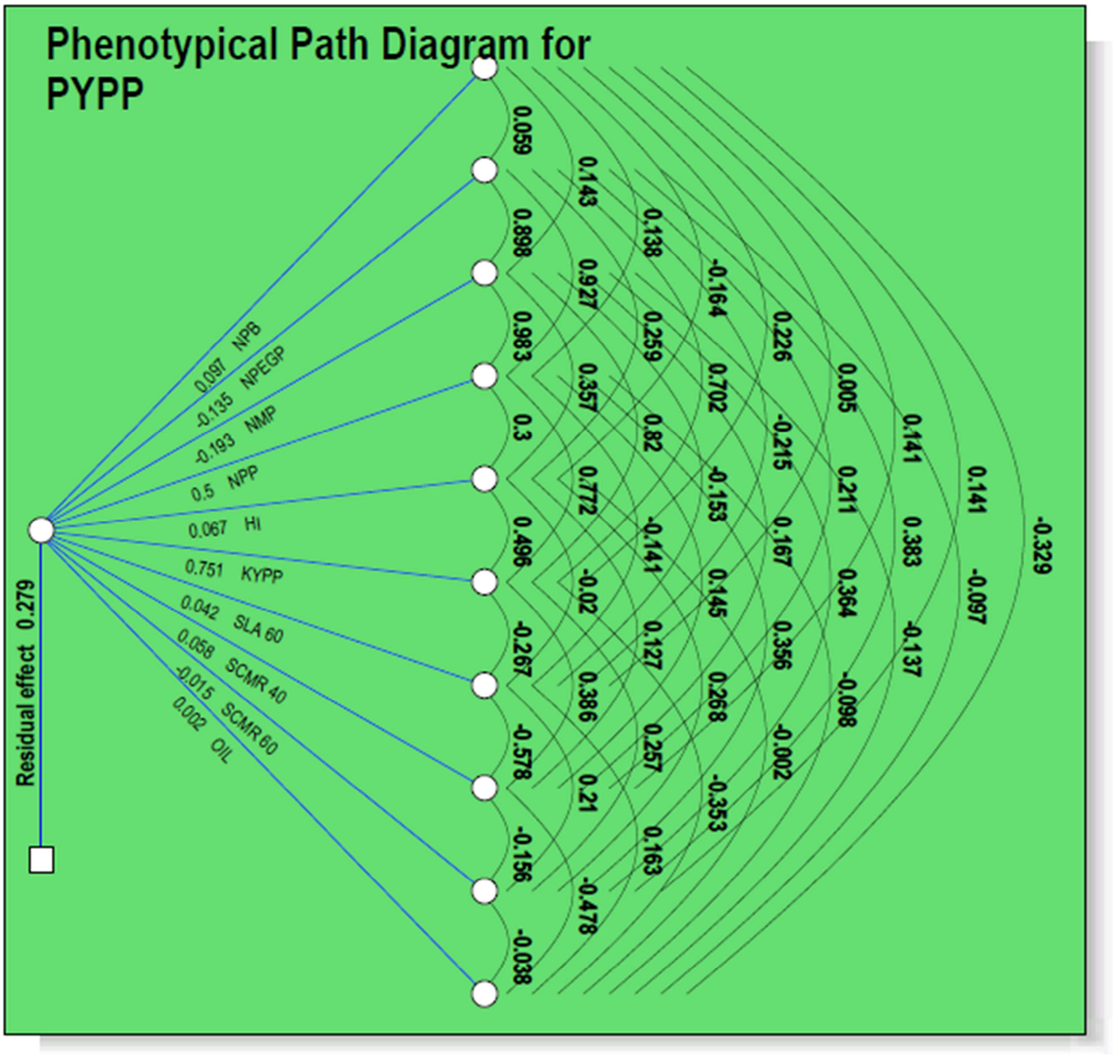

Fig. 4.6 Phenotypic path diagram for pod yield and its significantly correlated component traits under inorganic fertilizer management.

4.6.2.2 Number of pegs per plant

Number of pegs per plant exhibited negative direct effect (-0.1348) on pod yield per plant. Its significant positive correlation (0.7031) with pod yield per plant was due to its positive indirect effect through kernel yield per plant (0.5272), number of pods per plant (0.4635), harvest index (0.0174), SCMR at 40 DAS (0.0122), number of primary branches (0.0057).

On contrary positive direct effect of number of pegs per plant was reported by Trivikrama *et al*. (2017)

4.6.2.3 Number of mature pods per plant

A low negative direct effect was exhibited by number of mature pods per plant (-0.1929) on pod yield per plant. But its positive indirect effects through kernel yield per plant (0.6163), number of pods per plant (0.4915), harvest index (0.0241), number of primary branches (0.0140) and SCMR at 40 DAS (0.0097) resulted in its high positive correlation (0.8294) with pod yield per plant.

Negative direct effect of number of mature pods per plant was reported by Tulsiram *et al*. (2017a). On contrary positive direct effects were reported for number of mature pods per plant by Trivikrama *et al*. (2017) and Mahesh *et al*. (2018b)

4.6.2.4 Number of pods per plant

Number of pods per plant showed high positive direct effect (0.4999) on pod yield per plant. Its positive indirect effects through kernel yield per plant (0.5818), harvest index (0.0202), number of primary branches (0.0135) and SCMR at 40 DAS (0.0084) contributed for its high significant positive correlation (0.7960) with pod yield per plant.

On contrary negative direct effect of number of pods per plant was recorded by Trivikrama *et al.* (2017)

4.6.2.5 Harvest index

Harvest index exerted negligible positive direct effect (0.0673) on pod yield per plant. It's positive significant correlation (0.4723) than its direct effect is due to its positive indirect effects through kernel yield per plant (0.3725), number of pods per plant (0.1499) and SCMR at 40 DAS (0.0074). Positive direct effect of harvest index was reported by Giri (2009) and Yusuf *et al.* (2017b).

4.6.2.6 Kernel yield per plant

Kernel yield exhibited highest positive direct effect (0.7513) on pod yield per plant. The positive indirect effects of kernel yield through number of pods per plant (0.3861), harvest index (0.0334), SCMR at 40 DAS (0.0223) and number of primary branches (0.0220) were added to its high significant positive correlation (0.9465) with pod yield per plant.

Positive direct effects for kernel yield per plant was also reported by Giri (2009), John *et al.* (2015), Tulsiram *et al*. (2017a) and Mahesh *et al.* (2018b).

4.6.2.7 SLA at 60 DAS

SLA at 60 DAS showed negligible positive direct effect (0.0416) on pod yield per plant. Its significant negative correlation (-0.2080) with pod yield per plant is due to its negative indirect effects on pod yield per plant through kernel yield per plant (-0.2006), number of pods per plant (-0.0703), SCMR at 40 DAS (-0.0334), SCMR at 60 DAS (-0.0031) and harvest index (-0.0014).

4.6.2.8 SCMR at 40 DAS

A negligible positive direct effect (0.0578) was exhibited by SCMR at 40 DAS on pod yield per plant. But its significant positive correlation (0.3589) higher than its direct effect is contributed by its positive indirect effects through kernel yield per plant (0.2899), number of pods per plant (0.0723), number of primary branches (0.0138), harvest index (0.0086), and SCMR at 60 DAS (0.0023). On contrary negative direct effect of SCMR at 40 DAS was observed by Bhargavi *et al.* (2017)

4.6.2.9 SCMR at 60 DAS

SCMR at 60 DAS recorded negligible negative direct effect (-0.0150) on pod yield per plant. Its positive indirect effects through kernel yield per plant (0.1929), number of pods per plant (0.1778), harvest index (0.0181), number of primary branches (0.0137) and SLA at 60 DAS (0.0087) resulted in its significant positive correlation (0.2653) with the pod yield per plant. On contrary positive direct effect was reported by Bhargavi *et al.* (2017).

4.6.2.10 Oil content

Oil content showed negligible positive direct effect (0.0021) on pod yield per plant. But its significant negative correlation (-0.3250) with pod yield per plant was due to its negative indirect effects through kernel yield per plant (-0.2652), number of pods per plant (-0.0488), number of primary branches (-0.0321), SCMR at 40 DAS (-0.0277) and harvest index (-0.0001).

Positive direct effect of oil content on pod yield per plant was reported by Giri (2009), John *et al.* (2015), Rathod *et al.* (2015), Bhargavi *et al.* (2017) and Tulsiram *et al.* (2017a).

Under inorganic fertilizer management the residual effect observed was 0.2789 indicating the consideration of most of the characters in the study.

Under inorganic fertilizer management the traits kernel yield per plant and number of pods per plant exhibited high positive direct effects on pod yield per plant. The traits number of pegs per plant, number of mature pods per plant, number of pods per plant, harvest index and SCMR at 40 DAS showed moderate to high indirect effects through kernel yield per plant on pod yield per plant whereas the traits number of pegs per plant, number of mature pods per plant, kernel yield per plant showed moderate to high indirect effects through number of pods per plant. Hence in inorganic fertilizer managements kernel yield per plant and number of pods per plant can be considered as selection criteria.

Based on overall path analysis, it is concluded that kernel yield per plant registered high positive direct effect under both organic and inorganic fertilizer managements. Under inorganic fertilizer management number of pods per plant also exhibited high positive direct effect on pod yield per plant. These results specified that by keeping the other traits constant selection for kernel yield per plant under organic management and for kernel yield per plant and number of pods per plant under inorganic fertilizer management will result in an increased pod yield per plant under respective environments.

The overall analysis showed that the genotypes showed differential ranking performance for various characters under organic and inorganic conditions. Under organic conditions the genotypes TCGS-1157, ICG-10384, ICG-11322 and ICG-7153 showed better performance for pod yield per plant and kernel yield per plant. In addition to these, TCGS-1330 and Dharani registered high pod yield per plant and kernel yield per plant, respectively. Similarly, the genotype TCGS-1157 showed better performance for pod yield, water use efficiency and quality characters and the pod yield is on par with the highest pod yield under inorganic fertilizer management. Hence these genotypes should be further tested under organic fertilizer managements and can be recommended for organic farming or they can be utilized in further breeding programmes to develop suitable varieties for organic fertilizer managements. Further the crosses TCGS-1157 X K-7 bold, TCGS-1157 X K-1789, TCGS-1330 X K-7 bold and Dharani X K-7 bold can be utilized to get transgressive segregants for pod yield, water use efficiency and quality traits under organic fertilizer managements.

Under inorganic fertilizer management, ICG-7153, K-9, ICG-11322 and TCGS-1330 showed better performance for pod yield per plant and kernel yield per plant. Similarly, K-7 bold and Dharani also exhibited high pod yield per plant and kernel yield per plant respectively. Hence these genotypes can be further tested and utilized for development of varieties under inorganic fertilizer management. The crosses K-9 X ICG-11651, Dharani X ICG-11651, K-9 X K-7 bold, Dharani X K-7 bold and TCGS-1330 X ICG-11651 can be utilized for the development of transgressive segregants for pod yield and water use efficiency traits under inorganic fertilizer management. These experiments showed that the performance of genotypes is not same in organic and inorganic conditions indicating the need for development of varieties specifically for different conditions.

Chapter ~ V

Summary & Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation entitled “Genetic analysis of yield, yield components and water use efficiency traits under organic and inorganic fertilizer managements in groundnut (*Arachis hypogaea* L.)” was carried out in order to study the variability, heritability, genetic advance as per cent of mean, degree of association between yield and its component traits and to assess the direct and indirect contribution of each component character towards yield among the thirty groundnut genotypes under organic and inorganic fertilizer managements.

The two separate field experiments were conducted at dryland farm of Sri Venkateswara Agricultural College, Tirupati, Acharya N.G. Ranga Agricultural University during *Kharif* 2017 in a Randomized Block Design with three replications. Data was recorded on twenty two characters *viz.*, days to 50 % flowering, days to maturity, plant height (cm), number of primary branches, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, number of pods per plant, hundred kernel weight (g), shelling percentage (%), harvest index (%), kernel yield per plant (g), pod yield per plant (g), SLA at 40 DAS, SLA at 60 DAS, SCMR at 40 DAS and SCMR at 60 DAS, relative water content (%), oil content (%), protein content (%), carbohydrate content (%) and total free amino acids (mg g^{-1}).

Analysis of variance revealed significant differences for all the characters studied in both organic and inorganic fertilizer managements indicating the presence of ample amount of variability among the genotypes in both the environments. Observations of the mean data for yield and different yield contributing attributes under these two trials clearly showed change in ranking order of the genotypes for most of the characters. Under organic fertilizer management, the genotypes TCGS-1157, ICG-10384, ICG-11322, ICG-7153 and TCGS-1330 showed high mean performance for yield and its component traits. On contrary, the genotypes ICG-7153, K-9, ICG-11322, TCGS-1330 and Dharani showed high mean performance for yield and its components in inorganic fertilizer management. Considering both the trials, the genotypes ICG-7153, TCGS-1330 and ICG-11322 showed high *per se* performance for pod yield and its component traits.

High estimates of GCV and PCV were observed for number of immature pods per plant, kernel yield per plant, pod yield per plant and total free amino acids in both organic and inorganic fertilizer managements whereas number of pegs per plant, number of mature pods per plant and number of pods per plant showed high GCV and PCV in only inorganic fertilizer management indicating the presence of genetic variability for these traits and less influence of environment. Thus, direct selection for these traits would result in further improvement of pod yield under respective environment. Moderate GCV and high PCV were observed by number of pegs per plant, number of mature pods per plant and number of pods per plant in organic fertilizer management and by number of primary branches in inorganic fertilizer management. The characters days to 50% flowering, harvest index, SLA at 40 DAS and SCMR at 60 DAS exhibited low GCV and moderate PCV under organic fertilizer management whereas in inorganic fertilizer management the characters hundred kernel weight, harvest index and SLA at 40 DAS showed low GCV and moderate PCV.

Under organic fertilizer management moderate GCV and PCV were observed for plant height, number of primary branches, hundred kernel weight, SLA at 60 DAS and carbohydrate content whereas in inorganic fettilizer management it was observed for plant height, SLA at 60 DAS and carbohydrate content. The characters days to maturity, shelling percentage, SCMR at 40 DAS, relative water content, oil content and protein content exhibited low GCV and PCV in organic fertilizer management while in inorganic fertilizer management low GCV and PCV was observed for the characters days to 50% flowering, days to maturity, shelling percentage, SCMR at 40 DAS, SCMR at 60 DAS, relative water content, oil content and protein content which indicated little scope for further improvement of these characters through selection.

The characters total free amino acids and carbohydrate content exhibited high heritability coupled with high genetic advance as percent of mean under both organic and inorganic fertilizer managements whereas SLA at 60 DAS and hundred kernel weight showed high heritability coupled with high genetic advance as percent of mean in organic fertilizer management and plant height, number of pegs per plant, number of mature pods per plant, number of pods per plant and kernel yield per plant in inorganic fertilizer management. High heritability and moderate genetic advance as percent of mean was observed by days to 50% flowering in both organic and inorganic fertilizer management and by SCMR at 60 DAS in inorganic fertilizer management, respectively.

The characters oil content and protein content showed high heritability coupled with low genetic advance as percent of mean under both organic and inorganic fertilizer managements whereas days to maturity and shelling percentage in organic fertilizer management and SCMR at 40 DAS in inorganic fertilizer management showed high heritability coupled with low genetic advance as percent of mean. Moderate heritability coupled with moderate genetic advance as percent of mean was observed for number of primary braches per plant and harvest index in both organic and inorganic fertilizer managements and by plant height and SCMR at 60 DAS in organic and hundred kernel weight in inorganic fertilizer managements.

Moderate heritability coupled with high genetic advance as percent of mean was observed for the characters number of pegs per plant, kernel yield per plant, number of pods per plant, number of immature pods per plant, number of mature pods per plant and pod yield per plant under organic fertilizer management and by number of immature pods per plant, pod yield per plant and SLA at 60 DAS in inorganic fertilizer management. Moderate heritability coupled with low genetic advance as percent of mean was observed for the characters SCMR at 40 DAS in organic fertilizer management and for days to maturity and relative water content in inorganic fertilizer managements. The traits SLA at 40 DAS and relative water content in organic fertilizer management and shelling percentage and SLA at 40 DAS in inorganic fertilizer management exhibited low heritability coupled with low genetic advance as percent of mean.

Using D^2 analysis, 30 genotypes of groundnut were grouped into seven clusters in organic and five clusters in inorganic fertilizer managements. The characters oil content in organic and plant height in inorganic fertilizer management contributed more towards genetic divergence. Based on inter cluster distances the clusters III vs VII, IV vs VII and II vs VII in organic and the clusters II vs III, II vs V and II vs IV were found to be divergent. The crosses TCGS-1157 X K-7 bold, TCGS-1157 X K-1789, TCGS-1330 X K-7 bold and Dharani X K-7 bold under organic fertilizer management and K-9 X ICG-11651, Dharani X ICG-11651, K-9 X K-7 bold, Dharani X K-7 bold and TCGS-1330 X ICG-11651 under inorganic fertilizer management can be utilized for development of transgressive segregants for yield, water use efficiency and quality traits.

Character association analysis revealed that the characters viz., number of primary branches, number of pegs per plant, number of mature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SCMR at 40 DAS and SCMR at 60 DAS showed significant positive correlation with pod yield per plant under both organic and inorganic fertilizer managements. Thus, selection criterion if emphasized on the traits that showed significant positive association with pod yield per plant would result in improvement of pod yield under both the managements. On contrary the characters oil content and SLA at 60 DAS showed significant negative correlation with pod yield per plant.

Path analysis was conducted with the traits which were significantly correlated with pod yield per plant under both the fertilizer managements. It was observed that kernel yield per plant under organic fertilizer management and kernel yield per plant and number of pods per plant in inorganic fertilizer managements exhibited high positive direct effect on pod yield per plant.

Under organic fertilizer management the traits number of primary branches per plant, number of pegs per plant, number of mature pods per plant, number of pods per plant, hundred kernel weight, harvest index and SCMR at 40 DAS showed high positive indirect effects through kernel yield per plant on pod yield per plant whereas in inorganic fertilizer management the traits number of pegs per plant, number of mature pods per plant, number of pods per plant, harvest index and SCMR at 40 DAS showed moderate to high indirect effects through kernel yield per plant on pod yield per plant whereas the traits number of pegs per plant, number of mature pods per plant and kernel yield per plant showed moderate to high indirect effects through number of pods per plant. Hence more importance could be given for kernel yield per plant under organic fertilizer management and for kernel yield per plant and number of pods per plant under inorganic fertilizer management during selection for pod yield improvement in groundnut.

Overall analysis revealed that the genotypes TCGS-1157, ICG-10384, ICG-11322, ICG-7153, TCGS-1330 and Dharani under organic fertilizer management and the genotypes ICG-7153, K-9, ICG-11322, TCGS-1330, K-7 bold and Dharani under inorganic fertilizer management performed better for yield and other component characters. Hence these genotypes can be further utilized for development of varieties suitable for respective fertilizer managements.

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APPENDICES

Appendix A

JEEVAMRUTHAM PREPARATION

Materials required:

- Water : 200 litres
- Cow dung : 10 kg (Indigenious Cows, Preferably)
- Cow urine : 5 litres (Indigenious Cows, Preferably)
- Jaggery : 2 kg
- Flour of any pulse : 2 kg
- Soil from same land : one handfull.

Preparation process:

First 200 litres of water was taken in a drum and all the above mentioned ingredients were added and mixed well. Then the drum was covered with a gunny bag and the mixture was stirred properly once in a day for 5 days and then used.

Appendix B

PANCHAGAVYA PREPARATION

Materials required:

- Cow dung : 7 kg
- Cow ghee : 1 kg
- Cow urine : 10 litres
- Water : 10 litres
- Cow milk : 3 litres
- Cow curd : 2 litres
- Tender coconut water : 3 litres
- Jaggery : 3 kg
- Well ripened banana : 12

Preparation process:

A wide mouthed plastic tub was taken and cow dung and cow ghee was added to it. It was mixed thoroughly twice a day for three days. On the fourth day, all the remaining ingredients were added and the mixture was stirred twice a day for the next fifteen days and then used. The container was covered with a plastic bag to avoid houseflies from laying eggs.

Appendix C

BRAMHASTHRAM PREPARATION

Materials required:

Cow urine	: 10 litres (Indigenious Cows, Preferably)
Neem leaves	: 3 kg
Sitaphal leaves	: 2 kg
Papaya leaves	: 2 kg
Guava leaves	: 2 kg
White datura leaves	: 2 kg

Preparation process:

All the above mentioned leaves were made into paste and boiled in 10 litres of cow urine. The mixture was kept for cooling and stirred once in a day for two days and used for spraying.

GENETIC ANALYSIS OF YIELD, YIELD COMPONENTS AND WATER USE EFFICIENCY TRAITS UNDER ORGANIC AND INORGANIC FERTILIZER MANAGEMENTS IN GROUNDNUT (*Arachis hypogaea* L.)

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ABSTRACT

A study was conducted at dryland farm of S.V. Agricultural college, Tirupati, during *kharif* 2017 to study the variability and genetic parameters, character association and path analysis in thirty groundnut genotypes under organic and inorganic fertilizer managements.

Analysis of variance revealed significant differences for all the characters studied under both organic and inorganic managements indicating the presence of ample amount of variability among the genotypes. Higher estimates for GCV and PCV for number of immature pods per plant, kernel yield per plant, pod yield per plant and total free amino acids and high heritability coupled with high genetic advance as percent of mean for total free amino acids and carbohydrate content was observed under both fertilizer managements.

Using D^2 analysis thirty genotypes of groundnut were grouped into seven and five clusters under organic and inorganic fertilizer managements. The characters oil content in organic and plant height in inorganic contributed more towards genetic divergence. The crosses TCGS-1157 X K-7 bold, TCGS-1157 X K-1789, TCGS-1330 X K-7 bold and Dharani X K-7 bold under organic management and K-9 X ICG-11651, Dharani X ICG-11651, K-9 X K-7 bold, Dharani X K-7 bold and TCGS-1330 X ICG-11651 under inorganic management can be utilized for development of transgressive segregants for yield, water use efficiency and quality traits.

Character association analysis revealed that number of primary branches, number of pegs per plant, number of mature pods per plant, number of pods per plant, harvest index, kernel yield per plant, SCMR at 40 DAS and SCMR at 60 DAS showed significant positive correlation with pod yield per plant under both fertilizer managements. Path analysis revealed that kernel yield per plant under organic management and kernel yield per plant and number of pods per plant in inorganic management exhibited high positive direct effect on pod yield per plant.