

**GENETIC DIVERSITY ANALYSIS
FOR DROUGHT RESISTANCE
AND WATER USE EFFICIENCY
TRAITS 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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2018

**GENETIC DIVERSITY ANALYSIS FOR
DROUGHT RESISTANCE AND WATER
USE EFFICIENCY TRAITS
IN GROUNDNUT
(*Arachis hypogaea* L.)**

BY
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THESIS SUBMITTED TO THE
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CHAIRPERSON: Dr. R. P. VASANTHI



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2018

DECLARATION

I, **Ms. K. SARITHA**, hereby declare that the thesis entitled **“GENETIC DIVERSITY ANALYSIS FOR DROUGHT RESISTANCE AND WATER USE EFFICIENCY TRAITS 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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Date :

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CERTIFICATE

Ms. **K. SARITHA** has satisfactorily prosecuted the course of research and that thesis entitled “**GENETIC DIVERSITY ANALYSIS FOR DROUGHT RESISTANCE AND WATER USE EFFICIENCY TRAITS 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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CERTIFICATE

This is to certify that the thesis entitled “**GENETIC DIVERSITY ANALYSIS FOR DROUGHT RESISTANCE AND WATER USE EFFICIENCY TRAITS 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. K. SARITHA** 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 the 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
>	:	Greater than
°	:	Degree
$\bar{X}$	:	Grand mean
ANOVA	:	Analysis of Variance
bp	:	base pairs
CD	:	Critical Difference
cm	:	centimetre
CV	:	Co-efficient of Variation
DAS	:	Days After Sowing
DNA	:	Deoxy Ribose Nucleic Acid
dNTP	:	Deoxyribo Nucleotide Triphosphate
g	:	gram
GA	:	Genetic Advance
GAM	:	Genetic Advance as percent of Mean
GCV	:	Genotypic Co-efficient of Variation
$h^2(b)$	:	heritability (broad sense)
ha	:	hectare
HI	:	Harvest Index
Kg	:	kilogram
LAD	:	Leaf Area Duration
LAI	:	Leaf Area Index
m	:	meters
ml	:	Millilitre

mM	:	Millimoles
Mt	:	Million tonnes
N	:	Nitrogen
ng	:	nano gram
no.	:	Number
PCA	:	Principal Component Analysis
PCV	:	Phenotypic Co-efficient of Variation
RBD	:	Randomized Block Design
rg	:	genotypic correlation coefficient
rp	:	phenotypic correlation coefficient
rpm	:	Revolutions per minute
RWC	:	Relative Water Content
SCMR	:	SPAD Chlorophyll Meter Reading
SEm	:	Standard error of Mean
SLA	:	Specific Leaf Area
SSR	:	Simple Sequence Repeats
WUE	:	Water Use Efficiency
μl	:	Microlitre

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ABSTRACT

The present investigation was carried out during *Kharif*, 2017 and *rabi*, 2017-18 to study the genetic divergence, variability, character association and path co-efficients in 32 genotypes of groundnut. The experiment was laid out at Regional Agricultural Research Station, Tirupati in a randomized block design with four replications in *kharif* and two replications in *rabi*. Data were recorded on 19 characters in *kharif* and six characters in *rabi*.

Analysis of variance indicated existence of significant genotypic differences for all the characters. In *kharif*, the genotypes viz., SG 99, TCGS-1694, R-2001-3-1, ALG-06-320 and TCGS-1653 while in *rabi*, the genotypes viz., TCGS-1694, ALG-06-320, TCGS-1622, SG 99 and TCGS-1157 showed high mean performance for pod yield as well as for most of yield components with desirable attributes that contribute for WUE and drought resistance.

Analysis of genetic parameters revealed that GCV, PCV, heritability (broad sense) and genetic advance as per cent of mean were high for all the traits except shelling percentage in *kharif* indicating that these traits are amenable for phenotypic selection while in *rabi* pod yield per plant, SLA at 60 DAS and 100-seed weight recorded high to moderate GCV, PCV, heritability(broad sense) and genetic advance as per cent of mean indicating simple phenotypic selection could be followed for their improvement. Low GCV, PCV, high to moderate heritability and low GAM were observed for SCMR at 60 DAS, RWC and shelling percentage indicating that phenotypic selection would not be that effective to improve these characters.

Genetic divergence studies by Mahalanobis's D^2 analysis revealed considerable diversity among 32 genotypes of groundnut and were grouped into seven and eight clusters based on physiological, yield and yield attributes in *kharif* and *rabi* respectively. The characters, angle between main axis and primary branches at 60 DAS (72.58%) in *kharif* and SLA at 60 DAS (33.67%) in *rabi* contributed maximum to the diversity. This was confirmed by canonical analysis. Based on these studies, cross combinations between genotypes in cluster VII and cluster III in *kharif* and cluster VIII and cluster II, cluster VIII and cluster V in *rabi* are proposed to get transgressive segregants for physiological, yield and yield parameters.

SSR marker studies detected a high level of genetic variation among the ten groundnut genotypes selected. A high degree of polymorphism was obtained with the primers, PM 45 (0.95) and SEQ5D05 (0.75). The similarity index values ranged from 0.34 to 0.703 indicating a wide range of genetic diversity.

Character association studies revealed significant positive correlation of number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, mature pods per plant, immature pods per plant and harvest index with pod yield per plant. Path co-efficient analysis also indicated that these characters were important attributes directly influencing the pod yield in groundnut. Hence, these characters should be considered in formulating selection criteria in breeding programme aimed at improvement of yield in groundnut.

Chapter ~ I

Introduction

Chapter I

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) ($2n = 40$), highly self-pollinated legume crop grown in tropical and sub-tropical regions of the world, is a good source of oil and protein. It is a segmental allotetraploid, belongs to family fabaceae and is the major oilseed crop in India and in Andhra Pradesh. Groundnut is considered as king of vegetable oilseeds and also called as wonder legume. This annual legume is native to South America (Brazil), but now grown throughout the tropical and warm temperate regions of the globe between latitudes 40° N to 40° S.

Groundnut seeds are the rich source of edible oil and protein content. The seeds contain about 36-54 per cent oil, 22-36 per cent protein and 18 per cent carbohydrates and are rich source of B-complex vitamins, especially thiamine and nicotinic acid but deficient in fat soluble vitamins A and D and almost lacking vitamin C. Groundnut oil contains a higher proportion of unsaturated fatty acids including essential fatty acids like linolenic acid and linoleic acids (Desai *et al.*, 1999).

Groundnut is not only a major oilseed crop but also an important food crop in India. India groundnut occupies an area of 40.68 lakh ha with production of 66.15 lakh tonnes and productivity of 1626 kg ha^{-1} in *Kharif* season (2017-18). In *rabi-summer*, it is being grown in 8.39 lakh ha with production of 16 lakh tonnes with productivity of 1909 kg ha^{-1} (2017-18). In Andhra Pradesh, in *Kharif* season, it is cultivated in an area of 6.48 lakh ha with production of 8 lakh tonnes and productivity of 1238 kg ha^{-1} . In *rabi* season, it is cultivated in 0.90 lakh ha with production of 2.07 lakh tonnes and productivity of 2300 kg ha^{-1} (AICRP on Groundnut, Annual Report, 2017).

Our productivity in the state as well as in our country is still low in both irrigated and rainfed conditions in comparison with USA (3540 kg ha^{-1}) and

China (2624 kg ha⁻¹) whereas the average productivity was 938 kg ha⁻¹ in India during the last decade.

Over two thirds of the global peanut production occurs in rainfed regions where erratic and insufficient rainfall is a major constraint. Drought of various intensities and duration severely limits peanut productivity. Although some agronomic interventions to conserve soil moisture and enhance water use efficiency (WUE) are available, developing peanut varieties tolerant to drought and efficient in water use offers the best long term and cost effective solution to the uncertainty of availability of water. Various characters viz., high SCMR (SPAD Chlorophyll Meter Reading), low SLA, high RWC, deep root system have been reported to be involved in drought resistance and water use efficiency mechanism.

Drought resistance can be enhanced by improving the ability to mine water from soil. This might be achieved by selection for large root systems for better adaptation to drought conditions. Very limited information has been available for the relationships between WUE and large root systems under different water regimes. To better understand how peanut genotypes behave in response to different water levels and to investigate the relationships between WUE and large root systems and other related traits (SLA and SCMR), further investigations are required. (Songsri *et al.*, 2008).

The Mahalanobis D² statistic has been used to quantify the degree of divergence among a set of genotypes (Ariyo, 1987, Nair *et al.*, 1998 and Pintu *et al.*, 2007). This statistical tool gives information on the divergent parental genotypes to be used in a breeding programme. Along with divergence, it is necessary to know the variability for different characters governing superior performance in different situations i.e., rainfed, irrigated with different constraints i.e., drought in rain-fed and biotic stresses in irrigated situation (Makinde and Ariyo, 2010).

The variation at molecular level is yet to be documented in greater depth in groundnut. It would be further helpful in selection of genotypes for hybridisation and also the documentation of genotypes developed in the breeding programme at molecular level in this era of competition to establish the uniqueness of the genotypes along with morphological and physiological characterization.

With these views in sight, the present study was planned with the following objectives,

1. To study the diversity among genotypes developed in different breeding programmes for drought resistance and WUE.
2. To estimate the variability parameters for yield and drought related characters.
3. To study the extent of association among different yield, drought resistance and WUE traits .
4. To identify the characters that contribute for drought conditions directly or indirectly.
5. Validation of reported SSR markers for drought resistance traits among the selected genotypes.

Chapter ~ II

Review of Literature

Chapter II

REVIEW OF LITERATURE

In groundnut, a self-pollinated annual legume, crop improvement is mainly through hybridization and selection in segregating generations with the ultimate goal of developing high yielding pure line homozygous variety. The parents for hybridization are chosen mostly depending on the characters/breeding objectives along with high yield. Effectiveness of selection after hybridization depends upon the variability for yield, yield attributes and specific objectives of hybridization. Hence, it is necessary to choose parents carefully for which diversity assessment among different germplasm/advanced breeding lines/released varieties that are available.

After making crosses, selection is exercised to select superior plants/progenies. In this context, studies on variability, heritability and genetic advance helps us the type of selection procedure to be followed. Among a set of genotypes, this helps in identification of traits that show higher variation and amenable for selection through phenotype/genotype and the generation when selection should be practiced. Hence, it is important to review the literature on these aspects to draw logical conclusions about the material under study.

A brief review of available literature related to the objectives of present investigation in groundnut (*Arachis hypogaea* L.) is presented under the following headings.

2.1 Variability and Genetic Parameters

2.2 Genetic Divergence

2.3 Character Association

2.4 Path Co-Efficient Analysis

2.1 GENETIC PARAMETERS (Variability, Heritability and Genetic

Advance as per cent of mean)

The success of any breeding programme depends on the amount of variability present for different characters in a population and its efficient management. The genetic co-efficient of variability gives an 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 [$h^2_{(b)}$] as it measures the relative amount of the heritable portion of variability. Genetic advance (GA) 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.

Table 2.1 Review of literature on variability for various quantitative characters in groundnut

Character	Range	References
SCMR	Low	Kumar (2004) Devi (2004) Venkateswarlu (2005) Kumar (2005) Hugar and Savithramma (2015) Srivali and Nadaf (2016) Bhargavi <i>et al.</i> (2016) Shashikumara <i>et al.</i> (2016) Bhavya <i>et al.</i> (2017)

	Moderate	Vasanthi <i>et al.</i> (2003)
	High	Rostini <i>et al.</i> (2000) Madhava <i>et al.</i> (2003) Mallikarjun and Savithramma (2017)
SLA	Low	Anuradha (1995) Srivalli and Nadaf (2016) Shashikumara <i>et al.</i> (2016)
	Moderate	Sudhir <i>et al.</i> (2008) John <i>et al.</i> (2011) Bhavya <i>et al.</i> (2017)
	High	Suneetha (2007) Hugar and Savithramma (2015)
RWC	Low	Savita <i>et al.</i> (2014) Srivalli and Nadaf (2016)
	Moderate	Savita <i>et al.</i> (2014)
LAI	Low	Anuradha (1995)
	Moderate	John <i>et al.</i> (2011) Mohammad (2015)
	High	Suneetha (2007) Preetha and Raveendran (2007)
LAD	High	Suneetha (2007)
Angle between main axis and primary branches	Moderate	Lodhi <i>et al.</i> (2014)
Root dry mass	Low	Jayalakshmi <i>et al.</i> (2001)
	Moderate	Jayalakshmi <i>et al.</i> (2001)
	High	Jayalakshmi (1997) Jayalakshmi <i>et al.</i> (2001)

		Makhan Lal <i>et al.</i> (2003) Jayalakshmi and Reddy (2003)
Number of primary branches per plant	Low	Naik <i>et al.</i> (2000) Vijayasekhar (2002) Devi (2004) Kumar (2005) John <i>et al.</i> (2009) Balaraju and Kenchanagoudar (2016)
	Moderate	Manoharan and Ramalingam (1993) Vijayasekhar (2002) Vasanthi <i>et al.</i> (2003) Shukla and Rai (2014) Gupta <i>et al.</i> (2015)
	High	Alam <i>et al.</i> (1985) Kandaswami <i>et al.</i> (1986) Naidu <i>et al.</i> (1987) Rao <i>et al.</i> (1988) Uddin <i>et al.</i> (1995) Khurram <i>et al.</i> (1998) Nath and Alam (2002) Parameshwarappa <i>et al.</i> (2005) Gupta <i>et al.</i> (2015) Vasanthi <i>et al.</i> (2015) Hugar and Savithramma (2015) Aparna <i>et al.</i> (2018)
Number of secondary branches per plant	Moderate	Vasanthi <i>et al.</i> (2003)
	High	Patil <i>et al.</i> (1982)

		Kandaswami <i>et al.</i> (1986) John <i>et al.</i> (2009) Korat <i>et al.</i> (2009) John <i>et al.</i> (2011) Balaraju and Kenchanagoudar (2016)
Plant height	Low	Kumar (1991) Vijayasekhar (2002)
	Moderate	Vijayasekhar (2002) Sudhir <i>et al.</i> (2008) Hugar and Savithramma (2015) Balaraju and Kenchanagoudar (2016) Gaikwad <i>et al.</i> (2015) Gupta <i>et al.</i> (2015)
	High	Kandaswami <i>et al.</i> (1986) Kumar (1991) Manoharan and Ramalingam (1993) Uddin <i>et al.</i> (1995) Kumar <i>et al.</i> (1998) Naik <i>et al.</i> (2000) Nath and Alam (2002) Makhan lal <i>et al.</i> (2003) Parameshwarappa <i>et al.</i> (2005) Zaman <i>et al.</i> (2011) Thakur <i>et al.</i> (2011) Maurya <i>et al.</i> (2014) Patidar <i>et al.</i> (2014)

		Rao <i>et al.</i> (2014) Satish (2014) Gupta <i>et al.</i> (2015) Rao (2016) Mallikarjun and Savithramma (2017)
Number of pegs per plant	High	Patil <i>et al.</i> (1982) Gaikwad <i>et al.</i> (2015) Aparna <i>et al.</i> (2018)
Number of mature pods per plant	Low	Vijayasekhar (2002) Venkateswarlu (2005)
	Moderate	Manoharan and Ramalingam (1993) Vijayasekhar (2002) Kumar (2004) Vasanthi <i>et al.</i> (2003) Sudhir <i>et al.</i> (2008) Bhargavi <i>et al.</i> (2016)
	High	Deshmukh <i>et al.</i> (1986) Naidu <i>et al.</i> (1987) Vaddoria and Patel (1990) Islam and Rasul (1998) Makhan lal <i>et al.</i> (2003) Kumar (2005) John <i>et al.</i> (2009) Zaman <i>et al.</i> (2011) Vekariya <i>et al.</i> (2011) Satish (2014) Gupta <i>et al.</i> (2015)

		Gaikwad <i>et al.</i> (2015) Rao (2016) Aparna <i>et al.</i> (2018)
Number of immature pods per plant	Moderate	Vasanthi <i>et al.</i> (2003)
	High	John <i>et al.</i> (2009) Zaman <i>et al.</i> (2011) Gaikwad <i>et al.</i> (2015) Aparna <i>et al.</i> (2018)
100 seed weight		John <i>et al.</i> (2011) Gaikwad <i>et al.</i> (2015)
	Moderate	Kumar (1991) Manoharan and Ramalingam (1993) Kumar (2004) Sudhir <i>et al.</i> (2008) Gupta <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016)
	High	Alam <i>et al.</i> (1985) Deshmukh <i>et al.</i> (1986) Reddy <i>et al.</i> (1986a) Vaddoria and Patel (1990) Kumar (1991) Uddin <i>et al.</i> (1995) Naik <i>et al.</i> (2000) Vijayasekhar (2002) Kumar (2005) Suneetha (2007) John <i>et al.</i> (2009)

		Zaman <i>et al.</i> (2011) Vekariya <i>et al.</i> (2011) Thakur <i>et al.</i> (2011) Narasimhulu <i>et al.</i> (2012) Rao <i>et al.</i> (2014) Satish (2014) Gupta <i>et al.</i> (2015) Vasanthi <i>et al.</i> (2015) Haj Hussein <i>et al.</i> (2018)
Shelling percentage	Low	Manoharan and Ramalingam (1993) Naik <i>et al.</i> (2000) Kumar (2004) Devi (2004) Venkaetswarlu (2005) Kumar (2005) John <i>et al.</i> (2011) Narasimhulu <i>et al.</i> (2012) Gaikwad <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016) Bhargavi <i>et al.</i> (2016)
	Moderate	Sudhir <i>et al.</i> (2008) Hugar and Savithramma (2015)
	High	Singh <i>et al.</i> (1996) Vijayasekhar (2002) John <i>et al.</i> (2009) Thakur <i>et al.</i> (2011)
Harvest index	Low	Venkateswarlu (2005)

	Moderate	Kumar (1991) Kumar (2004) Kumar (2005) Sudhir <i>et al.</i> (2008) Gaikwad <i>et al.</i> (2015)
	High	Vaddoria and Patel (1990) Kumar (1991) Vijayasekhar (2002) Jayalakshmi and Reddy (2003) Kumar (2004) Suneetha (2007) Vekariya <i>et al.</i> (2011) Gupta <i>et al.</i> (2015) Vasanthi <i>et al.</i> (2015) Bhargavi <i>et al.</i> (2016) Balaraju and Kenchanagoudar (2016)
Pod yield per plant	Low	Venkateswarlu (2005)
	Moderate	Kumar (1991) Manoharan and Ramalingam (1993) Nath and Alam (2002) Vasanthi <i>et al.</i> (2003) Sudhir <i>et al.</i> (2008) Shukla and Rai (2014) Gupta <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016)
	High	Kandaswami <i>et al.</i> (1986)

		Kumar (1991) Reddy and Gupta (1992) Singh <i>et al.</i> (1996) Khurram <i>et al.</i> (1998) Parameshwarappa <i>et al.</i> (2005) Kumar (2005) John <i>et al.</i> (2009) Meta and Monpara (2010) Narasimhulu <i>et al.</i> (2012) Maurya <i>et al.</i> (2014) Patidar <i>et al.</i> (2014) Satish (2014) Hugar and Savithramma (2015) Bhargavi <i>et al.</i> (2016) Rao (2016) Mallikarjun and Savithramma (2017) Haj Hussein <i>et al.</i> (2018) Aparna <i>et al.</i> (2018)
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Table 2.2 Review of literature on heritability for various quantitative characters in groundnut

Character	Range	References
SCMR	Low	John <i>et al.</i> (2011)
	Moderate	Rostini <i>et al.</i> (2000) Vasanthi <i>et al.</i> (2003) Venkateswarlu (2005) Bhargavi <i>et al.</i> (2016) Shashikumara <i>et al.</i> (2016)

		Srivalli and Nadaf (2016)
	High	Kumar (2004) Serraj <i>et al.</i> (2004) Devi (2004) Painawadee <i>et al.</i> (2009) Hugar and Savithramma (2015) Rao (2016) Shashikumara <i>et al.</i> (2016) Srivalli and Nadaf (2016) Bhavya <i>et al.</i> (2017) Mallikarjun and Savithramma (2017)
SLA	Moderate	Jayalakshmi and Reddy (2003) John <i>et al.</i> (2011) Srivalli and Nadaf (2016)
	High	Suneetha (2007) Painawadee <i>et al.</i> (2009) Hugar and Savithramma (2015) Srivalli and Nadaf (2016) Bhavya <i>et al.</i> (2017) Mallikarjun and Savithramma (2017)
RWC	Moderate	Srivalli and Nadaf (2016)
	High	Srivalli and Nadaf (2016)
LAI	Moderate	John <i>et al.</i> (2011)
	High	Suneetha (2007)
LAD	High	Suneetha (2007)
Root length	High	Painawadee <i>et al.</i> (2009)
Root dry mass	Low	Makhan Lal <i>et al.</i> (2003)

	Moderate	Jayalakshmi <i>et al.</i> (2001) Shreya (2014)
	High	Jayalakshmi (1997) Jayalakshmi <i>et al.</i> (2001) Jayalakshmi and Reddy (2003) Painawadee <i>et al.</i> (2009)
Number of primary branches per plant	Low	Vaddoria and Patel (1990) Vijayasekhar (2002) Vasanthi <i>et al.</i> (2015)
	Moderate	Manoharan and Ramalingam (1993) Vijayasekhar (2002) John <i>et al.</i> (2011) Vishnuvardhan <i>et al.</i> (2013) Maurya <i>et al.</i> (2014) Gupta <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016)
	High	Kandaswami <i>et al.</i> (1986) Naidu <i>et al.</i> (1987) Reddy <i>et al.</i> (1987) Uddin <i>et al.</i> (1995) Naik <i>et al.</i> (2000) Devi (2004) Mahalakshmi <i>et al.</i> (2005) Korat <i>et al.</i> (2009) Hiremath <i>et al.</i> (2011) Patidar <i>et al.</i> (2014) Hugar and Savithramma (2015) Aparna <i>et al.</i> (2018)

Number of secondary branches per plant	High	Mahalakshmi <i>et al.</i> (2005) Korat <i>et al.</i> (2009) John <i>et al.</i> (2011) Vishnuvardhan <i>et al.</i> (2013) Balaraju and Kenchanagoudar (2016)
Plant height	Low	Vijayasekhar (2002) John <i>et al.</i> (2011)
	Moderate	Alam <i>et al.</i> (1985) Naik <i>et al.</i> (2000) Vijayasekhar (2002) Mahalakshmi <i>et al.</i> (2005) Shoba <i>et al.</i> (2009) John <i>et al.</i> (2011) Gupta <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016)
	High	Kandaswami <i>et al.</i> (1986) Reddy <i>et al.</i> (1987) Kumar (1991) Manoharan and Ramalingam (1993) Uddin <i>et al.</i> (1995) Kumar <i>et al.</i> (1998) Makhan lal <i>et al.</i> (2003) Korat <i>et al.</i> (2009) Hiremath <i>et al.</i> (2011) Zaman <i>et al.</i> (2011) Maurya <i>et al.</i> (2014) Patidar <i>et al.</i> (2014) Hugar and Savithramma (2015)

		Gaikwad <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Rao (2016) Haj Hussein <i>et al.</i> (2018) Aparna <i>et al.</i> (2018)
Number of pegs per plant	Moderate	Aparna <i>et al.</i> (2018)
	High	Gaikwad <i>et al.</i> (2015) Kadam <i>et al.</i> (2016)
Number of mature pods per plant	Low	Vijayasekhar (2002) Makhan lal <i>et al.</i> (2003) Venkateswarlu (2005) Vishnuvardhan <i>et al.</i> (2013) Gupta <i>et al.</i> (2015)
	Moderate	Kandaswamy <i>et al.</i> (1986) Vijayasekhar (2002) Vasanthi <i>et al.</i> (2003) Vasanthi <i>et al.</i> (2015)
	High	Naidu <i>et al.</i> (1987) Vaddoria and Patel (1990) Manoharan and Ramalingam (1993) Kumar (2004) Suneetha <i>et al.</i> (2005) Mahalakshmi <i>et al.</i> (2005) Vekariya <i>et al.</i> (2011) Zaman <i>et al.</i> (2011) Gaikwad <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Aparna <i>et al.</i> (2018)

Number of immature pods per plant	Moderate	Vasanthi <i>et al.</i> (2015)
	High	Mahalakshmi <i>et al.</i> (2005) Zaman <i>et al.</i> (2011) Vishnuvardhan <i>et al.</i> (2013) Gaikwad <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Aparna <i>et al.</i> (2018)
100 seed weight	Low	Alam <i>et al.</i> (1985) Naidu <i>et al.</i> (1987) Reddy <i>et al.</i> (1987) Manoharan and Ramalingam (1993) Vasanthi <i>et al.</i> (1998) Vijayasekhar (2002) Reddy (2003) Kumar (2004) Devi (2004) Suneetha <i>et al.</i> (2005) John <i>et al.</i> (2011)
	Moderate	Alam <i>et al.</i> (1985)
	High	Vaddoria and Patel (1990) Kumar (1991) Manoharan and Ramalingam (1993) Uddin <i>et al.</i> (1995) Vasanthi <i>et al.</i> (1998) Naik <i>et al.</i> (2000) Vijayasekhar (2002) Kumar (2004) Korat <i>et al.</i> (2009)

		Meta and Monpara (2010) Hiremath <i>et al.</i> (2011) Patidar <i>et al.</i> (2014) Gaikwad <i>et al.</i> (2015) Gupta <i>et al.</i> (2015) Vasanthi <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Rao (2016) Balaraju and Kenchanagoudar (2016) Haj Hussein <i>et al.</i> (2018) Aparna <i>et al.</i> (2018)
Shelling percentage	Low	Naidu <i>et al.</i> (1987) John <i>et al.</i> (2011) Maurya <i>et al.</i> (2014) Vasanthi <i>et al.</i> (2015)
	Moderate	Kandaswamy <i>et al.</i> (1986) Venkateswarlu (2005) Vishnuvardhan <i>et al.</i> (2013) Hugar and Savithramma (2015)
	High	Naidu <i>et al.</i> (1987) Reddy <i>et al.</i> (1987) Manoharan and Ramalingam (1993) Vasanthi <i>et al.</i> (1998) Vijayasekhar (2002) Reddy (2003) Kumar (2004) Devi (2004) Suneetha <i>et al.</i> (2005)

		Mahalakshmi <i>et al.</i> (2005) Korat <i>et al.</i> (2009) Hiremath <i>et al.</i> (2011) Zaman <i>et al.</i> (2011) Patidar <i>et al.</i> (2014) Gaikwad <i>et al.</i> (2015) Gupta <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016) Bhargavi <i>et al.</i> (2016) Kadam <i>et al.</i> (2016) Rao (2016) Shashikumara <i>et al.</i> (2016) Mallikarjun and Savithramma (2017) Aparna <i>et al.</i> (2018)
Harvest index	Low	Reddy <i>et al.</i> (1986a)
	Moderate	Kandaswamy <i>et al.</i> (1986) Devi (2004) John <i>et al.</i> (2011) Gupta <i>et al.</i> (2015) Aparna <i>et al.</i> (2018)
	High	Vaddoria and Patel (1990) Kumar (1991) Vijayasekhar (2002) Jayalakshmi and Reddy (2003) Devi (2004) Venkateswarlu (2005) Mahalakshmi <i>et al.</i> (2005) Korat <i>et al.</i> (2009)

		Vishnuvardhan <i>et al.</i> (2013) Gaikwad <i>et al.</i> (2015) Vasanthi <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016) Bhargavi <i>et al.</i> (2016)
Pod yield per plant	Low	Kandaswami <i>et al.</i> (1986) Reddy <i>et al.</i> (1986a) Makhan lal <i>et al.</i> (2003) Venkateswarlu (2005) John <i>et al.</i> (2011)
	Moderate	Kandaswamy <i>et al.</i> (1986) Naik <i>et al.</i> (2000) Vasanthi and Raja Reddy (2002) Jayalakshmi and Reddy (2003) Devi (2004) Vasanthi <i>et al.</i> (2003) Shoba <i>et al.</i> (2009) Balaraju and Kenchanagoudar (2016) Aparna <i>et al.</i> (2018) Vasanthi <i>et al.</i> (2015)
	High	Naidu <i>et al.</i> (1987) Reddy <i>et al.</i> (1987) Kumar (1991) Manoharan and Ramalingam (1993) Khurram <i>et al.</i> (1998) Vasanthi and Raja Reddy (2002) Reddy (2003) Devi (2004)

		Suneetha <i>et al.</i> (2005) Korat <i>et al.</i> (2009) Vekariya <i>et al.</i> (2011) Maurya <i>et al.</i> (2014) Patidar <i>et al.</i> (2014) Hugar and Savithramma (2015) Gupta <i>et al.</i> (2015) Bhargavi <i>et al.</i> (2016) Kadam <i>et al.</i> (2016) Shashikumara <i>et al.</i> (2016) Mallikarjun and Savithramma (2017) Haj Hussein <i>et al.</i> (2018)
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Table 2.3 Review of literature on genetic advance for various quantitative characters in groundnut

Character	Range	References
SCMR	Low	Devi (2004)
		Venkateswarlu (2005)
		John <i>et al.</i> (2011)
		Hugar and Savithramma (2015)
		Shashikumara <i>et al.</i> (2016)
		Bhargavi <i>et al.</i> (2016)
		Srivalli and Nadaf (2016)
		Bhavya <i>et al.</i> (2017)
	Moderate	Vasanthi <i>et al.</i> (2003)
	High	Rao (2016)
		Mallikarjun and Savithramma (2017)
SLA	Low	Jayalakshmi and Reddy (2003)

		Shashikumara <i>et al.</i> (2016) Srivalli and Nadaf (2016)
	Moderate	Jayalakshmi and Reddy (2003) John <i>et al.</i> (2011) Shashikumara <i>et al.</i> (2016) Srivalli and Nadaf (2016) Bhavya <i>et al.</i> (2017) Mallikarjun and Savithramma (2017)
	High	Suneetha (2007) Hugar and Savithramma (2015)
RWC	Low	Srivalli and Nadaf (2016)
LAI	High	Suneetha (2007) John <i>et al.</i> (2011)
LAD	High	Suneetha (2007)
Root dry mass	High	Jayalakshmi and Reddy (2003) John <i>et al.</i> (2011) Shreya (2014)
Number of primary branches per plant	Low	Manoharan and Ramalingam (1993) Vijayasekhar (2002) Devi (2004) Vishnuvardhan <i>et al.</i> (2013) Vasanthi <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016)
	Moderate	Uddin <i>et al.</i> (1995) Mahalakshmi <i>et al.</i> (2005) Hiremath <i>et al.</i> (2011) John <i>et al.</i> (2011)

		Maurya <i>et al.</i> (2014) Gupta <i>et al.</i> (2015) Haj Hussein <i>et al.</i> (2018)
	High	Naidu <i>et al.</i> (1987) Reddy <i>et al.</i> (1987) Uddin <i>et al.</i> (1995) Korat <i>et al.</i> (2009) Patidar <i>et al.</i> (2014) Hugar and Savithramma (2015) Aparna <i>et al.</i> (2018)
Number of secondary branches per plant	High	Mahalakshmi <i>et al.</i> (2005) Korat <i>et al.</i> (2009) John <i>et al.</i> (2011) Vishnuvardhan <i>et al.</i> (2013) Balaraju and Kenchanagoudar (2016)
Plant height	Low	Vijayasekhar (2002)
	Moderate	Kumar (1991) Manoharan and Ramalingam (1993) Uddin <i>et al.</i> (1995) Mahalakshmi <i>et al.</i> (2005) Shoba <i>et al.</i> (2009) John <i>et al.</i> (2011) Gupta <i>et al.</i> (2015)
	High	Alam <i>et al.</i> (1985) Reddy <i>et al.</i> (1987) Kumar (1991) Uddin <i>et al.</i> (1995) Kumar <i>et al.</i> (1998)

		Korat <i>et al.</i> (2009) Hiremath <i>et al.</i> (2011) Zaman <i>et al.</i> (2011) Maurya <i>et al.</i> (2014) Patidar <i>et al.</i> (2014) Hugar and Savithramma (2015) Balaraju and Kenchanagoudar (2016) Gaikwad <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Rao (2016) Aparna <i>et al.</i> (2018)
Number of pegs per plant	High	Gaikwad <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Aparna <i>et al.</i> (2018)
Number of mature pods per plant	Low	Manoharan and Ramalingam (1993) Vijayasekhar (2002) Makhan lal <i>et al.</i> (2003) Kumar (2004) Venkateswarlu (2005) Vasanthi <i>et al.</i> (2015)
	Moderate	Kumar (2004) Vasanthi <i>et al.</i> (2003) Gupta <i>et al.</i> (2015)
	High	Naidu <i>et al.</i> (1987) Vaddoria and Patel (1990) Reddy and Gupta (1992) Islam and Rasul (1998) Suneetha <i>et al.</i> (2005)

		Mahalakshmi <i>et al.</i> (2005) Vekariya <i>et al.</i> (2011) Zaman <i>et al.</i> (2011) Vishnuvardhan <i>et al.</i> (2013) Gaikwad <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Aparna <i>et al.</i> (2018)
Number of immature pods per plant	Moderate	Vasanthi <i>et al.</i> (2015)
	High	Mahalakshmi <i>et al.</i> (2005) Zaman <i>et al.</i> (2011) Vishnuvardhan <i>et al.</i> (2013) Gaikwad <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Aparna <i>et al.</i> (2018)
100 seed weight	Low	John <i>et al.</i> (2011) Gaikwad <i>et al.</i> (2015)
	Moderate	Kumar (1991) Manoharan and Ramalingam (1993) Uddin <i>et al.</i> (1995) Kumar (2004) Patidar <i>et al.</i> (2014)
	High	Labana <i>et al.</i> (1980) Alam <i>et al.</i> (1985) Reddy <i>et al.</i> (1986a) Vaddoria and Patel (1990) Kumar (1991) Uddin <i>et al.</i> (1995) Vasanthi <i>et al.</i> (1998)

		Yadava <i>et al.</i> (1998) Naik <i>et al.</i> (2000) Vijayasekhar (2002) Kumar (2004) Korat <i>et al.</i> (2009) Meta and Monpara (2010) Hiremath <i>et al.</i> (2011) Gupta <i>et al.</i> (2015) Vasanthi <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Rao (2016) Balaraju and Kenchanagoudar (2016) Haj Hussein <i>et al.</i> (2018) Aparna <i>et al.</i> (2018)
Shelling percentage	Low	Naidu <i>et al.</i> (1987) Manoharan and Ramalingam (1993) Uddin <i>et al.</i> (1995) Reddy (2003) Kumar (2004) Devi (2004) Suneetha <i>et al.</i> (2005) Venkateswarlu (2005) Mahalakshmi <i>et al.</i> (2005) Hiremath <i>et al.</i> (2011) John <i>et al.</i> (2011) Vasanthi <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016) Bhargavi <i>et al.</i> (2016)

		Gaikwad <i>et al.</i> (2015)
	Moderate	Reddy <i>et al.</i> (1987) Korat <i>et al.</i> (2009) Zaman <i>et al.</i> (2011) Vishnuvardhan <i>et al.</i> (2013) Patidar <i>et al.</i> (2014) Hugar and Savithramma (2015) Gupta <i>et al.</i> (2015) Kadam <i>et al.</i> (2016) Rao (2016)
	High	Reddy and Gupta (1992) Vasanthi <i>et al.</i> (1998) Vijayasekhar (2002) Maurya <i>et al.</i> (2014) Shashikumara <i>et al.</i> (2016) Mallikarjun and Savithramma (2017) Aparna <i>et al.</i> (2018)
Harvest index	Low	Varman and Raveendran (1996)
	Moderate	Kumar (1991) Devi (2004) Korat <i>et al.</i> (2009)
	High	Vaddoria and Patel (1990) Kumar (1991) Reddy and Gupta (1992) Vijayasekhar (2002) Jayalakshmi and Reddy (2003) Devi (2004) Venkateswarlu (2005)

		Mahalakshmi <i>et al.</i> (2005) John <i>et al.</i> (2011) Gaikwad <i>et al.</i> (2015) Gupta <i>et al.</i> (2015) Vasanthi <i>et al.</i> (2015) Balaraju and Kenchanagoudar (2016) Bhargavi <i>et al.</i> (2016) Aparna <i>et al.</i> (2018)
Pod yield per plant	Low	Manoharan and Ramalingam (1993) Makhal lal <i>et al.</i> (2003) Venkateswarlu (2005) John <i>et al.</i> (2011)
	Moderate	Kumar (1991) Vasanthi and Raja Reddy (2002) Jayalakshmi and Reddy (2003) Devi (2004) Suneetha <i>et al.</i> (2005) Vasanthi <i>et al.</i> (2003) Balaraju and Kenchanagoudar (2016)
	High	Naidu <i>et al.</i> (1987) Reddy <i>et al.</i> (1987) Kumar (1991) Reddy and Gupta (1992) Khurram <i>et al.</i> (1998) Yadava <i>et al.</i> (1998) Naik <i>et al.</i> (2000) Vasanthi and Raja Reddy (2002) Reddy (2003)

		Devi (2004) Korat <i>et al.</i> (2009) Shoba <i>et al.</i> (2009) Vekariya <i>et al.</i> (2011) Vishnuvardhan <i>et al.</i> (2013) Maurya <i>et al.</i> (2014) Patidar <i>et al.</i> (2014) Hugar and Savithramma (2015) Gupta <i>et al.</i> (2015) Vasanthi <i>et al.</i> (2015) Bhargavi <i>et al.</i> (2016) Kadam <i>et al.</i> (2016) Shashikumara <i>et al.</i> (2016) Mallikarjun and Savithramma (2017) Haj Hussein <i>et al.</i> (2018) Aparna <i>et al.</i> (2018)
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2.2 GENETIC DIVERGENCE

2.2.1 Mahalanobis's D^2 analysis

The success of any breeding programme is determined by the amount of variability present for different characters in a population and its efficient management. Morphological similarity, eco-geographic diversity, phylogenetic relationships *etc.*, were the few earlier methods used for discriminating divergent populations which are reinstated by more scientific and advanced biometric techniques viz., multivariate analysis based on Mahalanobis's D^2 statistic and semigraphic method of metroglyph analysis. By Mahalanobis generalized distance estimated by D^2 statistic (Maurya and Singh, 1977) estimation of degree of divergence between biological populations and computation of relevant contributions of different

components to total divergence is done. Selection of parents for hybridization programme based on Mahalanobis's D^2 statistic is more reliable method as the requisite knowledge in respect of a mass of characters is available prior to crossing programme.

Prabhakar (1985) reported grouping of 49 genotypes of groundnut into nine clusters which include 14 valencia, 23 virginia and 12 spanish types collected from different geographic regions. Plant spread had contributed maximum towards divergence followed by number of pods and pod yield.

Nadaf *et al.* (1986) studied genetic diversity using Mahalanobis D^2 statistic. 83 genotypes from 18 countries on the basis of yield per plot and other six agronomic characters were grouped into nine clusters that were not related to their geographical origin. Pod yield accounted for 88 per cent of the total variation between clusters, but number of developed pods, days to 50 per cent flowering and 100-seed weight were important in accounting for divergence within clusters.

48 groundnut genotypes were grouped into eleven clusters based on D^2 analysis by Kumar (1991). The characters, harvest index and shelling out turn were the major contributing traits towards divergence.

Golakia and Makne (1992) carried out genetic diversity analysis using Mahalanobis D^2 statistic in 35 Virginia runner groundnut genotypes which were grouped into seven clusters. The genotypes of common geographic origin were grouped into different clusters which suggested a lack of relationship between genetic and geographic diversity.

Reddy and Reddy (1993) assessed 48 genotypes from different geographical origin and grouped them into six clusters and confirmed the existence of variability between the genotypes for all the 12 characters studied. Geographical diversity was not related to genetic diversity. 100-pod weight (36%), number of secondary branches per plant (31%) and harvest index (15%) accounted for more than 82 per cent of the total divergence.

Anuradha (1995) through canonical root analysis grouped 30 genotypes into 13 clusters and reported maximum contribution of harvest index, pod yield and kernel yield towards divergence.

Choudhary *et al.* (1998) carried out D^2 analysis of yield components of 30 groundnut genotypes and grouped them into five clusters.

Through Mahalanobis D^2 analysis 65 genotypes formed ten clusters in a study by Vijayasekhar (2002). The mode of distribution of genotypes into various clusters was at random suggesting that there was no correlation between geographical distribution and genetic diversity. The characters harvest index, 100-seed weight and shelling percentage contributed maximum towards genetic divergence in both D^2 analysis and canonical root analysis.

Jain *et al.* (2003) reported that the highest contribution towards total divergence was through haulms yield per plant (26.22%) followed by dry pod yield per plant (19.66%) and opined that the genotypes involved in the diverse clusters could be used as promising parents in intermating for obtaining high heterotic response and better segregants.

Kumar (2004) studied diversity by employing Mahalanobis D^2 and reported 54 genotypes formed 11 clusters based on morphological and biochemical characters whereas 17 clusters based on physiological characters respectively. The mode of distribution of genotypes different clusters based on morphological and biochemical characters was at random and independent of each other suggesting that there was no relationship between geographical origin and genetic diversity. While clustering pattern of genotypes for physiological characters was related to geographical origin, no regular demarcation was discernible in the pattern of constellation of genotypes into various clusters.

Garjappa *et al.* (2005) carried out genetic divergence studies in 200 genotypes of groundnut through Mahalanobis's D^2 statistic and principal component analysis (PCA). They were grouped into 12 clusters in case of D^2

analysis and 15 clusters through principal component analysis. They reported that number of secondary branches per plant contributed maximum towards divergence followed by days to maturity and total drymatter per plant.

Upadhyaya (2005) evaluated 184 mini core entries, consisting of 37 *fastigiata*, 58 *vulgaris*, 85 *hypogaea*, two *peruviana*, and one each of *aequitoriana* and *hirsuta* and four control cultivars viz., M13, Gangapuri, ICGS 44 and ICGS 76). The PCA was used to provide a reduced dimension model that would indicate measured differences among 18 selected entries and four control cultivars. PC 1, which is the first and most important component, accounted for 29.83% and the PC 2 accounted for 12.61% of total variation. The last PC considered for clustering, PC 15, contributed 1.16% of the total variation. Cluster analysis was carried out by first 15 principal component scores which resulted in four clusters.

Lakshmiddevamma *et al.* (2006) studied genetic divergence in 81 groundnut genotypes by utilizing Mahalanobis D^2 analysis. Based on the genetic distance groundnut accessions were grouped into 16 clusters. Test weight, days to maturity and oil content were the most potential traits contributing to the total divergence.

Kumar *et al.* (2010a) collected and evaluated 64 groundnut genotypes. Data recorded on 14 characters were subjected to multivariate analysis to study the variability within the genotypes and to classify them. The first three axes of PCA captured 59.52 % of the total variability and jointly identified final pod yield per plant, kernel yield per plant and oil yield per plant as characters contributing most to total variation. The first three axes of canonical analyses accounted for 99% of total variation. Ward's clustering method has grouped the genotypes into 3 distinct clusters.

Analysis of genetic divergence in sixty four genotypes of groundnut by Kumar *et al.* (2010b) revealed wide range of D^2 values ranging between 4.52 and 27.75 suggesting the presence of considerable amount of genetic diversity

in the genotypes studied, they were grouped in to seven clusters. Contribution of various characters towards total divergence revealed highest contribution by Specific leaf area (27.67%) to the total divergence.

Makinde and Ariyo (2010) evaluated 22 groundnut genotypes and the data collected on 33 characters were subjected to PCA. Results from the PCA revealed that only five of the thirty three principal components had eigen values greater than 3.0. The first five principal axes together explained above 70 per cent of the total variation.

Zaman *et al.* (2010) conducted diversity studies on 34 groundnut genotypes. The genotypes were grouped into five clusters. Days to 50 per cent flowering, days to maturity, number of branches per plant, number of matured nuts per plant and karnel size were the most important contributors based on the latent vector.

Nirmala *et al.* (2013) evaluated thirty genotypes of groundnut for 19 yield and physiological traits. All the 30 genotypes were grouped into 14 clusters with a variable number of entries in each cluster revealing the presence of a considerable amount of genetic diversity in the material. Among the various traits, the highest contribution towards divergence was found for number of secondary branches per plant (29.89%), followed by crop growth rate (CGR) at 75 days after sowing to harvest (18.39%), CGR at 30-75 DAS (10.57%), 100-seed weight (8.51%), plant height (8.51%), SPAD chlorophyll metre reading (6.9%) and harvest index (5.75%).

Suneetha *et al.* (2013) analysed diversity among twentynine released and pre-release groundnut genotypes based on 16 morphological, yield and yield attributes and grouped into nine clusters. Maximum contribution to diversity was from harvest index (33.50%) followed by days to emergence (17.00%) and length of main axis (8.62%), leaflet length (1.4%). The characters, 100 seed weight, pod yield per plant, leaf length contributed 5.91, 5.17 and 4.68 per cent respectively. Minimum contribution was by number of

mature pods per plant. Constellation of genotypes into different clusters was not completely at random and it showed relationship with respect to their pedigree and place of breeding.

Anthony (2014) assessed the variation among 50 genotypes through principal component analysis based on the morphological traits. Four of the nine principal components extracted, had Eigenvalue greater than one and accounted for 76.92 per cent of the total variation among 50 genotypes. The first principal component accounted for (31.01%) of the total variation. The variation in principal component I was mainly attributed to number of pods per plant followed by pod yield, shelling percentage, number of seeds per pod, canopy spread, plant height, pod length. The principal component II contributed 19.94 per cent of the total divergence, principal component III constituted 14.82 per cent of the total variation and principal component IV described an additional 11.13 per cent of the total variation.

Sixty genotypes of groundnut (*Arachis hypogaea* L.) were evaluated for the genetic diversity by Yadav *et al.* (2014). D² analysis indicated existence of wider genetic variability in the population of sixty genotypes which were grouped in to twelve clusters.

Vasanthi *et al.* (2015) studied genetic diversity among 29 genotypes based on ten physiological attributes- LAD, LAI, CGR, NAR, SLA, SCMR, seedling vigour index, germination percentage, harvest index and pod yield per plant. LAD at 54 DAS contributed maximum (34.48%) followed by LAI at 72 DAS (20.20%), LAD at 72 DAS (12.81%), CGR at 72 DAS (12.32%), CGR at 54 DAS (8.37%), harvest index (4.68%) and SLA at 72 DAS (3.21%). The distribution of genotypes into different clusters was related to the objective with which the genotypes were bred i.e. the 11 genotypes in cluster I were derived from WUE breeding programme.

Patil *et al.* (2015) carried out divergence studies in forty nine groundnut genotypes. The genotypes were grouped into fourteen clusters. Pod yield per

plant, days to 50 per cent flowering, 100 kernel weight, kernel weight per plant, number of pod bearing nodes were the most important contributors.

Gaikwad *et al.* (2015) studied genetic diversity studies in 50 genotypes of groundnut. On the basis of D^2 values, all the fifty genotypes were grouped into five clusters with substantial genetic divergence between them. Maximum contribution to diversity was from dry haulm yield per plant (31.83%) followed by number of pegs per plant (28.49%) and 100 kernel weight (10.69%).

Venkatesh *et al.* (2015) evaluated fifty drought tolerant groundnut genotypes for their genetic diversity with regards to kernel yield and yield attributing characters. The genotypes were classified into nine clusters, based on Mahalanobis D^2 statistic. 100 kernel weight contributed maximum (58.78%), followed by haulm yield per plant (33.47%) towards the total divergence.

Vivekananda *et al.* (2015) carried out diversity studies on 31 genotypes of groundnut for five agro-morphological characters. Based on Tocher's method, 31 genotypes were grouped into seven clusters. Contribution of character towards divergence was observed maximum in 100-kernel weight (63.14%) followed by dry pod yield per plant (34.27 %) and minimum in shelling percentage (0.55 %).

Bhakal and Lal (2015) studied genetics divergence using D^2 analysis of 40 genotypes of groundnut (*Arachis hypogaea* L.) of different geographic origins revealed existence of considerable diversity for eleven quantitative and qualitative characters. The genotypes were grouped into seven clusters.

Gupta *et al.* (2015) analysed divergence among sixty groundnut genotypes using Mahalanobis's D^2 statistic. The genotypes were grouped into thirteen clusters. Protein content (42.82%) followed by oil content (22.60%), 100-pod weight (19.72 %), 100-kernal weight (7.06%), biological yield per

plant (3.79%) and kernel yield per plant (1.02%) contributed maximum towards divergence.

Kushwah *et al.* (2016) evaluated 29 breeding lines for 12 traits including yield. On the basis of critical D^2 values 29 genotypes were classified into eight clusters. Based on D^2 analysis shelling percentage contributed to maximum divergence followed by harvest index, kernel yield per plant, hundred kernel weight. The canonical analysis revealed that the important characters responsible for genetic divergence were shelling percentage and kernel yield per plant in the first axis and harvest index and kernel yield per plant in the second axis.

The nature and degree of genetic diversity among 21 promising Spanish bunch groundnut genotypes of different agro-climatic regions were evaluated by Gantait *et al.* (2017). Based on the D^2 values, 21 genotypes were grouped into four distinctive non-hierarchical clusters. Pod yield as an economically important trait was found to be the key contributor towards the genetic divergence followed by days to maturity.

Waghmode *et al.* (2017) assessed genetic diversity for one hundred and twenty one groundnut genotypes. These genotypes were grouped into seven clusters variance of cluster means 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.

Based on D^2 values, 36 genotypes were classified into 10 clusters by Sardar *et al.* (2017). Haulm yield per plant contributed maximum towards divergence followed by pod yield per plant, kernel yield and kernel number per plant. Shelling per cent contributed least divergence.

Thirty drought tolerant groundnut genotypes were evaluated for their genetic diversity with respect to kernel yield and yield component traits by Lokeshwar *et al.* (2017). The genotypes were classified into six clusters. In

this study, oil content (44.37%), followed by free proline content (31.26%), protein content (19.31%) and 100 kernel weight (1.38%) contributed maximum towards the total divergence.

Fifty peanut stem necrosis tolerant groundnut varieties were evaluated for their genetic diversity with respect to kernel yield, yield attributing characters and qualitative traits by Niveditha *et al.* (2017). The genotypes were classified into eight clusters, based on Mahalanobis D² statistic. SCMR at 60 days after sowing, protein content, harvest index per cent and 100 kernel weight accounted for 80.98 per cent of the total genetic divergence indicating their importance in the choice of parents for hybridization programme.

2.2.2 Divergence at molecular level using SSR markers

Recent achievements in the development of marker protocols such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP) and simple sequence repeats (SSRs) (also known as microsatellites) have revolutionized the genetic analysis and opened new possibilities in the study of complex traits in the crop plants. SSRs belong to the co-dominant marker class, are easy to manipulate, highly reproducible, and targets hypervariable regions of the genome. They are tandem repeats of DNA sequences of only a few basepairs (1-6 bp) in length (Gupta *et al.*, 1996). Variation in the number of repeated core sequence of nucleotides at a SSR locus among different genotypes provides the basis for polymorphism that can be used in plant genetic studies. SSRs are therefore excellent choice of DNA markers for genetic mapping in plants. Unlike RFLPs, for instance SSR technology is PCR based, requires only nanograms of DNA, and is readily automatable. Unlike RAPDs, SSR markers have proven to be reliable and reproducible. Unlike AFLPs, they are co-dominant and species specific. Moreover, they are both size, sequence specific and species specific. Validation and use of markers linked with drought tolerance that are previously reported across different populations would enhance the efficiency of MAS.

Dwivedi and Varma (2002) studied molecular diversity in 37 groundnut genotypes with SSR primers and reported that differences in DNA profiles were observed in 537 of the 666 pair-wise comparisons analyzed among 37 drought tolerant genotypes. The dissimilarity ranged from 0.11 to 0.78. ICGV 94100 with ICGV 94106, ICGV 97068, ICGV 99247 and Chico; and ICGV 97068 with CSMG 84-1, ICGV 99231, ICGV 99247 and ICGV 99236 showed large difference at molecular level in their DNA profiles.

Krishna *et al.* (2004) selected 48 cultivated Valencia peanut genotypes and analyzed using 18 fluorescently labeled SSR (f-SSR) primer pairs. These primer pairs amplified 120 polymorphic loci among the genotypes screened and amplified from 3 to 19 alleles with an average of 6.9 alleles per primer pair. The f-SSR marker data was further analyzed using cluster algorithms and principal component analysis. The results indicated that considerable genetic variations were discovered among the analyzed genotypes.

Moretzsohn *et al.* (2004) developed a total of 67 new microsatellite markers (mainly TTG motif) for *Arachis*. Only three of these markers, however, were polymorphic in cultivated peanut. These three new markers plus five other markers characterized previously were evaluated for number of alleles per locus and gene diversity using 60 accessions of *A. hypogaea*. Genetic relationships among these 60 accessions and a sample of 36 wild accessions representative of section *Arachis* were estimated using allelic variation observed in a selected set of 12 SSR markers. Results showed that the Brazilian peanut germplasm collection has considerable levels of genetic diversity detected by SSR markers. Similarity groups for *A. hypogaea* accessions were established, which is a useful criteria for selecting parental plants for crop improvement.

Kottapalli *et al.* (2006) genotyped seventy-two peanut accessions from the U.S. peanut mini core with 73 SSR markers, but six produced reliable, polymorphic bands. Moderate levels of genetic variation were found with genetic distance values among accessions ranging from 0.088 to 0.254.

Distinct groupings of the accessions based on subspecies classification and on botanical type groupings were established.

Tang *et al.* (2007) assessed the genetic variation using thirty four SSR markers among four sets of twenty four accessions each from the four botanical varieties of the cultivated peanut. Among the tested accessions, ten to sixteen pairs of SSR primers showed polymorphisms. The maximum differentiation index, which was defined as the degree of genetic differentiation, was as high as 0.992 in the tested accessions. Each accession could be discriminated by a specific set of polymorphic SSR primers, and the intra-variety genetic distance was determined among accessions, with an average of 0.59 in var. *fastigiata*, 0.46 in var. *hypogaea*, 0.38 in var. *vulgaris*, and 0.17 in var. *hirsuta*. Dendrograms based on genetic distances were constructed for the four botanical varieties, which revealed the existence of different clusters.

Naito *et al.* (2008) assessed diversity among 201 accessions of groundnut and 13 accessions of *Arachis* wild species with a selected set of 13 SSR primers. Genetic similarities among accessions were estimated based on Jaccard's similarity. A UPGMA phenogram was constructed for all 214 accessions, tetraploid accessions were distinguished from diploid accessions.

Varshney *et al.* (2009) studied genetic variation among 189 groundnut (*Arachis hypogaea* L.) accessions comprising landraces, cultivars, mutants, advanced breeding lines and others (unknown genetic background) which represents 29 countries and 10 geographical regions, using 25 SSR loci and detected high number of alleles in the range of 3 to 20 with an average of 10.6 alleles per locus. The PIC content varied from 0.38 to 0.88 with an average of 0.70. Cluster analysis grouped the accessions into 4 clusters and reported presence of high level of diversity in South America and South Asian accessions.

Shoba *et al.* (2010) evaluated eleven groundnut genotypes consisting of ten late leaf spot and rust resistant genotypes. Among the 17 SSR primer pairs used for assessing the genetic diversity, six primer pairs (24.0 per cent) were polymorphic. The genotype TMV 2 was susceptible to rust and late leaf spot diseases and it was separately clustered in the dendrogram and among the eleven foliar disease resistant genotypes, the genotypes viz., COG 0423, COG 0436 and COG 0432 were distantly clustered from TMV 2.

Ravi *et al.* (2011) identified candidate QTLs for drought tolerance, from a comprehensive and refined genetic map containing 191 SSR loci based on a single mapping population (TAG 24 $\times$ ICGV 86031), segregating for drought and surrogate traits was developed. Genotyping data and phenotyping data collected for more than ten drought related traits in 2–3 seasons were analyzed in detail for identification of main effect QTLs (M-QTLs) and epistatic QTLs (E-QTLs) using QTL Cartographer, QTL Network and Genotype Matrix Mapping (GMM) programmes. The identification of few major, many minor M-QTLs and QTL $\times$ QTL interactions during the present study confirmed the complex and quantitative nature of drought tolerance in groundnut.

Gautami *et al.* (2012) identified quantitative trait loci (QTL) for drought tolerance, from two new recombinant inbred line (RIL) mapping populations, namely ICGS 76 $\times$ CSMG 84-1 (RIL-2) and ICGS 44 $\times$ ICGS 76 (RIL-3). After screening of 3,215 simple sequence repeat (SSR) markers on the parental genotypes of these populations, two new genetic maps were developed with 119 (RIL-2) and 82 (RIL-3) SSR loci. Together with these maps and the reference map with 191 SSR loci based on TAG24 $\times$ ICGV 86031 (RIL-1), a consensus map was constructed with 293 SSR loci distributed over 20 linkage groups, spanning 2,840.8 cM. as all these three populations segregate for drought-tolerance-related traits. A few key genomic regions were selected on the basis of the QTL identified in each region, and their expected role in drought adaptation is reported.

Boontang *et al.* (2013) evaluated four peanut genotypes at two water regimes and data was recorded for specific leaf weight (SLW) and relative water content (RWC), and 256 SSR markers were used to detect genetic difference. 89 SSR markers could detect polymorphism among peanut genotypes (48.9%). KK 4 was clustered distinctly from the others genotypes. Whereas ICGV 98324, ICGV 98353 and ICGV 98303 were grouped in the same cluster far from KK 4.

John *et al.* (2013) evaluated eight groundnut genotypes using 45 SSR primers to study the level of diversity among them. Among 45 primers, 10 primers produced clear polymorphic bands. Genetic relationships among eight genotypes were estimated using Jaccard's similarity co-efficient and the similarity index values ranged from 23.5 per cent to 77.8 per cent indicating the presence of substantial molecular diversity among eight genotypes.

Roomi *et al.* (2014) screened 30 SSR markers among twenty peanut accessions. Fifteen out of thirty primers generated polymorphic bands among the selected accessions. In total, forty different polymorphic loci were determined across the selected accessions. The range of number of polymorphic loci detected ranged from 2 to 4 for each primer, with an average of 2.6 loci per primer. Polymorphic Information Content (PIC) value was calculated for each marker. The dendrogram was constructed on the basis of allelic data from fifteen SSR markers across the selected accessions. All the accessions were divided into six clusters at 0.67 coefficients of similarity.

Ren *et al.* (2014) used one hundred and forty-six highly polymorphic simple sequence repeat (SSR) markers to assess the genetic diversity and population structure of 196 peanut (*Arachis hypogaea* L.) cultivars which had been extensively planted in different regions in China. Sixty-four SSR markers did not amplify in most of the accessions, and therefore were eliminated from the analysis. The remaining 146 SSR markers amplified 440 polymorphic bands with an average of 2.99 with 2 to 9 per primer pair. The polymorphism information content (PIC) for the SSR loci ranged from 0.01 to

0.75 and the average PIC value was 0.38. The genetic diversity index ranged from 0.01 to 0.51, with an average of 0.11. Eighty-six rare alleles with a frequency less than one per cent were identified at 66 loci in this study. The ratio of cultivars with rare alleles was the highest in cultivars from the south and was the lowest in cultivars from the north.

A study conducted by Gaikpa *et al.* (2015), to find molecular diversity among cultivated groundnut using SSR markers. 13 SSR markers were polymorphic with 76.9 per cent of them showed PIC values above 0.50. Clustering analysis showed genetic similarities from 60 per cent to 90 per cent across the 20 genotypes and the genotypes were grouped into one group at 60 per cent similarity, whereas six well separated groups at 75 per cent similarity. Cluster analysis in this study showed that most *hypogaea* subspecies were separated from *fastigiata* ones at the molecular level.

Oteng-Frimpong *et al.* (2015) screened a total of 53 SSR and 25 were found to be polymorphic with an average polymorphic information content (PIC) value of 0.57. Of the 48 groundnut genotypes studied, 67 per cent showed very close relationship (~100% similarity) with one or more genotypes among themselves. The remaining 33 per cent of the groundnut genotypes were distant from each other and could therefore serve as effective parental material for future work.

Kanyika *et al.* (2015) analysed a total of 799 SSRs comprising of di- and tri-nucleotide motifs from both genomic and expressed sequence tag (EST) were screened across 16 cultivated groundnut varieties indigenous to Africa. The SSR markers amplified 817 loci and were graded on a scale of 1 to 4 according to successful amplification and ease of scoring of amplified alleles. Of these, 376 markers exhibited Polymorphic Information Content (PIC) values ranging from 0.06 to 0.86, with 1476 alleles detected at an average of 3.7 alleles per locus. The remaining 423 markers were either monomorphic or did not work well. The best performing polymorphic markers were subsequently used to construct a dissimilarity matrix that

indicated the relatedness of the varieties in order to aid selection of appropriately diverse parents for groundnut improvement.

Pereira *et al.* (2015) evaluated fourteen intraspecific top lines (F₇) to identify drought tolerant materials based on SSR markers. Thereafter, the selected lines were submitted to 10 days (d) of water stress and analyzed by physiological (stomata conductance, transpiration and photosynthesis) and biochemical (organic solutes and antioxidative enzymes) traits. SSR markers obtained from 18 genotypes were scored for their presence '1' or absence '0' of bands for each primer. The binary data were used to estimate levels of polymorphism by dividing the polymorphic bands by the total number of scored bands. Pair-wise similarity matrix was generated by Jaccard's coefficient using NTSYS-pc. A dendrogram was constructed by UPGMA method to identify the phenetic representation of genotypes. Lines grouped in same cluster of BR 1 were chosen for further physiological and biochemical assays.

2.3 CHARACTER ASSOCIATION

Yield is a polygenically controlled character and highly influenced by the environment. Selection merely based on yield is not effective. Selection based on its component traits increases yield as they are not only less complex but also relatively simply inherited and are much less influenced by environmental deviations. Character association analysis measures the actual relationship between various plant characters and helps the plant breeder in formulating selection criteria for pod yield in parental lines and segregating populations. 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). Correlation coefficient reveals the type, nature and magnitude of correlation between any pair of characters.

Both yield and drought tolerance cannot be considered as a single trait. Hence the response of yield to drought condition may not distinctly be explained by the responses of rooting traits alone without considering their association with physiological response of the genotype. Several studies have reported on the correlation of physiological characters with increased yield after drought stress such as Relative Water Content (RWC), Specific Leaf Area (SLA) and SPAD Chlorophyll Meter Reading (SCMR). However, those reports were limited to experiments under greenhouse conditions and with only a few genotypes and did not reveal the relationship between the physiological and rooting characters for contributing to pod yield under intermittent drought stress. There is an immediate need to study the mechanism of response of root traits along with physiological traits for the pod yield under drought stress in field conditions. In this background, it was proposed in this study to evaluate 32 groundnut genotypes for root and physiological traits and their correlated response to pod yield under irrigated and rain-fed conditions.

Alam *et al.* (1985) observed that pod yield per plant had positive association with number of pods per plant, days to maturity, secondary branches/plant and plant height. Shelling percentage had negative association with 100-kernel weight.

Reddy *et al.* (1987) reported that primary yield components of groundnut viz., shelling percentage, kernel yield and number of mature pods per plant showed positive correlation with each other and with pod yield..

Madhavi (1988) identified that LAI in the initial stages had positive correlation with pod yield, kernel yield and number of pods. She also observed strong correlation of LAI from 60 days with pod yield, kernel yield and total dry matter. She concluded that initial LAI together with initial dry matter could be employed profitably as selection criteria to select productive genotypes in groundnut breeding.

208 accessions of groundnut germplasm were evaluated by Rao *et al.* (1988) for association analysis. The study revealed that pod yield was strongly correlated with plant height, number of primary branches, number of nodes on first primary branch, leaf length, leaf breadth, number of flowers, number of pegs, number of mature pods, peg to flower ratio, and shelling percentage.

Yield of mature pods per plant had positive association with number of mature pods, number of immature pods, 100-kernel weight, yield of immature pods and biological yield (Sharma and Varshney, 1990).

Vaddoria and Patel (1992) reported that pod yield in *Virginia* runner type had positive significant association with harvest index, shelling percentage, number of mature pods per plant, 100-seed weight and number of primary branches per plant.

Wright *et al.* (1994) identified significant negative association of specific leaf area with harvest index. They concluded that selection for low specific leaf area in peanuts may be appropriate in water limited systems, where both pod yield for human consumption and vegetative yield for animal fodder need to be maximised.

Patra *et al.* (1995) found that LAI at 50 and 70 DAS had positive significant influence on number of pods per plant, shelling percentage, 100-kernel weight and pod yield. It was concluded that LAI at 70 DAS along with drymatter accumulation at 70 DAS were key growth variables positively influencing pod and oil yields in groundnut.

Arjunan *et al.* (1997) observed positive non-significant association of pod weight with specific leaf area and non-significant negative association of specific leaf area with harvest index.

Vasanthi *et al.* (1998) reported that pod weight per plant possessed significant positive correlation with sound mature kernel percentage and

significant negative association with days to 50 per cent flowering in a study involving advanced breeding lines.

Rostini *et al.* (2000) observed positive genetic correlation between yield and chlorophyll content at 16 days after flowering and negative genotypic correlation between yield and leaf angle and leaf number.

Reddy *et al.* (2003a) reported a positive correlation between SCMR and seed yield and negative correlation between SCMR and SLA and substantiated the conclusion that SCMR was a potential physiological trait to employ as a surrogate for transpiration efficiency.

Kumar (2004) found significant positive association of kernel yield per plant with mature pods per plant, 100-kernel weight and harvest index and positive non-significant association with shelling percentage.

Upadhyaya *et al.* (2005) reported that SCMR and SLA are negatively correlated. SCMR values were more strongly correlated with pod yield and other economic traits such as 100-seed weight at both 60 and 80 DAS than SLA.

Patil *et al.* (2006) conducted correlation analysis in thirteen genotypes along with four check varieties (JL-24, GPBD-4, Dh-86 and Dh-3-3-30) at six different locations and observed that pod yield per plant had significant positive association with number of pods per plant, shelling percent and sound mature kernel per cent in at least three locations.

Songsri *et al.* (2008) studied correlation among traits associated with drought tolerance and pod yield and found high magnitude of positive correlations among drought tolerance index (DTI), pod yield, root length density (RLD) and harvest index (HI), indicating that RLD in deeper soil contributed to pod yield and HI under drought conditions.

Boontang *et al.* (2010) evaluated 10 groundnut genotypes at two water regimes. Drought increased SCMR,SLW and reduced biomass,pod yield and

seed size whereas HI and no. of pods per plant were not significantly affected. SCMR and SLW were well associated and they had significant positive correlation with biomass and pod yield. SCMR seemed to be more stable than SLW and it is recommended to be used as a surrogate trait for drought tolerance in peanut.

Korat *et al.* (2010) evaluated 80 bunch groundnut genotypes and observed that yield contributing characters like 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. And they also noticed that the genotypic correlations of above said yield components with pod yield were also strong and with similar sign.

From correlation studies involving thirty four genotypes of groundnut Zaman *et al.* (2011) concluded that seed yield per plant showed highly significant and positive association with nut size, number of nuts per plant, kernel size and days to 50 per cent flowering.

Hamidou *et al.* (2012) studied 247 lines belonging to the reference collection of groundnut under well watered (WW) and intermittent water stress (WS) conditions in India and Niger for two years following similar experimental protocols. In water stress situation, the reduction in pod yield was from 31-46 per cent, in haulm yield from 8-55 per cent and in harvest index from 1-10 per cent. A close relationship was observed between yield and pod growth rate ($r^2 = 0.51$) and partitioning ($r^2 = 0.33$) under WS conditions. Whereas no significant relationship was found between yield under WS and SCMR or specific leaf area (SLA).

Sadeghi and Niyaki (2012) evaluated twenty three groundnut genotypes in order to study interrelationships among various agronomic traits under drought stress and irrigated conditions and reported that in both

conditions, 100- seed weight, total no. of kernels per plant, total no. of pods per plant and biomass had a high positive correlation with seed yield.

Alam (2014) carried out association analysis studies for pod yield and its yield component characters in 45 genotypes of groundnut and found that pod yield showed significant positive association with secondary branches per plant, harvest index, 100-pod weight, 100-kernel weight, pod size, disease incidence and canopy temperature indicating that these are important components for improvement of pod yield in groundnut.

Rao *et al.* (2014) analysed 50 groundnut genotypes and revealed that dry pod yield had significant positive association with kernel yield, number of pods per plant, hundred kernel weight and dry haulm yield.

Shukla and Rai (2014) reported that pod yield was positively correlated with kernel yield, pod yield per plant, hundred kernel weight, shelling percent and kernel uniformity.

Pavankumar *et al.* (2014) reported that kernel yield was significantly and positively associated with pod yield per plant, number of mature pods per plant, shelling percentage, harvest index, sound mature kernel percentage, specific leaf weight at 60 days after sowing, protein content and oil content in an experiment with sixty six genotypes of groundnut.

Satish (2014) evaluated sixteen genotypes of groundnut and observed significant and positive genotypic correlations of pod yield with number of pods per plant followed by number of branches, days to 50 per cent flowering and 100 seed weight, whereas with plant height pod yield showed negative and non-significant correlation.

Drought at pod filling reduces growth, yield and seed quality of peanut (*Arachis hypogaea* L.) great root system can reduce yield loss under water stress. Pot experiments were conducted by Junjittakarn *et al.* (2014) to determine the relationship between rooting traits and peanut yield under

terminal drought. In conclusion, drought stress decreased root traits, dry matter, and harvestable yield in peanut. Root length had a positive correlation with biomass, genotypes having large root system could maintain peanut yield under drought condition.

Vasanthi *et al.* (2015) in a study of 29 released/pre-release groundnut cultures observed significant positive association of number of mature pods per plant, number of primary branches per plant, and 100- seed weight with pod yield per plant.

Rasheed *et al.* (2015) observed that plant height, pod /plant and shelling percentage revealed positive non significant correlation with pod yield but kernelplant⁻¹, 100 kernel weight and pod length displayed negative and non-significant association with pod yield.

Shreya *et al.* (2015) studied correlation for yield and yield contributing characters in F₃ generation derived from four crosses of groundnut (involving parents viz., ICGV 05163, ICGV 06045, ICGV 93261, TCGS 1043 and TCGS 913; TCGS 1043 was used as common female parent) and reported that yield was significant and positively associated with number of primary branches per plant (0.273 to 0.401), plant height per plant (0.179 to 0.404cm), pegs number per plant (0.478 to 0.613), total biomass per plant (0.779 to 0.819 g), shoot weight per plant (0.448 to 0.542 g), root weight per plant (0.311 to 0.458 g), number of mature pods per plant (0.742 to 0.853), number of immature pods per plant (0.161to 0.387) , harvest index (0.435 to 0.572 %) and kernel weight per plant (0.950 to 0.980 g) in all the four crosses.

Jain *et al.* (2016) carried out correlation analysis for pod yield and its component characters in 24 genotypes of groundnut and noticed genotypic correlation coefficients of relatively higher magnitude than the corresponding phenotypic correlation coefficients, indicating strong inherent association between the characters. Pod yield per plant displayed significant positive association with kernel yield per plant, mature pods per plant and plant height.

Eighteen local collections of groundnut were evaluated by Kamdi *et al* (2017) along with checks (TAG -24 and Kopergoan-3) for assessment correlation analysis. Positive significant genotypic and phenotypic correlations between number of mature pods per plant and weight of dry pods in kg /ha were observed. Height of main axis had positive significant association with number of primary and secondary branches plant. They reported positive association between number of primary and secondary branches per plant.

Reddy *et al.* (2017) carried out character association studies for kernel yield and its component characters in six parents and their 15 F₁ crosses in groundnut. Kernel yield per plant possessed significant positive association with pod yield per plant, mature pods per plant, 100-kernel weight, pods per plant, pegs per plant, harvest index and shelling percentage at both the genotypic and phenotypic levels.

Bhakal and Lal (2017) reported plant height at 40 DAS (0.9215 and 0.8915), was significantly and positively correlated with pod yield q/ha (0.2897 and 0.2637) and hundred kernel weight (0.8981 and 0.4804) was positively correlated with pod yield per plant.

Hugar and Savithramma (2017) identified physiological traits related to Water Use Efficiency, SLA and SCMR were negatively associated to each other with the latter being associated positively and the former associated negatively with pod yield.

Ninety genotypes along with three check varieties viz., JL TG37A, PM-2 and UG-5 were evaluated for association analysis by Ram *et al.* (2017) and they observed 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.

Hampannavar *et al.* (2018) studied 144 groundnut genotypes and reported significant positive correlation of kernel yield per plant, mature pods

per plant, sound mature kernel and haulm yield per plant had with dry pod yield per plant.

2.4. PATH CO-EFFICIENT ANALYSIS

Path coefficient analysis is an effective statistical tool developed by Wright (1921) which partitions the correlation co-efficients into direct and indirect effects of independent variable on dependent variable indicating the direction of selection to be practiced. It helps in identification of traits that should be given emphasis in selection process. Hence, path analysis of much importance in any plant breeding programmes. The available literature on path coefficient analysis is furnished here under.

Sudarshanam (1985) reported that the number of mature pods per plant and 100-seed weight had maximum positive direct effect on pod yield in Spansih group whereas 100-kernel weight had maximum direct effect in Virginia group.

Reddy *et al.* (1986b) observed that maximum positive direct effect of kernel yield had on pod yield followed by number of mature pods per plant.

Abraham (1990) reported that kernels per plant and 100-kernel weight had high positive direct effect on kernel yield of 42 bunch varieties. The indirect effects of pods per plant and shelling percentage via kernels per plant and sound mature kernels and shelling percentage via 100-kernel weight were appreciable and positive indicating that kernels per plant and 100-kernel weight were the major yield contributors.

Patra *et al.* (1995) identified that LAI at 50 and 70 DAS had positive and significant influence on number of pods per plant, shelling percentage, 100-kernel weight, pod yield and oil content.

Path coefficient analysis conducted for 23 groundnut genotypes by Uddin *et al.* (1995) and reported that days to maturity, primary branches per plant and nuts per plant had large direct effects on seed yield per plant.

Hoque and Chowdhury (1997) in a study involving 25 genetically diverse groundnut genotypes and reported that the direct effects of 100-pod weight, primary branches per plant and mature pods per plant were significant with pod yield.

Moinuddin (1997) observed strong positive association of pod yield with number of mature pods per plant, 100-kernel weight and biomass per plant and also their direct effects were positive and high in almost all environments. Haulm yield and shelling per cent exhibited negative association and negative direct effect on pod yield.

Jayalakshmi (1997) identified that harvest index was positively associated with SLA in parents and F_1 (but exhibited non-significant association in F_3 generation).

Vasanthi *et al.* (1998) carried out association studies and observed high positive direct effect of 100-pod weight on pod yield followed by 100-kernel weight.

Khan *et al.* (2000) evaluated thirteen geographically diverse peanut genotypes and reported that 100-kernel weight had the highest direct effect on pod yield followed by pods per plant, seeds per pod and sound mature kernel per cent. They also indicated that the kernel weight affected pod yield negatively via indirect influence of pods per plant, seeds per pod, sound mature kernel per cent and shelling percentage.

Singh and Singh (2001) reported that the number of primary branches had maximum positive direct effect on pod yield. It was followed by 100-kernel weight, sound mature kernel percentage, harvest index and number of fruiting nodes. Main shoot height had largest negative direct effect via number of primary branches and also via 100-kernel weight, sound mature kernel percentage and harvest index.

Studies of Vijayasekhar (2002) indicated maximum direct effect of kernel yield per plant on pod yield followed by pods per plant and harvest index. High and positive indirect effect of kernel yield per plant was exerted through harvest index while pods per plant and harvest index contributed through kernel yield per plant.

Reddy (2003) reported high positive direct effect of pod yield, mature pods per plant, pods per plant, 100-kernel weight and harvest index on kernel yield in groundnut.

Kumar (2004) observed positive moderate indirect effect of SLA on kernel weight through SCMR, negative indirect effect through SLA at 60 DAS was also observed. The direct effect of pod weight per plant on kernel weight per plant was high. High positive indirect effects were observed through LAI at 90 days and harvest index.

In parents, SPAD chlorophyll meter reading and in crosses sound mature kernel per cent exhibited high positive direct effect on pod yield per plant in a study by Devi (2004).

Suneetha *et al.* (2005) carried out association studies and reported that harvest index exerted the highest positive direct effect on pod yield per plant followed by 100-kernel weight. Days to maturity, number of primary branches, number of mature pods, shelling percentage and 100-pod weight also exhibited positive direct effect but of lower magnitude while days to 50 per cent flowering, height of main axis had high negative direct effects.

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

Venkateswarlu *et al.* (2007) evaluated 28 F_1 s derived out of 8 X 8 diallel mating system involving eight parents and reported 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.

Korat *et al.* (2010) carried out genotypic and phenotypic path analysis in eighty bunch groundnut genotypes and found highest positive direct effects of biological yield per plant and harvest index towards pod yield. They also found that hundred-kernel weight contributed indirectly via biological yield per plant and harvest index.

Vekariya *et al.* (2011) evaluated fifty diverse genotypes of bunch groundnut and path analysis revealed that the kernel yield per plant, biological yield per plant and harvest index had high and positive direct effects on pod yield per plant.

Zaman *et al.* (2011) carried out path coefficient analysis in a study involving thirty four genotypes of groundnut revealed 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 per cent flowering and days to maturity.

In order to study interrelationships among various agronomic traits under drought stress and irrigated conditions, Sadeghi and Niyaki (2012) studied twenty three groundnut genotypes and reported that under irrigated condition, total number of kernels per plant, 100-seed weight and total number of pods per plant and in drought stress condition, 100-seed weight, total number of kernels per plant, total number of pods per plant and biomass had greatest positive direct effects on seed yield. They also noticed that high indirect contribution was via 100-seed weight and total number of kernels per plant.

Pavankumar *et al.* (2014) from a study involving sixty six genotypes of groundnut reported that pod yield per plant and shelling percentage had high positive direct effect on kernel yield signifying the importance of these traits in the improvement of seed yield. Hence these characters should be given more importance in the improvement of kernel yield.

Satish (2014) carried out association studies in 16 genotypes of groundnut and reported that pod yield per plant followed by 100 seed weight, number of branches per plant and days to 50 per cent flowering had positive direct effect on number of pods per plant signifying the importance of these traits in the improvement of pod yield.

Association studies were carried out in set of 50 groundnut genotypes by Rao *et al.* (2014) and observed highest direct positive effect of kernel yield, days to maturity no of pods per plant and hundred kernel weight was revealed on pod yield.

Vasanthi *et al.* (2015) analysed 29 groundnut cultivars and observed that high positive direct effect on pod yield per plant was exhibited by the traits viz., number of mature pods per plant, length of main axis, 100-seed weight, number of primary branches per plant, number of immature pods per plant, harvest index, weight of immature pods per plant, shelling percentage and days to 50 per cent flowering.

John and Reddy (2016) evaluated twenty four F₁s along with six lines and four testers of groundnut and reported that the maximum positive direct effect on pod yield per plant was contributed by days to maturity, SPAD chlorophyll meter reading at 40 days after sowing and 60 days after sowing, specific leaf area at 60 days after sowing, specific leaf area at 40 days after sowing and 60 days after sowing, dry haulms yield per plant and harvest index indicating that these traits are the important yield contributing characters.

24 genotypes of groundnut were evaluated by Jain *et al.* (2016) and reported high direct effects of kernel yield per plant, plant height and matured pods per plant on pod yield per plant.

Eighteen local collections of groundnut, along with two checks were studied and path co-efficient analysis was carried out by Kamdi *et al.* (2017) and indicated that number of mature pods per plant, number of primary branches per plant and days to 50 per cent flowering had positive direct effect on weight of dry pods. Hence, proper attention should be given to increase the number of mature pods plant, number of primary branches per plant and days to 50 per cent flowering for improving pod yield of groundnut.

Hugar and Savithramma (2017) reported that pods per plant, kernel yield and primary branches per plant had positive direct effect indicating that the correlation between these characters with pod yield is due to direct effect of the characters.

Ninety genotypes along with three check varieties viz., JL TG37A, PM-2 and UG-5 were evaluated for association analysis by Ram *et al.* (2017). They observed highest positive direct effect on dry pod yield by kernel yield per plant (2.28) followed by days to maturity (0.57), oil content (0.31) and days to 50 per cent flowering (0.22). This indicates that increase in kernel yield per plant, 100-kernel weight and sound mature kernels would improve the dry pod yield per plant of groundnut.

Hampannavar *et al.* (2018) studied 144 groundnut genotypes and reported kernel yield per plant (0.9809) had highest direct effect on dry pod yield. The traits like number of mature pods per plant (0.0029), sound mature kernels (0.0024) and haulm yield (0.0018) had high and positive indirect effect on dry pod yield via kernel yield.

Chapter ~ III

Material and Methods

Chapter III

MATERIAL AND METHODS

3.1 LOCATION OF THE EXPERIMENTAL SITE

The present investigation was carried out during *kharif*, 2017 and *rabi*, 2017-18 at Regional Agricultural Research Station, Tirupati situated at an altitude of 182.90 m above mean sea level, 13° N latitude and 79° E longitude. The soil is sandy clay loam with medium fertility. The material used and methods followed pertaining to the present investigation are presented here under.

3.2 MATERIAL

The experimental material consisted of 32 genotypes of groundnut. The material was made available for the study by the Principal Scientist (Genetics and Plant Breeding), Regional Agricultural Research Station, Tirupati.

3.3 METHODS

3.3.1 Field Layout

In the present study, two experiments were laid out, Exp: 1-Irrigated and Exp: 2-Rainfed, in a randomised block design each with two replications. The crop was sowed on 14th July 2017. Each genotype was sown in two rows of 5 m length and 0.9 m width with a spacing of 30 cm between the rows and 10 cm between the plants within rows. But, due to uniform rainfall distribution throughout the crop season during *kharif*, 2017, there was no difference with respect to moisture stress in both the experiments (weather parameters given in Appendix I). Thus, the two experiments were clubbed and considered as a single experiment with four replications. An experiment was laid out in *rabi*, 2017-18 on 18th December 2017 with two replications under irrigated conditions to record observations on relative water content along with other water use efficiency traits, SCMR and SLA as it could not be taken

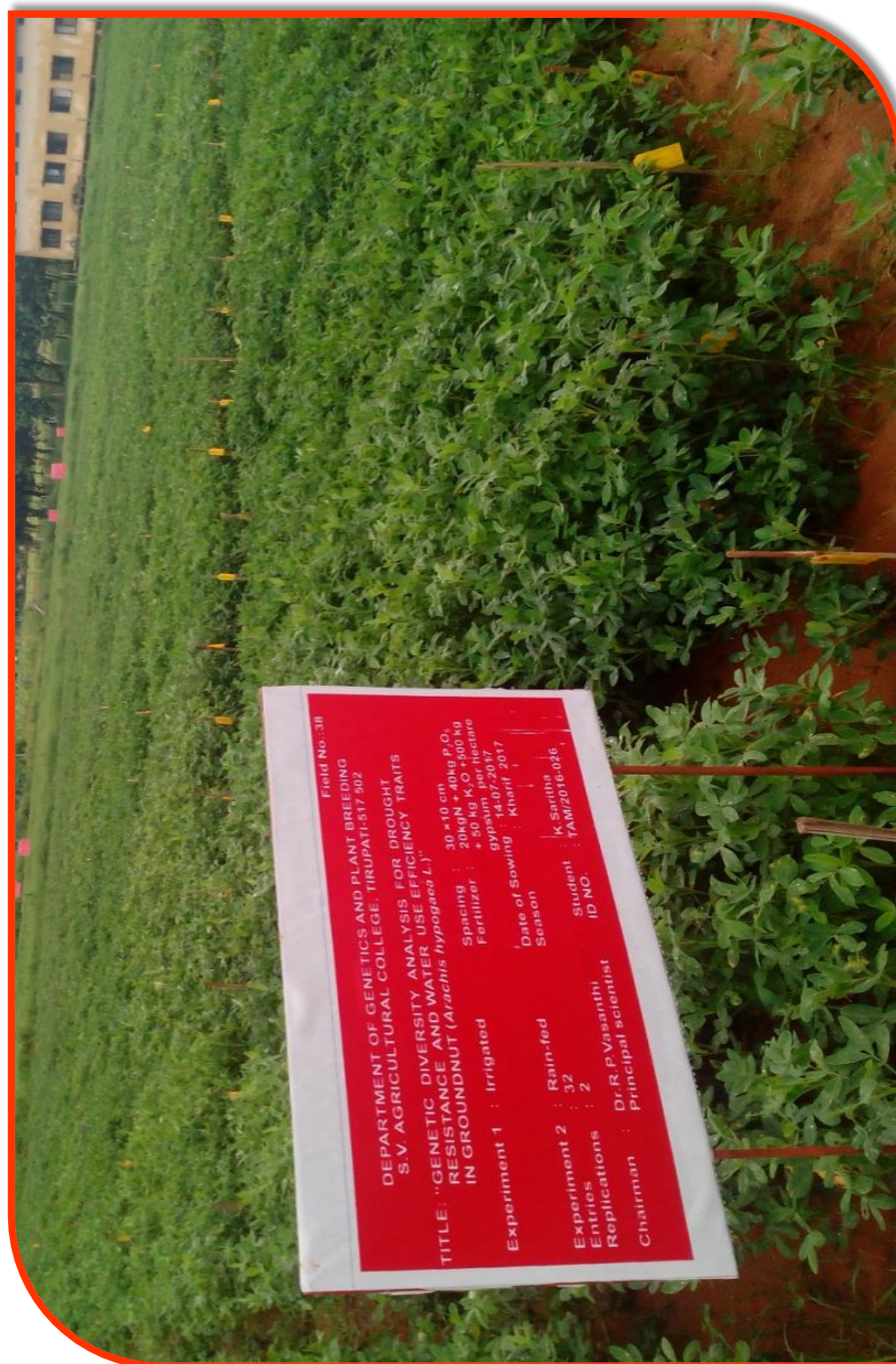


Plate 1. View of experimental plot (kharif, 2017)

during *kharif*, 2017 as crop did not experience moisture stress at any stage during the crop period. Each genotype was sown in two rows of 5 m length and 0.9 m width with a spacing of 22.5 cm between the rows and 10 cm between the plants within rows. During rabi season, only mild moisture stress could be imposed by withholding irrigation for a period of 15 days.

Table 3.1. Pedigree of 32 groundnut genotypes included in the present study

S. No	Genotype	Pedigree
1	TCGS-1694	K 6 × ICG (FDRS) 79
2	TCGS-1696	ICG (FDRS) 79 × Tirupati-4
3	TCGS-1630	Tirupati-1 × ICG (FDRS) 79
4	TCGS-1653	TCGS-45 × TCGS-876
5	TCGS-1616	K 6 × Dharani
6	TCGS-1622	K 6 × Dharani
7	TCGS-1073	TCGS-29 × JAL-30
8	TCGS-1157	TAG-24 × Jyothi
9	R-2001-2-1	ICGS 11 x ICG 4728
10	GPBD-4	KRG-1 × ICGV 86855
11	R-2001-3-1	ICGS 11 x ICG 4728
12	J 89	ALR-3 × TG 26
13	R 2001-3	ICGS 11 x ICG 4728
14	SG 99	ICGV 86529 x ICGV 87160
15	R 2001-2	ICGS 11 x ICG 4728
16	ALG-06-320	(J 11 x CG 52) x ICGV 86015
17	K 1805	(ICGV92069 X ICGV93184) X (ICGS44 X ICGS76)
18	K 1725	Kadiri 7 bold x TAG24

19	K 9	Kadiri 4 x Vemana
20	K. Harithandra	9157-2xPI476177
21	K. Anantha	Vemana x Girnar
22	TCGS-1097	TAG-24 × TCGS-522
23	GG 16	JSP-14 × JSSP-4
24	K 1847	Kadiri 8 bold x TAG24
25	K 1789	(ICGV92069 X ICGV93184) X[(ICGV87121XICGV87853)X ICGV92093]
26	K 1811	(ICGV92069XICGV93184) SIL4 X ICGV98300
27	ICGS 76	TMV 10 x Chico
28	ICG 86325	ICGS 20 x G 201
29	Dharani	VRI-2 × TCGP-6
30	Narayani	JL 24 × Ah 316/s
31	GG 20	GAUG 10 × Robut 33-1
32	K 6	JL 24 × Ah 316/s

3.3.2 Crop Husbandry

The field was ploughed and harrowed until a fine tilth of soil was obtained. The crop was raised under rainfed conditions during *kharif*, 2017 and under irrigated conditions during *rabi*, 2017-18 and was fertilized at 20 kg N, 40 kg P₂O₅, 50 kg K₂O and 500 kg gypsum ha⁻¹ in the form of urea, single super phosphate and muriate of potash respectively. Weeding and plant protection operations were taken up as and when needed during the crop growth uniformly to all genotypes.

3.3.3 Data Recording

Observations were recorded on randomly chosen five competitive plants in each genotype in each replication for all morphological, yield and

physiological parameters. The mean values of selected competitive plants were averaged and expressed as mean of the respective characters. The details of data recorded were as follows.

3.3.3.1 Morphological, yield and yield attributes

3.3.3.1.1 Number of primary branches per plant

Number of all primary branches originating from the main axis were counted as number of primary branches per plant at the time of harvest.

3.3.3.1.2 Number of secondary branches per plant

Number of all secondary branches originating from the primary branches were counted as number of secondary branches per plant at the time of harvest.

3.3.3.1.3 Plant height (cm)

Height of the plant was measured in centimetres using a scale as the vertical distance of the main axis from ground level to the apical leaflet.

3.3.3.1.4 Number of pegs per plant

Number of pegs was determined by counting all pegs at the time of harvest.

3.3.3.1.5 Number of mature pods per plant

Number of well filled and matured pods per plant were counted and mean value of total number of mature pods stripped from five plants gave the number of mature pods per plant.

3.3.3.1.6 Number of immature pods per plant

The number of immature pods per plant was estimated from the average of total number of immature pods collected from five plants.

3.3.3.1.7 100-seed weight (g)

Hundred kernels at random were counted and weighed for each genotype in each replication and recorded as 100-seed weight.

3.3.3.1.8 Shelling percentage (%)

Shelling percentage was calculated using the formula

$$\text{Shelling percentage} = \frac{\text{Kernel yield plant}^{-1} \text{ (g)}}{\text{Pod yield plant}^{-1} \text{ (g)}} \times 100$$

100 g pods were taken and shelled to get shelling percentage of each genotype. The observed values of shelling percentage are angular transformed.

3.3.3.1.9 Harvest Index (%)

Harvest Index was calculated by using the formula

$$\text{HI} = \frac{\text{Economic yield plant}^{-1} \text{ (g)}}{\text{Biological yield plant}^{-1} \text{ (g)}} \times 100$$

Mean value of five sample plants per replication was recorded as harvest index in percentage. The observed values of HI were angular transformed.

3.3.3.1.10 Pod yield per plant (g)

Weight of mature pods per plant was taken and the mean value of weight of mature pods from five plants was recorded as weight of mature pods per plant.

3.3.3.2 Physiological characters

Data for the following characters were recorded on sampled plants.

3.3.3.2.1 SCMR (SPAD chlorophyll meter reading)

Soil Plant Analytical Development (SPAD) chlorophyll meter readings (SCMR) was recorded at 60 DAS in *kharif*, 2017 and in *rabi*, 2017-18 with SPAD chlorophyll meter (SPAD-502, Minolta corp., Ramsey, NJ). Measurements were made on the 3rd leaf from top of main axis of five plants.

3.3.3.2.2 Specific leaf area (SLA) (cm² g⁻¹)

Specific leaf area (SLA) was recorded at 60 DAS in *kharif*, 2017 and in *rabi*, 2017-18. Leaves were collected from five plants from each genotype in each replication and leaf area was estimated using a leaf area meter (LICOR Model-3100). They were dried in a hot air oven at 80°C for two days and dry weight was recorded. The formula used was

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

3.3.3.2.3 Relative water content (%)

Relative water content was recorded at 80 DAS in *rabi* season. Measurements were made on the 3rd leaf from top of main axis of five plants. RWC was calculated by using following formula and expressed in percentage.

$$RWC = \frac{\text{Fresh weight-Dry weight}}{\text{Turgid weight-Dry weight}} \times 100$$

3.3.3.2.4 Leaf area index (LAI)

Leaf area index (LAI) was estimated at 60 and 80 DAS using the formula

$$LAI = \frac{\text{Total leaf area}}{\text{Unit ground area}}$$

Three plants leaf area was measured by using leaf area meter (LICOR model-3100) and the average was taken.

3.3.3.2.5 Leaf area duration (LAD) (dm² day)

Leaf area duration (LAD) was recorded at 80 DAS. Leaves were collected from three plants from each treatment in each replication for calculating LAD. Leaf area was estimated using a leaf area meter (LI-COR Model-3100). The formula used was

$$\text{LAD} = \frac{A_1 + A_2}{2} \times (t_2 - t_1)$$

Where,

A_1 = leaf area at time t_1

A_2 = leaf area at time t_2 .

3.3.3.2.6 Angle between main axis and first two primary branches at 60 and 80 DAS (°)

Five plants were selected randomly from each genotype in each replication and angle between main axis and first two primary branches was recorded using a protractor in field itself.

3.3.3.2.7 Root length (cm)

At maturity, the field was well irrigated and five plants from each genotype in each replication were lifted carefully and root length was recorded in centimetres from base to tip of main root.

3.3.3.2.8 Root dry mass (g)

Roots were collected from five plants from each genotype in each replication and they were dried in a hot air oven at 80°C for two days and dry weight was recorded.

3.4 STATISTICAL ANALYSIS

The data collected on competitive plants in all the entries in different replications were averaged replication wise and mean values were subjected for statistical analysis as follows

- i. Analysis of variance
- ii. Estimation of genetic parameters viz., genotypic and phenotypic coefficients of variation, heritability (broad sense), genetic advance and genetic advance as per cent of mean.
- iii. Estimation of genetic divergence using Mahalanobis's D^2 analysis.
- iv. Estimation of phenotypic and genotypic correlations and
- v. Path co-efficient analysis.

3.4.1 Analysis of Variance

The data for different characters were statistically analysed as per Panse and Sukhatme (1961).

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

where,

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

μ = General mean

g_i = Effect of i th genotype

γ_j = Effect of j th replication

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

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

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	F ratio
Replication	(r-1)	RSS	M_r	M_r / M_e
Genotypes	(t-1)	VSS	M_v	M_v / M_e
Error	(r-1) (t-1)	ESS	M_e	-
Total	(rt-1)	TSS		

Where,

r = number of replications

t = number of genotypes

M_r = Mean sum of squares due to replications

M_v = Mean sum of squares due to genotypes

M_e = Mean sum of squares due to error

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

3.4.2 Estimation of Genetic Parameters

The data obtained from the analysis of variance were used to estimate the following genetic parameters.

3.4.2.1 Variance

The genotypic and phenotypic variances were calculated as per the formula proposed by Lush (1940)

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

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

$$\sigma_g^2 = \text{Genotypic variance}$$

$$\sigma_e^2 = \text{Error variance}$$

3.4.2.2 Genotypic and phenotypic coefficient of variation

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

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

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

Where, σ_p , σ_p and $\bar{X}$ 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

Heritability in broad sense refers to the proportion of genotypic variance to the total variance of the population. Heritability in broad sense [$h^2_{(b)}$] was calculated by the formula given by Allard (1960).

$$\text{Broad sense Heritability} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

where,

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

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance ($\sigma_g^2 + \sigma_e^2$)

σ_e^2 = Environmental variance

As suggested by Johnson *et al.* (1955), 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.* (1955).

$$GA = k \sigma_p h^2_{(b)}$$

where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

$h^2_{(b)}$ = 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 percent mean)

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

$$\text{GA as per cent of mean} = \frac{\text{GA}}{\bar{X}} \times 100$$

where,

GA = Genetic advance

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

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

Less than 10% - Low

10 – 20 % - Moderate

More than 20% - High

3.4.3 Genetic Divergence

3.4.3.1 Mahalanobis's generalized distance (D^2)

Genetic diversity between genotypes was estimated using D^2 statistic given by Mahalanobis (1936).

3.4.3.1.1 Test of significance

Variances were calculated for all the sixteen characters 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 character, a simultaneous test of significance of differences between 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 utilized Wilk's ' Λ ' criterion (Wilks, 1932). The sum of squares and sum of products of error and error plus

Variety Variance, Covariance matrix were used for this purpose. The estimation of λ (Wilk's criterion) was done using the following relationship:

$$\lambda' = \frac{|E|}{|E + V|}$$

where,

$$|E| = \text{Determinant of error matrix}$$

$$|E + V| = \text{Determinant of error + varieties matrix}$$

The significance of ' λ ' was tested by

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

where,

$$m = n - (P + q + 1)/2 \text{ with } pq \text{ degree of freedom}$$

$$n = \text{Degrees of freedom of error + varieties}$$

$$p = \text{Number of characters}$$

$$q = \text{Number of genotypes} - 1$$

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

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 reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e., $\sum d_i^2$

3.4.3.1.3 Computation of D^2 values

The D^2 value between ' i^{th} ' and ' j^{th} ' genotypes for ' p ' characters was calculated as

$$D_{ij} = p \sum_{t=1} (\bar{Y}_{it} - \bar{Y}_{jt})$$

where,

$\overline{Y_{it}}$ = Uncorrelated mean value of 'ith' genotype for 't' character

$\overline{Y_{jt}}$ = Uncorrelated mean value of 'jth' genotype for 't' character

D_{ij} = D^2 value between 'ith' and 'jth' genotypes

3.4.3.1.4 Testing the significance of D^2 values

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

3.4.3.1.5 Determination of group constellations (or) clusters

Grouping of genotypes into different clusters was done by using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two varieties belonging to the same cluster should atleast, on an average show a smaller D^2 values of the combinations of each genotype arranged in increasing (ascending) order of their magnitudes in a tabular form as described by Singh and Choudhary (1977).

To start with two genotypes having the smallest distance from each other were considered, to which a third genotype having the smallest average D^2 value from the first two genotypes was added. Similarly, the nearest next fourth genotype was considered and this procedure was continued. At certain stage when it was felt that after adding a particular genotype, there was an abrupt increase in the average D^2 , that population was not considered for including in that cluster.

The groups of the first cluster were then omitted and the rest were treated in similar way. This process was continued till all the populations were included into one or the other cluster.

After the formation of the clusters, the average inter and intra cluster divergence (distances) were calculated.

3.4.3.1.6 Average intra-cluster distance

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

$$\Sigma D_i^2 / n$$

where,

ΣD_i^2 = the sum of distance between all possible combinations (n) of the genotypes included in a cluster.

3.4.3.1.7 Average inter- cluster distance

Clusters are taken one by one and their distance from other clusters were calculated. The distance between two clusters was the sum of the product of number of genotypes in both the clusters under consideration.

3.4.3.1.8 Cluster diagram

The clusters and their mutual relationship 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 the combinations, each cluster was ranked on the basis of their combination towards divergence between two entries ($d_{ij} = Y_{it} - Y_{jt}$). Rank one is given to the highest mean difference and rank 'p' to the lowest difference, where 'p' is the total number of characters. Percentage contribution of each character (X) towards genetic divergence is calculated using formula:

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

where,

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

M = All possible combinations of number of genotypic pairs.

3.4.3.2 Canonical analysis

Canonical analysis was used to verify the clustering pattern obtained by Mahalanobis's D^2 statistic. The canonical vectors or roots were calculated to represent the genotypes in the graphical form (Rao, 1952).

3.4.3.2.1 Calculation of sum of squares and sum of products

The correlated standard means were transformed into uncorrelated standardized variables. For each character and character contributions, sum of squares and sum of products were computed using the transformed variables to obtain the matrix of variances and covariances (matrix A). From matrix A, matrix $(A)^p$ was derived where 'p' is the number of characters.

3.4.3.2.2 Calculation of the first vector

The first approximate trial vector was obtained by first getting the column totals of matrix $(A)^p$ and then by dividing each of the column totals by the highest quantity among them. The canonical vectors were determined by iteration starting with the trial vector. The second approximation vector was obtained by multiplying each column of matrix $(A)^p$ with the first trial vector by the highest value among them. This new vector was then used as a trial vector and the procedure was repeated till the elements of the two approximation vectors were same. The vectors were then standardized by dividing them by the correlated sum of squares of these vectors. The first root ' λ_1 ' was calculated as the p^{th} root of the highest column total of the last approximation.

3.4.3.2.3 Calculation of the second vector

For getting the second vector ' λ_2 ' the original (A) ^p matrix was transformed and represented as (B) ^p. Each (I, j) th element in (B) ^p was calculated as follows:

$$(I, j)^{\text{th}} \text{ element} = (A)^p - \lambda_1 X_i^{\text{th}} \text{ element of the first vector}$$

The procedure followed in case of matrix 'A' was repeated to obtain second canonical root.

3.4.3.2.4 Estimation of 'Z' values

From the values of $Y_1, Y_2, \dots, Y_{ij}$, the mean values of characters Z_1, Z_2, Z_3 were calculated as, $Z_1 = (Y) (V_1); Z_2 = (Y) (V_2); Z_3 = (Y) (V_3)$.

3.4.3.2.5 Contribution of vectors towards divergence

Total contribution of all vectors was given by sum of diagonal elements in matrix A.

$$\text{Per cent of vector 1 } (\lambda_1) = \frac{\lambda_1 \times 100}{\text{Total contribution of all vectors}}$$

$$\text{Per cent of vector 2 } (\lambda_2) = \frac{\lambda_2 \times 100}{\text{Total contribution of all vectors}}$$

3.4.3.3 Divergence studies by using SSR markers

Detection of molecular polymorphism among 10 selected genotypes of groundnut was performed using SSR markers. The genotypes were selected based on SCMR and SLA values. 10 genotypes with contrasting drought characteristics like SCMR, SLA and RWC were selected.

3.4.3.3.1 Plant materials

The materials used for the study comprised of 10 genotypes of groundnut. The genotypes were sown in pots under sterile conditions.

Afterwards healthy leaf samples collected from 14 days old seedlings were used for DNA extraction.

3.4.3.3.2 Extraction of plant DNA

DNA was extracted as per modified CTAB (Cetyl trimethyl ammonium bromide) method given by Doyle and Doyle (1990).

- a) Healthy leaves were collected from young plants (14 days old) and brought to laboratory.
- b) The leaves were cut into small pieces and homogenized completely with liquid nitrogen using pestle and mortar.
- c) Leaf powder was taken into 2 ml eppendorf tube, and 1 ml of pre heated (65°C) extraction buffer (containing 2% (CTAB, 100 mM Tris, 20 mM EDTA, 1.4 M NaCl, 1% PVP and 1% β - mercaptoethanol) was added and mixed thoroughly.
- d) Contents were mixed by vortexing for few minutes and incubated at 65°C for 1 hr. Tubes were shaken once in 15 minutes.
- e) Samples were kept aside for 5 minutes.
- f) Samples were centrifuged at 10,000 rpm for 10 minutes at 37°C.
- g) Supernatant was collected and to the supernatant equal volume of phenol and chloroform (1:1) was added and centrifuged at 10,000 rpm for 10 minutes.
- h) Collect supernatant and add equal volume of Chloroform: Isoamyl Alcohol (23:1); mix gently and centrifuge at 37°C @10,000 rpm for 10 min.
- i) Supernatant was collected. 2 μ l RNAase was added and incubate at 37°C for 30 min. Then equal volume of Chloroform: Isoamyl Alcohol (23:1) was added; mix gently and centrifuge at 37°C @10,000 rpm for 10 min.
- j) Supernatant was collected and to it half volume of 5 M NaCl and double the volume of 90% ethanol was added. Tubes were kept at -20°C for 1 hour.

- k)** Samples were centrifuged at 15,000 rpm for 15 minutes at 4⁰c.
- l)** Supernatant was discarded. To the pellet 100 µl of 75% ethanol was added and centrifuged at 15,000 rpm for 15 minutes at 4⁰c.
- m)** Pellet was allowed to dry and after drying pellet was dissolved in 50 µl of TE buffer and stored at -20°C for further use.

3.4.3.3.3 Simple Sequence Repeat (SSR) or microsatellite markers analysis

The reaction mixture composition for the polymerase chain reaction was prepared by using following reagents for each of the DNA sample.

10X Taq buffer (New England BioLabs)	:	1.0 µl
10 mM dNTPs (New England BioLabs)	:	0.25 µl
25 mM Mgcl ₂ (New England BioLabs)	:	0.4 µl
Forward Primer (10 picomoles / µl)	:	1.0 µl
Reverse Primer (10 picomoles / µl)	:	1.0 µl
Taq polymerase enzyme (conc.5 U/µl)	:	0.1 µl
Template DNA (50ng / µl)	:	3.0 µl
Milli-Q-water	:	3.25 µl
Total	:	10 µl

3.4.3.3.4 PCR Conditions

Amplification was carried out on PCR machine (Eppendorf, Germany) adopting the following programme

The amplification profile was as follows,

No	Step	Temperature	Time	Number of cycles
a.	Initial denaturation	94°C	3 minutes	1 cycle
b.	Denaturation	94°C	30 seconds	35 cycles
c.	Primer annealing	As per T _m of SSR markers	30 seconds	
d.	Primer extension	72°C	45 seconds	
e.	Final extension	72°C	10 minutes	1 cycle
f.	Holding temperature	4°C	Till removed	

3.4.3.3.5 List of Primers Used

Twenty seven primers were used. The primer sequences used in SSR technique along with their annealing temperature are given in Table 3.2.

Table 3.2. List of SSR markers along with their nucleotide sequence used for PCR amplification in groundnut.

S. No	Primer	Primer sequence 5' - 3'	Annealing temperature (°C)
1	AH 041	(F) : CGCCACAAGATTAACAAGCACC	62.4
		(R) : GCTGGGATCATTGTAGGGAAGG	
2	AH 191	(F) : TTGTTGAGGAGGTGATGCTGGT	62.6

		(R) : CCCAAAGGCCGTAAATGAAGTC	
3	AH 229	(F) : GCAAACATCTTCCTTCCCAACA	61.6
		(R) : ATTGACGTAAGCTGCCAAGAGG	
4	AH 522	(F) : GTCAATGCCGAACCTCAACGTA	62.8
		(R) : TTCACCATCATCTCCAACGCTT	
5	GM 2350	(F) : GACTGTGTGGTTGGTGGTTTT	58.6
		(R) : CTCCTTGACCTCCTGGAGAAT	
6	GM 2724	(F) : CACTCTCACTTTCTCTTCTGCTT	57.6
		(R) : GGAAAAGAAGAGCAGCCACAT	
7	IPAH M 103	(F) : GCATTCACCACCATAGTCCA	58.7
		(R) : TCCTCTGACTTTCCTCCATCA	
8	IPAH M 105	(F) : CAGAGTTTGGAATTGATGCT	58.5
		(R) : GCCAGATCTGAGCAAGAACC	
9	IPAH M 108	(F):CTTGTCAAACCTCTGTGACTTAGCA	57.2
		(R) : CATGAACAATTACACCCAGTCA	
10	IPAH M 123	(F) : CGGAGACAGAACACAAACCA	58.7
		(R) : TACCCTGAGCCTCTCTCTCG	
11	IPAH M 165	(F) : CAACACGTTTCGCTTCCAGAT	59.8
		(R) : TCACTCTCATTTCGCCATT	
12	IPAH M 406	(F) : TGAAAGGGATTGGACCAAAA	59.1
		(R) : TGTTGGACAGGATTTACACA	

13	IPAH M 689	(F) : GATGACAATAGCGACGAGCA	58.9
		(R) : GTAAGCCTGCAGCAACAACA	
14	PM106	(F) : TGCATTGTGCTTGA ACTTCC	58.6
		(R) : AGCAAGCAGAGAGCAAAGAGA	
15	PM 3	(F):GAAAGAAATTATACACTCCAATTATGC	56.8
		(R) : CGGCATGACAGCTCTATGTT	
16	PM 375	(F) : CGGCAACAGTTTTGATGGTT	59.8
		(R) : GAAAAATATGCCGCCGTTG	
17	PM 418	(F):TCTAATGAAAACCGACAAGTTTAGA	57.1
		(R) : AGGCGTGCCAATAGAGTTTT	
18	PM 45	(F) : TGAGTTGTGACGGCTTGTGT	58.5
		(R) : GATGCATGTTTAGCACACTTGA	
19	PM 50	(F) :CAATTCATGATAGTATTTTATTGGACA	56.8
		(R) : CTTTCTCCTCCCAATTTGA	
20	SEQ3A 06	(F) : TGCATCAGCAAGCTACATACG	61
		(R) : GCGATTCACCATCAATCTCA	
21	SEQ3A 1	(F) : ATCATTGTGCTGAGGGAAGG	58.5
		(R) : CACCATTTTTCTTTTTCACCG	
22	SEQ2G 3	(F) : ATTCACAAGGGGACAGTTGC	58.7
		(R) : ATTCAAGCCTGGGAAACAGA	
23	SEQ2G	(F) : TTCTTGGTTCCTTTGGCTTC	58.4

	4	(R) : TGCTCAAGTGTCTTATTGGTG	
24	SEQ5D 05	(F) : AAAAGAAAGACCTTCCCCGA (R) : GCAGGTAATCTGCCGTGATT	58.8
25	TC3E0 5	(F) : CACCACTTGAGTTGGTGAGG (R) : CTTCTTCTTCTCCCGCAATG	61
26	TC4H0 2	(F) : ACCGCAAACATCCATCTC (R) : GATAGCGTCAGAGGCAGAGG	59
27	TC9F0 4	(F) : CCTAAACAACGACAAACACTCA (R) : AAGCACAACACAGAACCCTAAA	61

3.4.3.3.6 Agarose gel electrophoresis (AGE)

To the amplified product obtained after the PCR reaction (10 µl), 2 µl gel loading dye (Bromophenol Blue) was added and loaded into individual wells of 3% agarose gel. 50 bp ladder (Fermantas) was loaded in first lane as marker in 1 x TBE buffer. Electrophoresis was carried out at 120v for 3 h and the gel was stained with ethidium bromide (1µg/ml). After electrophoresis, the gel was observed under U.V. light using Alpha innotech corporation geldoc system.

3.4.3.3.7 Scoring and data analysis

Data were entered using a matrix in which all observed bands or characters were listed. The SSR pattern of each isolate was evaluated, assigning character state '1' to all the bands that could be reproducible and detected in the gel and '0' for the absence of band. Polymorphism information content (PIC) of each SSR marker was calculated using the formula (Anderson *et al.*, 1993)

$$PIC_i = 1 - \sum_{i=1}^k p_i^2$$

Where k is the total number of alleles (bands) detected for one SSR locus and p is the proportion of the cultivars or genotypes containing the allele (band) in all the samples analysed.

The data matrix thus generated was used to calculate Jaccard's similarity coefficient for each pair-wise comparison. The co-efficients were calculated in silico following Jaccard (1908) using the following formula.

$$\text{Similarity co-efficient} = a/n$$

Where, a = Number of matching bands for each pair of comparison

n = Total number of bands observed in two samples.

The similarity co-efficients were subjected to Unweighed Pair- Group Method of Arithmetic Average (UPGMA) cluster analysis to group the isolates based on their overall similarities. Statistical Package for Social Sciences (SPSS) was used for the cluster analysis and subsequent dendrogram preparation.

3.4.4 Character Association

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

3.4.4.1 Genotypic correlation co-efficients (r_g)

$$r_g(x_i x_j) = \frac{\text{CoV}_g(x_i x_j)}{\sqrt{V_g(x_i) V_g(x_j)}}$$

Where,

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

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

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

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

3.4.4.2 Phenotypic correlation coefficients (r_p)

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

Where,

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

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

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

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

3.4.5 Path Co-Efficient Analysis

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

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

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

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

$$\begin{array}{ccccccc}
 \cdot & \cdot & \cdot & \cdot & & \cdot & \cdot \\
 \cdot & \cdot & \cdot & \cdot & & \cdot & \cdot \\
 \cdot & \cdot & \cdot & \cdot & & \cdot & \cdot
 \end{array}$$

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

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:

$$\begin{array}{c} \text{A} \\ \left(\begin{array}{c} r_{1y} \\ r_{2y} \\ r_{3y} \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ r_{iy} \end{array} \right) \end{array} = \begin{array}{c} \text{C} \\ \left(\begin{array}{ccccccc} 1 & r_{12} & r_{13} & \dots & r_{1i} \\ r_{21} & 1 & r_{23} & \dots & r_{2i} \\ r_{31} & r_{32} & 1 & \dots & r_{3i} \\ \cdot & \cdot & \cdot & & \cdot \\ & \cdot & \cdot & & \cdot \\ \cdot & \cdot & \cdot & & \cdot \\ \cdot & \cdot & \cdot & & \cdot \\ r_{i1} & r_{i2} & r_{i3} & \dots & 1 \end{array} \right) \end{array} \begin{array}{c} \text{B} \\ \left(\begin{array}{c} p_{1y} \\ p_{2y} \\ p_{3y} \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ p_{iy} \end{array} \right) \end{array}$$

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

where,

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

Then, direct effects were calculated as follows:

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

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

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

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

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

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

Groundnut (*Arachis hypogaea* L.) is a good source of oil and protein, which is ranked as 5th most important oilseed crop in the world. It is a segmental allotetraploid ($2n = 40$), highly self-pollinated legume crop and grown successfully in tropical and sub-tropical areas of the world.

Groundnut is grown mainly in the arid and semiarid region where occurrence of drought is very frequent. Therefore productivity of the crop is highly variable. Hence, increasing the yield under drought conditions is an important breeding objective for the groundnut breeder. Further, identification of genotypes with greater ability to use limited available water more efficiently with enhanced productivity of the crop is the major breeding objective in groundnut. Water Use Efficiency (WUE) is one such important trait available to the breeder to augment the yield under drought environment. However, WUE is a quantitative character governed by many genes with small effect coupled with high environmental effect. Therefore selection for traits related to WUE would be important for the breeder to enhance the WUE coupled with high yield potential (Mallikarjun and Savithramma, 2017).

The knowledge of genetic divergence helps in making choice of parents to be used in hybridization programme to get good recombinants for desired characters. Correlation studies indicate the relationship between yield, its components and morpho-physiological attributes while path co-efficient analysis further partitions correlation coefficients into direct and indirect effects. Variability and heritability studies further are helpful in formulating effective selection procedures.

Keeping in view the above prospectives, the present investigation was undertaken. The data collected on physiological, yield and yield attributes of 32 groundnut genotypes were subjected to biometrical analysis *i.e.* variability,

genetic divergence (through D^2 statistic and SSR markers), character association and path co-efficient analysis. The results obtained from these investigations are furnished in this chapter under the following headings.

4.1 Mean performance

4.2 Genetic parameters

4.3 Genetic divergence

4.4 Character association

4.5 Path co-efficient analysis

4.1 MEAN PERFORMANCE

The data recorded on physiological, yield and yield attributes in *kharif* and *rabi* were subjected to analysis of variance and is presented in Table 4.1 and 4.2 respectively. The analysis of variance for *kharif* and *rabi* seasons was done separately for different physiological, yield and yield attributes.

The analysis of variance for all of the physiological, yield and yield attributes revealed significant differences among the genotypes. The mean performance of these thirty two genotypes in *kharif* and *rabi* is presented in Table 4.3 and 4.4 respectively.

4.1.1 SPAD Chlorophyll Metre Reading (SCMR)

SPAD chlorophyll meter reading gives a relative measure of the greenness or chlorophyll content of leaves and indication of leaf nitrogen status. Since SLN (Specific leaf nitrogen) determines the differences in WUE, it can be visualized that SCMR could reflect well in WUE differences (Veeraputhiran *et al.*, 2001).

The mean values of SCMR among the genotypes during *kharif*, 2017 ranged from 40.13 (Narayani) to 48.48 (K 9) with a general mean of 43.98.

Table 4.1. Analysis of variance for physiological, yield and yield attributes in 32 genotypes of groundnut during *kharif*, 2017

Sl. No.	Character	Replications	Treatments	Error
		(df = 3)	(df = 31)	(df = 93)
1	SCMR at 60 DAS	1.59	21.13 **	0.60
2	SLA at 60 DAS (cm ² g ⁻¹)	22.36	1005.56**	17.20
3	LAI at 60DAS	0.04	1.29**	0.02
4	LAI at 80DAS	0.03	2.62**	0.02
5	LAD at 80DAS (dm ² day)	94.04	4548.58**	170.49
6	Angle between main axis and primary branches at 60 DAS (°)	1	4.39**	0.61
7	Angle between main axis and primary branches at 80 DAS (°)	0.01	0.06**	0.01
8	Root length (cm)	0.01	200.78**	0.26
9	Root dry mass (g)	1.31	186.64**	0.52
10	Number of primary branches per plant	0.01	3.66**	0.16
11	Number of secondary branches per plant	0.02	3.69**	0.04
12	Plant height (cm)	1.63	172.23**	1.11
13	Number of pegs per plant	19.46	128.68**	15.81
14	Number of mature pods per plant	0.26	68.69**	2.17
15	Number of immature pods per plant	0.26	6.17**	0.58
16	Shelling percentage (%)	3.67	44.33**	2.99
17	Harvest Index (%)	6.98	178.87**	5.55
18	100-seed weight (g)	6.99	140.71**	5.28
19	Pod yield per plant (g)	7.66	19.94**	3.52

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

Table 4.2. Analysis of variance for physiological, yield and yield attributes in 32 genotypes of groundnut during *rabi* 2017-18

Sl. No.	Character	Replications	Treatments	Error
		(df = 1)	(df = 31)	(df = 31)
1	SCMR at 60 DAS	4.42	18.18**	3.9
2	SLA at 60 DAS (cm ² g ⁻¹)	7.76	559.12**	1.89
3	RWC at 80DAS (%)	0.54	49.06**	0.25
4	Shelling percentage (%)	1.26	82.13**	0.49
5	100-seed weight (g)	12.59	10.23**	3.19
6	Pod yield per plant (g)	0.25	13.85**	2.33

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

The genotype, K9 (48.48), K 1847 (48.33) and TCGS-1097 (47.38) showed higher SCMR values among the genotypes studied.

The mean values of SCMR among the genotypes during *rabi*, 2017-18 ranged from 43.2 (J 89) to 54.1 (K 9) with a general mean of 48.85. The genotypes, K 9 (54.1), K 1725 (53.15) and GG-16 (52.9) showed higher SCMR values among the genotypes studied. Fifteen genotypes were superior over the general mean (48.85). The genotype, K 9 recorded higher SCMR in both seasons.

4.1.2 Specific Leaf Area (SLA) ($\text{cm}^2 \text{g}^{-1}$)

The SLA is often considered as an indirect measure of leaf expansion. Higher SLA means higher leaf area per unit biomass and larger surface area for transpiration. On the other hand, if SLA is higher, lower will be the leaf thickness and hence low photosynthetic capacity and higher transpiration losses resulting in low WUE. Hence, low SLA is preferred trait in drought resistance breeding programme. The mean values of SLA in *kharif*, 2017 ranged from 151.35 to 207.67 with a general mean of 184.95. The genotype, TCGS-1653 (207.67) showed high mean SLA followed by GPBD-4 (205.64) while the genotype, K 9 (151.35) showed the lowest mean value.

The mean values of SLA in *rabi*, 2017-18 ranged from 108.22 to 171 with a general mean of 134.91. The genotype, GG-16 (171) showed high mean SLA followed by ICG 86325 (166.04) while the genotype, Narayani (108.22) showed the lowest mean value. Fifteen genotypes were superior over the general mean (134.91).

Madhava *et al.* (2003) observed a strong positive relationship of SCMR with WUE suggesting that SCMR could be a potential physiological trait to employ as a surrogate for selection for water use efficiency (WUE) in groundnut. The genotype, K 9 recorded highest SCMR value followed by K 1847, TCGS-1097, K 1725, K 1805, K. Anantha, TCGS-1157, TCGS-1073, TCGS-1694, GG-16, ALG-06-320 and SG-99 which showed SCMR values

above 44.0 in both *kharif* and *rabi* season. These genotypes also showed lower SLA values which ranged from 150-195 during *kharif* while in *rabi* the genotypes Narayani, TCGS-1696, TCGS-1630, TCGS-1653, TCGS-1622, TCGS-1073, GPBD-4, R-2001-3-1, R-2001-3, SG 99, K 9, TCGS-1097, K 1847 and Dharani showed lower SLA values which ranged from 108-130.

These genotypes bearing the traits of low SLA and high photosynthetic efficiency at grand growth phase could be directly useful as varieties if they have high yield potential or could be used in breeding programmes as genetic stocks for high WUE.

4.1.3 Relative Water Content (RWC) (%)

The values of RWC are often considered as the appropriate measure of plant water status and considered to be the sensitive index of plant water content especially when plants are exposed to cellular water deficit conditions (Painawadee *et al.*, 2009).

The genotype, K 1789 recorded maximum RWC (97.2%) followed by GG-16 (97.0%) while TCGS-1622 showed minimum value (79.9%) during *rabi* 2017-18. Fourteen genotypes were superior over the general mean (88.98%). The genotypes that showed high RWC (>90%) are TCGS-1630, TCGS-1073, J 89, ALG-06-320, K 1805, K 9, K. Anantha, K 1847, K 1811, ICGS 76, ICG 86325 and Dharani apart from the genotypes above mentioned. During *rabi* season, because of the climatic condition and the condition under which it is cultivated i.e. irrigated, in most of the genotypes RWC was above 80%.

Several scientists reported that RWC in groundnut and other crops varied significantly under moisture stress conditions (Rao, 1994; Babitha, 1996; Reddy *et al.*, 2003b). This trait can be exploited for screening the genotypes for drought tolerance especially under moisture stress or temperature stress conditions at any stage of crop growth.

4.1.4 Leaf Area Index (LAI)

At 60 DAS, the genotype, ICG 86325 recorded maximum LAI (4.35) while TCGS-1694 showed minimum value (1.97). Eighteen genotypes were superior over the general mean (3.09). LAI at 80 DAS ranged from 1.84 to 5.66 with a general mean of 2.92. The genotype, TCGS-1653 showed the highest LAI at 80 DAS (5.66) followed by GG-16 (4.34) while the genotype, K. Anantha showed the lowest mean value (1.84). In fourteen genotypes LAI increased from 60 DAS to 80 DAS and 18 genotypes showed decreasing trend of LAI from 60 DAS to 80 DAS.

Significant differences were found in the values of LAI from 60 to 80 DAS. Leaf area index (LAI) describes the size of assimilatory apparatus of a crop or the crop canopy expansion. Duncan *et al.* (1978) reported that maximum light interception occurred when the LAI was three. The genotypes, TCGS-1653, GG-16, ICGS 76, K 1805, SG-99, K 1847, TCGS-1630, ICG 86325, K. Harithandra and TCGS-1097 showed maximum LAI (>3) at both 60 and 80 DAS.

As per Williams *et al.* (1976), it is important to maintain high leaf area during pod filling period since sink seemed to be not limiting. Maintenance of high LAI is advantageous especially in *Kharif* season due to low photosynthetic rate under low light conditions. In some genotypes, viz., TCGS-1616, TCGS-1622, TCGS-1073, GPBD-4, R-2001-3-1, R-2001-3, SG 99, ALG-06-320, K. Harithandra, K. Anantha, TCGS-1097, K 1789, ICGV 86325, Dharani, Narayani, GG-20 and K 6 LAI at 80 DAS was lower than LAI at 60 DAS. This could be due to their early maturing nature or their susceptibility to foliar fungal diseases resulting in leaf fall consequently resulting in decreased LAI.

Though no difference was observed in SLW, N, P and K content between leaves of the upper and lower nodes of the main stem, due to higher

incidence of foliar diseases like rust and leaf spot, the leaf senescence was comparatively more during the monsoon season than in post-monsoon season and Spanish types show high percentage senescence of leaves (Narayanan and Chand, 1986) as observed in the present study i.e. decreased LAI in early maturing genotypes. Samdur *et al.* (2003) reported that LAI of bunch varieties spaced at 45×10 cm spacing was 1.7 at 60 DAE and reached 4.0 at 90 DAE while in the spreading varieties planted at 90×10 cm it was 0.5-1.2 at 60 DAE and 2-3.6 at 90 DAE. Reshma (2014) observed increase in LAI up to 60 DAS and thereafter declined at 75, 90 DAS and at harvest in all the groundnut genotypes studied.

4.1.5 Leaf Area Duration (LAD) (dm²day)

Leaf area duration (LAD) indicates persistence of greenness in crop duration of a genotype. It is a useful growth parameter indicating the efficiency of photosynthetic system with a high degree of association with dry matter accumulation. LAD is very useful trait for any genotype as it reflects the functional leaf area available for assimilation throughout the crop growth.

LAD at 80 DAS registered an overall mean of 179.49 dm²day with means ranging from 139.53 dm²day to 290.98 dm²day. The genotype, TCGS-1653 recorded maximum value (290.98 dm²day) followed by GG-16 (233.18 dm²day) while GPBD-4 exhibited minimum value (139.53 dm²day). LAD above 200 dm².day was recorded by nine genotypes viz., TCGS-1630, TCGS-1653, SG 99, K 1805, K 9, GG-16, K 1847, ICGS 76 and ICG 86325 though it is desirable, it may indicate their late maturing nature.

Pranusha (2011) found that LAD values gradually increased from 35 to 95 DAS. LAD is important for pod filling and improving shelling percentage. The maintenance of high LAD values during pod filling phase helps in sustained production of photosynthates and is a desirable attribute. Studies of Enyi (1977) on growth aspect of two varieties of groundnut, a sequential branching type, Natal common and an alternate type, 'Domodo

Edible' indicated greater grain to leaf ratio (grain weight at harvest/LAD between pod initiation and final sampling) in spreading types than bunch types. TCGS-1653 followed by GG-16, SG-99, K 1847, K 1805 recorded high LAD at 80 DAS.

Higher LAD during later stages of growth had positive effect resulting in higher number of pods per plant. The runner genotypes maintain more leaf area (higher active assimilation surface) and higher percentage of nitrogen in their leaves than the erect ones (Singh and Joshi, 1993). The growth traits of eight groundnut varieties having variation in pod yield, nodulation and N₂ fixation when analysed the LAD accounted for almost 70-75 per cent of variability in both nodulation and N fixed (Wynne and Gregory, 1981).

4.1.6 Angle between Main Axis and First Two Primary Branches (°)

Virginia bunch genotypes mostly show decumbent growth habit (decumbent 3). At 60 DAS, ICGS 76 showed maximum angle between main axis and first two primary branches of 85.92 ° followed by Dharani (85.42 °) while SG-99 showed minimum angle between main axis and primary branches at 60 DAS (48.67 °). Recently developed varieties like Dharani and K 9 show wider angle between main axis and primary branches though they behave as spanish bunch forms in other aspects like duration, main axis bearing and pod bearing habit.

Twenty genotypes recorded higher angle over the general mean (68.96). The angle between main axis and primary branches at 80 DAS ranged from 50.88 to 86.67 with a general mean of 71.03. The genotype, Dharani showed the highest angle between main axis and primary branches at 80 DAS (86.67) followed by ICGS 76 (86.0) while the genotype SG 99 minimum value (50.88). There was an increase in the angle between main axis and primary branches from 60 to 80 DAS in all the genotypes.

Wider the primary branch angle more will be the light interception and the higher the rate of photosynthesis. There is an increase in angle between

main axis and primary branch from 60 to 80 DAS. The genotypes viz., Dharani, ICGS 76, R-2001-2-1, K 1811 and GG-16 recorded $>80^\circ$ primary branch angle at both 60 and 80 DAS. In the genotypes with wider angle as in Dharani mutual shading is avoided and thus perform well under low light conditions which is usually the situation during *kharif* season.

4.1.7 Root Length (cm)

Root length is an important trait in drought resistance breeding programme. It decides the capacity to tap moisture from different layers of the soil in moisture stress situations. In groundnut, root is the place where nodules harbouring nitrogen fixing bacteria are present. As the root length was recorded in the field conditions and not in the special structures, the root length values recorded were low. This could be also due to continuous saturated condition the soil was maintained as the distribution of rainfall was very good during the season. The genotype, R-2001-2 showed maximum root length of 12.63 cm followed by TCGS-1694 (12.14 cm). R-2001-3-1 recorded minimum root length (7.10 cm). Seventeen genotypes were superior over the general mean of 10.29 cm.

4.1.8 Root Dry Mass (g)

Root mass is a trait that along with root length decides the drought tolerance capacity of a genotype. The mean values of root mass ranged from 0.44 to 1.09 g with a general mean of 0.62 g. The genotype, GPBD-4 showed highest root mass of 1.09 g followed by ALG-06-320 and K 1805 (0.78 g), while TCGS-1073 showed lowest root mass of 0.44 g.

Under drought stress conditions, the genotypes with large root systems had high WUE (Songsri *et al.*, 2008). The ability of genotypes with large root systems to better maintain water uptake through extraction/tapping of water from deeper layers of soil may explain their relatively high drought tolerance. The genotypes with long roots observed are R-2001-2, TCGS-1694, TCGS-

1630, R-2001-2-1 and TCGS-1073. The genotypes with high root mass observed are GPBD-4, ALG-06-320, K 1805 and TCGS-1653.

4.1.9 Number of Primary Branches per Plant

Number of primary branches per plant is an important yield attribute i.e. the higher the number higher the pod yield. In Virginia genotypes, the number is higher in comparison with Spanish and Valencia bunch genotypes. In yield improvement, breeder's objective is to improve the number of primary branches in early maturing background of Spanish bunch genotypes. Balance has to be struck between the number of primary branches, yield and shelling out-turn in a given agronomic situation.

Number of primary branches per plant ranged from 3.5 to 7.3 with a general mean of 4.86. SG-99 showed highest number of primary branches per plant (7.3) followed by R-2001-2 (6.85). The genotype, TCGS-1622 showed lowest number of primary branches per plant (3.50). Most of the genotypes possessed four branches per plant. In the present study, many improved genotypes showed mean primary branches number higher than 4.5 i.e. TCGS-1694, TCGS-1696, TCGS-1653, R 2001-2, GPBD-4, R 2001-3, SG 99, K 1805, K 1725, TCGS-1097, GG-16, K 1847, K 1789, K 1811, ICGS 76, ICGV 86325 and GG-20.

4.1.10 Number of Secondary Branches per Plant

Number of secondary branches contributes for increased leaf area. Secondary branches occur usually in Virginia types but occur rarely in Spanish bunch genotypes and almost absent in Valencia genotypes. However, most of the new improved varieties derived from intra-specific crosses (between sub- subspecies) though classified as Spanish bunch do possess secondaries and in-between characters. Number of secondary branches per plant ranged from 0.1 to 4.45 with a general mean of 0.97. SG-99 showed highest number of secondary branches per plant (4.45) followed by ICGS 76 (2.15), K 1805 (2.00), K 1725 (1.90) and TCGS-1157 (1.80).

4.1.11 Plant Height (cm)

Plant height had a positive relationship with LAI, crop growth rate, HI, leaf nitrogen content while it had negative relationship with number of branches, net assimilation rate and nitrogenase activity (Antony *et al.* 2000). The mean length of main axis ranged from 34.95 to 60.6 cm with a general mean of 45.71 cm. Among the genotypes, K. Anantha was the shortest (34.95 cm) and TCGS-1653(60.6 cm) was the tallest. Thirteen genotypes exceeded the general mean value.

4.1.12 Number of Pegs per Plant

Number of pegs per plant ranged from 17.1 to 39.7 with a general mean of 23.65. SG-99 recorded highest number of pegs per plant, while ICG 86325 recorded lowest number of pegs per plant. Twenty three genotypes produced more than 20 pegs per plant.

4.1.13 Number of Mature Pods per Plant

The genotype, TCGS-1653 recorded the highest number of mature pods per plant (24.32) while GG-16 registered the lowest number of mature pods per plant (8.35). Fifteen genotypes showed more number of matured pods per plant than the general mean (14.20). Among the genotypes with more number of mature pods per plant, TCGS-1653 (24.32), ALG-06-320 (23.18), SG 99 (22.45), TCGS-1694 (18.45), R-2001-2 (17.40) R-2001-3 (17.35) and TCGS-1630 (17.13) more number of primary branches per plant were observed in SG 99 (7.30), R-2001-2 (6.85) while in ALG-06-320 (3.80), TCGS-1694 (4.55) and TCGS-1630 (4.20) they were around four, the usual number observed in Spanish types. The yield depends on number of mature pods per plant and 100-seed weight (Basu and Nautiyal, 2004). Number of flowers, branches and pod number per plant depend on both the genotype and spacing adopted. In genotypes SG 99(7.65), K 1805 (5.80), R-2001-2 (4.35), ALG-06-320, J 89

(3.60) and K 6 (3.55) more number of immature pods per plant could be due to prolonged flowering period.

4.1.14 Number of Immature Pods per Plant

The mean ranged from 1.05 to 7.65 with a general mean of 2.65. In ten genotypes it was above the general mean value. The genotype, SG-99 recorded the highest (7.65) whereas ICG 86325 recorded the lowest value (1.05). Lower the immature pods, the higher will be shelling percentage and 100-seed weight. Synchrony in flowering lowers number of immature pods per plant.

4.1.15 Shelling Percentage

In *kharif*, the mean values of shelling percentage ranged from 64 to 76 per cent. The genotype, Dharani and TCGS-1097 recorded the highest shelling percentage (76%) while GPBD-4 registered the lowest shelling percentage (64%). The character general mean was (70.12%). Fourteen genotypes exceeded the general mean value.

While in *rabi*, the mean values of shelling percentage ranged from 57 to 72 per cent. The genotypes, TCGS-1694, K9 and ALG-06-320 recorded the highest shelling percentage (72%) while TCGS-1653 registered the lowest shelling percentage (57%). The character general mean was (65.59%). Sixteen genotypes exceeded the general mean value.

4.1.16 100-Seed Weight (g)

The 100-seed weight in *kharif* ranged from 26.25 to 50.25 g with a general mean of 35.60 g. GPBD-4 (26.25 g) and GG-16(50.25 g) recorded the lowest and highest 100-seed weight values respectively. Eighteen genotypes exceeded the general mean value (35.60 g).

The 100-seed weight in *rabi* ranged from 27 to 52 g with a general mean of 38.36 g. K 1847 (27 g) and TCGS-1622 (52 g) recorded the lowest

and highest 100-seed weight values respectively. Fifteen genotypes exceeded the general mean value (38.36 g).

4.1.17 Harvest Index (%)

The mean HI ranged from 28.33 to 61.83 with an average of 43.77. Among the genotypes, GPBD-4 recorded the lowest harvest index (28.33) while TCGS-1694 recorded the highest harvest index (61.83). Fourteen genotypes recorded higher harvest index than the general mean (43.77). The partitioning of photosynthates to fruit during pod filling stage is the most influential physiological factor in yield determination of groundnut.

Duncan *et al.* (1978) reported that partitioning of assimilates had the greatest effect on fruit yield and the estimates of partitioning to fruit ranged from 41% in Dixie runner released in 1943 to 98% in early bunch released in 1977. Suneetha (2007) reported HI that varied from 31.70 (Tirupati-3) to 63.66 (R-2001-2) in a study of 29 genotypes consisting of released and pre-release groundnut cultures. Vasanthi *et al.* (2003) observed HI ranging from 41% (TCGS-647) to 53% (JL 24) in post-rainy season.

4.1.18 Pod Yield per Plant (g)

The mean pod yield per plant in *kharif* ranged from 7.5 g to 17.9 g with a general mean value of 10.83 g. The genotype, SG-99 showed highest pod yield per plant (17.9 g) while GPBD-4 recorded the lowest pod yield per plant (7.5 g). Fifteen genotypes exceeded the general mean value (10.83 g).

The genotype, SG-99 recorded the highest pod yield per plant (17.90 g) followed by TCGS-1694 (14.85 g), R 2001-3-1 (13.15 g), ALG-06-320 (12.95 g) and TCGS-1653 (12.90 g). The increased pod yield per plant in SG-99 may be attributed to its superiority for number of primary branches per plant (7), number of secondary branches per plant (5), number of pegs per plant (40) and number of mature pods per plant (23). The genotype, TCGS-1694 also recorded high pod yield per plant (14.85 g) as it had highest harvest index

Table 4.3. Mean performance of 32 genotypes of groundnut for physiological, yield and yield attributes during

kharif, 2017

S. No.	Genotypes	SCMR at 60 DAS	SLA at 60 DAS	LAI at 60 DAS	LAI at 80 DAS	LAD at 80 DAS	Angle at 60 DAS	Angle at 80 DAS	RL	RDM	PB	SB	PH	PP	MP	IP	SP		100 SW	HI		PYP
																	O	T		O	T	
1	TCGS-1694	44.93	183.83	1.97	2.48	141.18	69.00	71.75	12.14	0.58	4.55	0.33	48.60	25.95	18.45	2.25	71.50	57.74	38.50	61.83	51.86	14.85
2	TCGS-1696	42.53	175.15	2.27	2.29	145.45	69.17	70.00	9.10	0.54	5.23	0.35	49.80	25.15	15.95	2.30	71.50	57.74	37.50	48.64	44.21	11.60
3	TCGS-1630	42.13	172.86	3.20	3.48	206.02	70.25	70.17	11.95	0.69	4.20	0.70	41.85	18.75	17.13	1.60	71.00	57.43	39.00	49.67	44.83	9.85
4	TCGS-1653	42.78	207.67	3.50	5.66	290.98	75.00	76.00	10.83	0.74	4.61	1.10	60.60	30.10	24.32	2.95	64.75	53.58	32.00	40.16	39.32	12.90
5	TCGS-1616	40.90	192.40	3.13	2.04	146.32	72.50	74.77	10.73	0.58	3.90	0.50	56.45	21.45	13.08	3.25	74.50	59.67	37.00	49.34	44.63	11.60
6	TCGS-1622	42.03	182.48	3.19	2.38	155.77	52.75	54.83	11.03	0.54	3.50	0.25	54.85	18.60	10.75	2.00	74.00	59.36	37.25	43.24	41.12	9.80
7	TCGS-1073	45.68	190.03	2.56	2.27	145.68	77.08	77.75	11.53	0.44	4.15	0.10	43.75	23.78	14.60	2.08	68.50	55.87	41.50	42.15	40.92	9.20
8	TCGS-1157	46.15	193.04	2.22	2.42	149.21	62.75	63.17	8.73	0.63	4.33	1.80	45.05	18.53	13.40	2.33	69.50	56.48	36.50	36.28	37.03	7.75
9	R-2001-2-1	41.85	203.47	2.72	3.16	174.59	84.75	85.75	11.88	0.63	4.60	0.15	44.23	24.90	17.40	2.55	67.00	54.94	28.75	49.16	44.53	11.45
10	GPBD-4	41.70	205.64	2.92	2.00	139.53	52.25	52.50	11.31	1.09	6.85	1.25	44.03	24.65	14.33	4.35	64.00	53.15	26.25	28.33	31.93	7.50
11	R-2001-3-1	42.48	197.06	3.43	2.96	175.72	73.67	75.00	7.10	0.53	5.40	0.75	46.75	34.35	17.23	2.43	69.00	56.17	27.50	52.66	46.54	13.15
12	J 89	40.93	152.73	2.53	2.76	163.11	58.83	59.50	11.33	0.53	4.35	0.50	40.93	23.15	12.90	3.60	64.50	53.43	28.50	44.52	41.84	10.75
13	R 2001-3	43.60	195.09	2.92	2.51	160.90	75.00	75.25	10.82	0.47	5.65	0.90	49.70	27.85	17.35	2.48	68.50	55.87	29.50	51.81	46.04	12.45
14	SG 99	44.10	184.97	3.88	3.63	230.89	48.67	50.88	9.70	0.72	7.30	4.45	38.48	39.70	22.45	7.65	68.50	55.87	38.00	47.64	43.65	17.90
15	R 2001-2	43.45	188.57	2.21	2.97	153.56	73.42	73.83	12.63	0.60	4.90	1.85	39.50	27.10	16.50	2.85	70.00	56.80	29.25	41.03	39.83	10.10
16	ALG-06-320	44.83	184.80	3.08	2.27	154.05	69.33	70.79	9.66	0.78	3.80	0.13	44.68	33.15	23.18	3.60	75.50	60.34	27.00	51.00	45.57	12.95
17	K 1805	46.55	155.84	3.10	3.75	213.58	72.25	72.00	9.73	0.78	6.45	2.00	39.70	29.65	15.30	5.80	68.00	55.56	30.25	40.98	39.83	12.40
18	K 1725	47.03	176.84	2.76	3.32	196.81	63.42	64.79	10.04	0.66	6.80	1.90	35.50	19.25	9.18	2.70	70.00	56.80	43.50	45.37	42.35	12.25
19	K 9	48.48	151.14	2.32	3.77	202.99	76.50	76.88	10.60	0.69	3.95	0.13	38.10	18.83	11.93	2.45	69.50	56.49	30.00	37.26	37.62	8.15
20	K.Harithandra	44.05	199.66	3.78	3.21	194.44	51.83	54.75	8.81	0.51	3.90	0.23	40.10	20.93	11.78	1.45	70.00	56.79	33.00	42.43	40.66	9.40

Cont.....

Table 4.3. cont...

Sl. No.	Genotypes	SCMR at 60 DAS	SLA at 60 DAS	LAI at 60 DAS	LAI at 80 DAS	LAD at 80 DAS	Angle at 60 DAS	Angle at 80 DAS	RL	RDM	PB	SB	PH	PP	MP	IP	SP		100 SW	HI		PYP
																	O	T		O	T	
21	K. Anantha	46.28	172.23	3.32	1.84	145.51	61.08	62.45	8.59	0.69	4.25	0.13	34.95	20.85	13.10	1.63	70.50	57.11	36.00	45.90	42.66	10.50
22	TCGS-1097	47.38	186.77	3.70	3.03	192.78	63.17	65.25	9.48	0.51	4.95	1.18	39.18	21.38	13.10	1.90	76.00	60.68	37.00	48.37	44.07	11.90
23	GG 16	44.50	188.96	3.71	4.34	233.18	81.00	83.88	9.80	0.63	4.55	1.30	54.70	20.78	8.35	1.38	67.00	54.94	50.25	35.37	36.50	9.40
24	K 1847	48.33	164.91	3.37	3.58	216.70	71.83	74.33	9.73	0.59	5.25	1.75	53.05	18.75	9.50	1.75	75.50	60.34	40.00	31.86	34.34	8.35
25	K 1789	42.88	155.17	3.04	2.25	154.16	69.16	72.00	10.38	0.52	4.80	1.63	47.60	23.60	14.45	2.15	64.50	53.44	30.50	42.81	40.88	10.70
26	K 1811	42.13	180.72	2.80	2.77	175.42	82.92	84.75	10.53	0.54	5.30	1.25	41.33	20.80	10.38	2.50	69.50	56.50	43.00	40.66	39.63	8.40
27	ICGS 76	44.93	181.86	3.65	3.80	222.51	85.92	86.00	9.24	0.68	5.90	2.15	45.23	21.35	10.30	2.10	70.00	56.79	38.00	36.21	37.00	11.50
28	ICG 86325	44.25	203.70	4.35	3.23	216.86	73.08	74.96	9.23	0.53	4.73	0.38	45.68	17.10	10.15	1.05	69.50	56.48	39.25	38.74	38.48	8.15
29	Dharani	42.50	202.38	3.42	2.04	148.91	85.42	86.67	9.80	0.59	4.20	0.13	51.43	17.20	9.80	1.83	76.00	60.69	37.25	48.52	44.16	9.35
30	Narayani	40.13	197.87	3.67	2.29	178.76	61.58	76.25	10.83	0.55	3.75	0.10	55.10	20.63	12.50	2.50	71.50	57.74	34.75	41.88	40.33	9.70
31	GG 20	47.03	196.32	3.45	2.65	176.58	62.42	69.25	11.33	0.59	4.90	1.55	40.20	18.25	8.70	1.85	70.50	57.11	47.75	43.50	41.28	9.85
32	K 6	41.08	194.27	2.70	2.19	141.69	60.92	67.00	10.70	0.71	4.40	0.10	51.70	30.25	16.83	3.55	73.50	59.03	34.75	43.25	41.11	12.60
	G. Mean	43.98	184.95	3.09	2.92	179.49	68.96	71.03	10.29	0.62	4.86	0.97	45.71	23.65	14.20	2.65	70.12	56.90	35.60	43.77	41.40	10.83
	C.V.(%)	1.76	2.23	4.95	4.82	9.29	0.60	0.83	13.44	9.77	8.23	18.76	2.30	13.36	10.10	25.22	-	1.91	6.40	-	3.40	17.35
	S.E.	0.39	2.06	0.08	0.07	8.33	0.21	0.29	0.69	0.03	0.20	0.09	0.53	1.58	0.72	0.33	-	0.54	1.15	-	0.70	0.94
	C.D. 5%	1.08	5.79	0.21	0.20	23.40	0.58	0.83	1.94	0.08	0.56	0.26	1.48	4.44	2.01	0.94	-	1.52	3.23	-	1.97	2.64

SCMR at 60 DAS- SPAD chlorophyll metre reading at 60 DAS; SLA at 60 DAS- Specific leaf area at 60 DAS ($\text{cm}^2 \text{g}^{-1}$); LAI at 60 DAS-Leaf area index at 60 DAS; LAI at 80 DAS- Leaf area index at 80 DAS; LAD at 80 DAS- Leaf area duration at 80 DAS($\text{dm}^2 \text{day}$); Angle at 60 DAS- Angle between main axis and first two primary branches at 60 DAS ($^\circ$); Angle at 80 DAS- Angle between main axis and first two primary branches at 80 DAS ($^\circ$); RL- Root length (cms); RDM- Root dry mass (g); PB- Number of primary branches per plant; SB- Number of secondary branches per plant; PH= Plant height (cms); PP- Number of pegs per plant; MP- Number of mature pods per plant; IP- Number of immature pods per plant; SP- Shelling percentage (%); 100 SW- 100 seed weight (g); HI- Harvest index (%); PYP- Pod yield per plant (g) and O- Observed values; T- Angular transformed values

Table 4.4. Mean performance of 32 genotypes of groundnut for physiological, yield and yield attributes during *rabi* 2017-18

Sl. No.	Genotypes	SCMR	SLA	RWC	Shelling %	100-seed weight	Pod yield per plant
1	TCGS-1694	49.65	132.52	80.80	72.00	45.50	13.05
2	TCGS-1696	46.75	110.47	86.90	68.00	46.00	8.82
3	TCGS-1630	45.45	120.55	93.40	68.00	40.00	8.75
4	TCGS-1653	47.60	120.49	88.65	57.00	34.00	8.99
5	TCGS-1616	49.90	159.09	84.65	71.00	41.00	6.68
6	TCGS-1622	47.25	128.76	79.90	70.00	52.00	11.81
7	TCGS-1073	51.45	120.37	91.80	69.00	50.00	7.53
8	TCGS-1157	52.45	132.16	83.75	67.00	42.00	11.59
9	R-2001-2-1	47.05	132.70	84.40	66.00	32.00	10.17
10	GPBD-4	44.25	118.34	82.75	67.00	34.00	6.38
11	R-2001-3-1	46.20	126.98	80.85	64.00	32.00	9.71
12	J 89	43.20	136.68	93.40	60.00	40.00	8.07
13	R 2001-3	48.50	120.05	85.90	65.00	30.00	11.05
14	SG 99	46.55	113.39	85.85	64.00	38.00	11.67
15	R 2001-2	46.55	146.50	86.30	65.00	31.50	11.53
16	ALG-06-320	48.20	147.59	90.60	72.00	40.00	12.87
17	K 1805	45.25	160.75	92.75	62.00	36.00	10.64
18	K 1725	53.15	135.09	84.75	64.00	47.00	8.17

Cont....

Table 4.4. cont...

Sl. No.	Genotypes	SCMR	SLA	RWC	Shelling %	100 seed weight	Pod yield per plant
19	K 9	54.10	123.99	94.05	72.00	35.50	9.38
20	K. Harithandra	52.00	162.18	87.85	66.00	44.00	5.97
21	K. Anantha	49.85	135.06	91.70	68.00	33.50	7.72
22	TCGS-1097	51.60	123.36	87.35	69.00	32.00	6.18
23	GG 16	52.90	171.00	97.00	61.00	47.00	3.78
24	K 1847	52.70	125.54	96.85	61.00	27.00	7.59
25	K 1789	45.10	143.32	97.20	63.00	31.00	6.18
26	K 1811	45.65	155.52	96.55	64.00	40.00	7.06
27	ICGS 76	52.80	137.83	94.30	62.00	42.00	5.80
28	ICG 86325	50.80	166.04	90.60	65.00	38.00	5.55
29	Dharani	48.85	121.64	91.25	67.00	35.00	5.98
30	Narayani	46.85	108.22	87.55	65.00	33.00	5.98
31	GG 20	51.90	138.81	89.00	61.00	45.50	3.80
32	K 6	48.60	142.08	88.70	64.00	33.00	4.21
	General Mean	48.85	134.91	88.98	65.59	38.36	8.21
	C.V.(%)	4.05	1.02	0.56	3.30	1.83	18.60
	S.E.	1.40	0.97	0.35	1.26	0.50	1.08
	C.D. 5%	4.03	2.81	1.02	3.646	1.43	3.11

(61.83%), optimum plant height (48.60 cm), 100-seed weight (38.50 g), LAI, higher number of mature pods per plant (18.45), moderate number of primaries (4.55) and high root length (12.14 cm). Similarly, ALG-06-320 showed fairly high pod yield per plant (12.95 g) due to high shelling percentage (75.50%), optimum plant height (44.68 cm), higher number of pegs (33.15), high HI (45.57%), optimum angle (69°) and moderate number of primaries (3.80). TCGS-1653 recorded relatively high pod yield per plant (12.90 g) due to its long stature.

Pod yield per plant was found to be highly related to the number of mature pods per plant, 100- seed weight, height and number of primary branches per plant (Labana *et al.*, 1980).

The mean pod yield per plant in *rabi* ranged from 3.78 g to 13.05 g with a general mean value of 8.20 g. The genotype, TCGS-1694 showed highest pod yield per plant (13.05 g) followed by ALG-06-320 (12.87), while GG-16 recorded the lowest pod yield per plant (3.78 g). Fourteen genotypes exceeded the general mean value (8.20 g). The genotype, TCGS-1097 (76%) and K 9 (72%) had the maximum shelling percentage in *kharif* and *rabi* respectively. The genotypes, GG-16 (50.25 g) and TCGS-1622 (52.00 g) showed the highest 100-seed weight in *kharif* and *rabi* respectively whereas ICG 86325 recorded least number of immature pods per plant (1.05). The above genotypes are worthy of utilization in improvement of the respective characters.

4.2 GENETIC PARAMETERS

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wide range of genetic variability helps in selecting desired genotypes. In genetic studies, characters with high genotypic coefficient of variation indicate the potential for effective selection. Heritability provides information about the extent to which a particular genetic character can be transmitted to the successive generations. Through

heritability estimates along with genetic advance, effectiveness of selecting the best individuals could be predicted successfully.

The estimates of variability (Genotypic and phenotypic co-efficients of variation), heritability (broad sense), genetic advance and genetic advance as per cent of mean for various physiological, yield and yield attributes in *kharif* and *rabi* are presented in Table 4.5 and 4.6 respectively

4.2.1. Kharif

All the characters exhibited high magnitude of PCV than GCV indicating the influence of environment in the expression of these traits. Similar kind of results were registered by Zaman *et al.* (2011), Satish (2014), Vasanthi *et al.* (2015) and Kamdi *et al.* (2017).

Genotypic co-efficient of variation (GCV) ranged from 3.56 per cent (shelling percentage) to 98.09 per cent (number of secondary branches per plant). High GCV values were recorded for the traits, viz. LAI at 80 DAS (27.84%), number of secondary branches per plant (98.09%), number of pegs per plant (22.25%), number of mature pods per plant (28.77%) and number of immature pods per plant (47.81%). Moderate GCV was observed for the traits viz. LAI at 60 DAS (18.20%), angle between main axis and primary branches at 60 DAS (14.53%), LAD at 80 DAS (19.42%), angle between main axis and primary branches at 80 DAS (13.59%), root dry mass (19.22%), number of primary branches per plant (19.28%), plant height (14.31%), 100-seed weight (16.20%) and pod yield per plant (18.71%). GCV was low for the traits viz. SCMR at 60 DAS (5.15%), SLA at 60 DAS (8.50%), root length (9.55%), shelling percentage (3.56%) and harvest index (9.32%).

Heritability ranged from 33.60 per cent (root length) to 99.80 per cent (angle between main axis and primary branches at 60 DAS). Except for the traits, root length (33.60%) and pod yield per plant (53.80%) for all the other 17 traits heritability was high *i.e.* > 60 per cent.

Genetic advance as per cent of mean (GAM) ranged from 6.46 per cent (shelling percentage) to 194.69 per cent (number of secondary branches per plant). Apart from the number of secondary branches per plant, GAM was high for the traits viz. LAI at 60 DAS (36.18%), LAI at 80 DAS (56.51%), LAD at 80 DAS (36.09%), angle between main axis and primary branches at 60 DAS (29.90%), angle between main axis and primary branches at 80 DAS (27.95%), root dry mass (35.29%), number of primary branches per plant (36.53%), plant height (29.10%), number of pegs per plant (39.30%), number of mature pods per plant (55.92%), number of immature pods per plant (87.12%), 100-seed weight (31.03%) and pod yield per plant (28.27%). GAM was moderate for SCMR at 60 DAS (10.04%), SLA at 60 DAS (16.94%), root length (11.40%) and HI (18.04%). It was low for only shelling percentage (6.46%).

GCV, heritability and GAM should be considered together to draw inference on the improvement or genetic gain that can be achieved in any particular trait (Johnson *et al.* 1955). For most of the traits included in the present study, moderate to high GCV coupled with high GAM were observed except shelling percentage indicating that the traits are amenable for phenotypic selection.

Gaikwad *et al.* (2015), Mahalakshmi *et al.* (2005) and Aparna *et al.* (2018) reported moderate to high PCV, GCV, heritability and moderate to high GAM for plant height, number of mature pods per plant, number of immature pods per plant, number of pegs per plant, harvest index and pod yield per plant. Gaikwad *et al.* (2015) and Patidar *et al.* (2014) observed low PCV, GCV, high heritability and moderate GCV for 100-seed weight. Nath and Alam (2002) reported moderate to high PCV, GCV, high heritability and GAM for number of primary branches per plant. Hiremath *et al.* (2011) and Bhargavi *et al.* (2016) observed low PCV, GCV, high heritability and low GAM for shelling percentage. Vasanthi *et al.* (2015) observed moderate PCV, GCV, high heritability and moderate to high GAM for plant height, number of

**Table 4.5. Genetic parameters for physiological, yield and yield attributes of 32 groundnut genotypes during
kharif, 2017**

Sl. No.	Character	Mean	Range		Variance		Co-efficient of variation		Heritability (Broad sense%)	Genetic Advance	Genetic Advance as per cent of mean(%)
			Min.	Max.	Geno- typic	Pheno- typic	Geno- typic (%)	Pheno- typic (%)			
1	SCMR at 60 DAS	43.98	40.13	48.48	5.13	5.73	5.15	5.44	89.60	4.42	10.04
2	SLA at 60 DAS	184.95	151.14	207.67	247.13	264.12	8.50	8.79	93.60	31.33	16.94
3	LAI at 60DAS	3.09	1.973	4.35	0.32	0.34	18.20	18.86	93.10	1.12	36.18
4	LAI at 80DAS	2.92	1.84	5.66	0.66	0.68	27.84	28.28	97.10	1.65	56.51
5	LAD at 80DAS	179.49	139.53	290.98	1214.74	1492.50	19.42	21.52	81.40	64.77	36.09
6	Angle between main axis and primary branches at 60 DAS	68.96	48.67	85.92	100.35	100.52	14.53	14.54	99.80	20.62	29.90
7	Angle between main axis and primary branches at 80 DAS	71.03	50.88	86.67	93.23	93.58	13.59	13.62	99.60	19.85	27.95
8	Root length	10.29	7.10	12.63	0.97	2.88	9.55	16.49	33.60	1.17	11.40
9	Root dry mass	0.62	0.44	1.09	0.01	0.02	19.22	21.56	79.50	0.22	35.29

Cont.....

Table 4.5. cont...

Sl. No.	Character	Mean	Range		Variance		Co-efficient of variation		Heritability (Broad sense%)	Genetic Advance	Genetic Advance as per cent of mean(%)
			Min.	Max.	Geno-typic	Pheno-typic	Geno-typic (%)	Pheno-typic (%)			
10	Number of primary branches per plant	4.86	3.50	7.30	0.88	1.04	19.28	20.97	84.60	1.77	36.53
11	Number of secondary branches per plant	0.97	0.10	4.45	0.91	0.95	98.09	96.29	96.34	1.89	194.69
12	Plant height	45.71	34.95	60.60	42.78	43.89	14.31	14.49	97.50	13.30	29.10
13	Number of pegs per plant	23.65	17.10	39.70	27.69	37.67	22.25	25.95	73.50	9.29	39.30
14	Number of mature pods per plant	14.20	8.35	24.33	16.68	18.74	28.77	30.49	89.00	7.94	55.92
15	Number of immature pods per plant	2.65	1.05	7.65	1.61	2.05	47.81	54.06	78.20	2.31	87.12
16	Shelling percentage	70.12	64.00	76.00	4.10	5.27	3.56	4.04	77.70	3.67	6.46
17	100-seed weight	35.93	26.25	50.25	33.86	39.14	16.20	17.41	86.50	11.15	31.03
18	Harvest Index	43.77	28.33	61.83	14.88	16.86	9.32	9.92	88.30	7.47	18.04
19	Pod yield per plant	10.83	7.50	17.90	4.10	7.63	18.71	25.52	53.80	3.06	28.27

primary branches per plant and pod yield per plant. Jayalakshmi and Reddy (2003) observed moderate to high PCV, GCV, high heritability and GAM for root dry mass. Shashikumara *et al.* (2016) reported low PCV, GCV, high heritability and moderate GAM for SLA and SCMR. The results of the present study were in accordance with these reports.

High heritability coupled with high genetic advance as percent of mean for LAI was in accordance with the results of John and Reddy (2014), Preetha and Raveendran (2007) in cotton and Rahaman (2015) in soybean. Whereas moderate heritability coupled with low genetic advance as per cent of mean for root length observed in the present study was similar to the report of Painwadee *et al.* (2009). High heritability and genetic advance as per cent mean for angle between main axis and primary branch was reported by Lodhi *et al.* (2014) in mustard and Sharanappa *et al.* (2014) in chickpea.

4.2.2. Rabi

GCV estimates were moderate to high for three traits – SLA at 60 DAS (12.37%), pod yield per plant (29.24%) and 100-seed weight (16.66%) while it was low for the remaining three traits – SCMR at 60 DAS (6.80%), RWC at 80 DAS (2.76%) and shelling percentage (4.79%).

Heritability was high for all the characters except for shelling percentage (52.40%) where it was moderate. GAM was high for SLA at 60 DAS (25.40%), 100-seed weight (34.11%) and pod yield per plant (50.83%) indicating that these traits are amenable for simple phenotypic selection. Low GCV, high heritability and low GAM was observed for the traits, SCMR at 60 DAS, RWC at 80 DAS and shelling percentage indicating that these traits are difficult to manipulate through simple selection procedures.

Bhavya *et al.* (2017) reported low to moderate PCV, GCV, high heritability and low to moderate GAM for SLA and SCMR, low PCV, GCV moderate heritability and GAM for shelling percentage and high PCV, GCV, heritability and GAM for pod yield per plant. Srivalli and Nadaf (2016)

Table 4.6. Genetic parameters for physiological, yield and yield attributes of 32 groundnut genotypes during *rabi* 2017-18

Sl. No.	Character	Mean	Range		Variance		Co-efficient of variation		Heritability (Broad sense %)	Genetic Advance	Genetic Advance as per cent of mean(%)
			Min.	Max.	Geno- typic	Pheno- typic	Geno- typic (%)	Pheno- typic (%)			
1	SCMR at 60 DAS	48.85	43.20	54.10	7.14	11.04	5.47	6.80	64.63	4.42	9.06
2	SLA at 60 DAS	134.91	108.22	171.00	278.61	280.51	12.37	12.42	99.33	34.27	25.40
3	RWC at 80DAS	88.98	79.90	97.20	24.40	24.65	5.55	5.58	98.88	10.12	11.37
4	Shelling percentage	65.59	57.00	72.00	3.52	6.71	3.47	4.79	52.40	2.80	5.17
5	100- seed weight	38.36	27.00	52.00	40.82	41.31	16.66	16.76	98.81	13.08	34.11
6	Pod yield per plant	8.21	3.78	13.05	5.76	8.09	29.24	34.66	71.20	4.17	50.83

observed low to moderate PCV, GCV, high heritability coupled with low genetic advance as per cent of mean for SLA, SCMR and RWC. Balaraju and Kenchanagoudar (2016) observed low GCV, PCV, high heritability and low GAM for shelling percentage and moderate GCV, PCV, high heritability and high GAM for 100-seed weight.

4.3. GENETIC DIVERGENCE

4.3.1 Genetic Divergence using Mahalanobis's D^2 Statistic based on Data of Physiological, Yield and Yield Attributes in *Kharif*

Genetic divergence among thirty two genotypes of groundnut was quantitatively assessed by adopting Mahalanobis's D^2 statistic and canonical root analysis based on pod yield and other morphological, physiological characters.

4.3.1.1 Test with wilks criterion and analysis of variance for dispersion of genotypes - *kharif*

Significant differences between genotypes based on the pooled effects of all the traits were tested by Wilks ' λ ' (statistic) criterion. The significance of ' λ ' (statistic) values was tested by ' χ^2 ' at 589 degrees of freedom. The ' λ ' statistic value (30710.58**) was significant indicating that the genotypes differed significantly when all the characters were considered simultaneously. The analysis of variance of dispersion of thirty two genotypes is presented in Table 4.7.

4.3.1.2 Mahalanobis's D^2 values

The mean values of thirty two genotypes $[(x_1)-(x_2)]$ were transformed into standardized uncorrelated mean values $[(y_1)-(y_2)]$. The D^2 values were computed for all the possible 32 $(32-1/2) = 496$ pairs of genotypes. The highest D^2 value of 3316.04 was found between the clusters III and VII.

Table 4.7. Analysis of variance for dispersion in 32 genotypes of groundnut for physiological, yield and yield attributes (*Kharif*, 2017)

Source of Variation	Degrees of freedom	Mean sum of squares
Genotype	31	9.9066E05**
Error	92	3.3381E05
Total	123	0.0000E00

** Significant at 1% level

**Table 4.8. Distribution of 32 genotypes of groundnut in different clusters
(Tocher's method) (*Kharif*, 2017)**

Cluster	Number of Genotypes	Genotypes
I	14	TCGS-1694, TCGS-1696, ALG-06-320, K 1789, TCGS-1630, R 2001-2, R-2001-3-1, R 2001-3, TCGS-1616, K 1847, ICG 86325, K1805, TCGS-1073, K 9
II	7	TCGS-1097, GG 20, K 1725, TCGS-1157, K. Anantha, K 6, J 89
III	5	R-2001-2-1, K 1811,Dharani, ICGS 76, GG 16
IV	3	TCGS-1622, K. Harithandra, GPBD-4
V	1	Narayani
VI	1	TCGS-1653
VII	1	SG 99

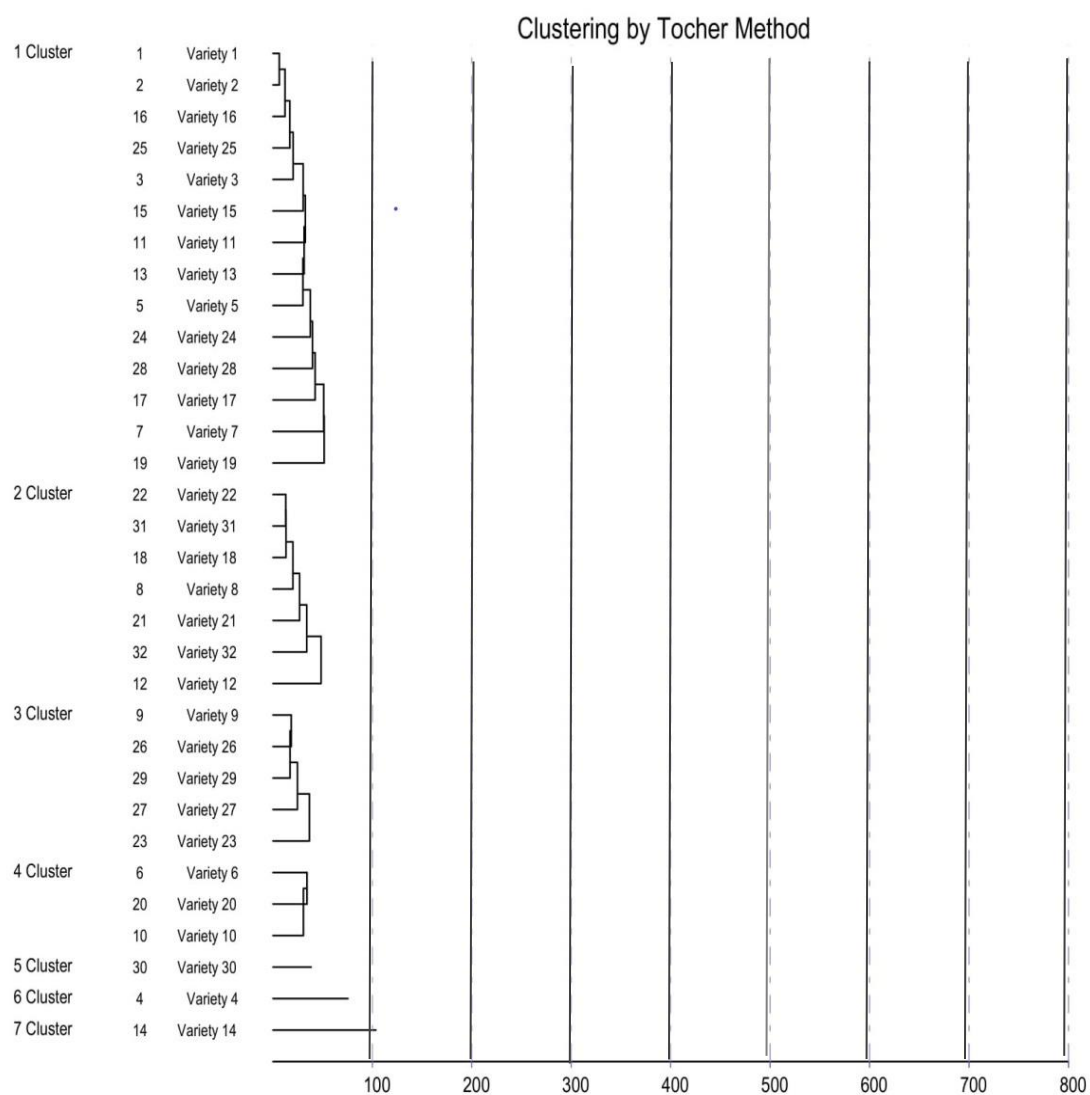


Fig 4.1. Dendrogram of 32 groundnut genotypes obtained through Tocher's method of classification (*Kharif*, 2017)

CLUSTER- I



TCGS-1694



TCGS-1696



ALG-06-320



K 1789



TCGS-1630



R-2001-2



R-2001-3-1



R-2001-3

Plate 2. Distribution of 32 groundnut genotypes in different clusters (Tocher's Method) (*kharif*, 2017)



TCGS-1616



K 1847



ICG 86325



K 1805



TCGS-1073



K 9

Plate 3. Distribution of 32 groundnut genotypes in different clusters (Tocher's Method) (*kharif*, 2017)

CLUSTER- II



TCGS-1097



GG-20



K 1725



TCGS-1157



K. Anantha



K 6



J 89

Plate 4. Distribution of 32 groundnut genotypes in different clusters (Tocher's Method) (*kharif*, 2017)

CLUSTER- III



R-2001-2-1



K 1811



Dharani



ICGS-76



GG-16

Plate 5. Distribution of 32 groundnut genotypes in different clusters (Tocher's Method) (*kharif*, 2017)

CLUSTER- IV



TCGS-1622



K. Harithandra



GPBD-4

CLUSTER- V



Naravani

CLUSTER-VI



TCGS-1653

CLUSTER- VII



SG 99

Plate 6. Distribution of 32 groundnut genotypes in different clusters (Tocher's Method) (*kharif*, 2017)

4.3.1.3 Grouping of genotypes

All the thirty two genotypes of groundnut were grouped into seven clusters using Tocher's method (Singh and Chaudhary, 1977). The distribution of the genotypes into clusters is presented in Table 4.8. and illustrated in Fig 4.1. Cluster I had maximum number of 14 genotypes, whereas cluster II comprised seven genotypes, cluster III had five genotypes, cluster IV had three genotypes, while cluster V, VI and VII were solitary clusters having one genotype each respectively.

Constellation of genotypes into different clusters based on physiological, yield and yield attributes in *kharif* was at random. Clustering pattern of genotypes into different clusters did not show any relationship with respect to their pedigrees and place of breeding. But, clustering pattern has clearly shown relationship with the characters/objective of the programme for which they were bred irrespective of place of breeding.

Clustering in twenty two genotypes by Makinde and Ariyo (2010) did not follow any pattern. The genotypes from different sources were grouped together while some genotypes from the same source were separated into eight different groups. Vasanthi *et al.* (2015) reported that clustering pattern was according to the objective for which they were bred. Zaman *et al.* (2010) and Islam *et al.* (2005) reported that genotypes of quite different pedigree and/or genotypes of common geographic origin or bred at same location were grouped into different clusters.

4.3.1.4 Intra and inter-cluster average distances

The average intra and inter-cluster D^2 and D values of various cluster are furnished in Table 4.9 Maximum intra-cluster D^2 (112.90) and D (10.63) distances were recorded by cluster I while minimum distance was noticed in clusters V, VI and VII as they had single genotype each. Inter-cluster average D^2 values ranged from 238.78 to 3316.04. Maximum inter-cluster D^2 value was observed between cluster III and VII (3316.04). Hence the genotypes

Table 4.9. Average intra and inter cluster D² and D values in 32 genotypes of Groundnut (*Kharif*, 2017)

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	112.90 (10.63)	363.62 (19.07)	454.29 (21.31)	1050.3 (32.41)	304.55 (17.45)	304.12 (17.44)	1612.33 40.15)
Cluster 2		102.86 (10.14)	1312.14 (36.22)	317.86 (17.83)	238.78 (15.45)	793.22 (28.16)	686.1 26.19)
Cluster 3			93.76 (9.68)	2539.13 (50.39)	986.94 (31.42)	401.63 (20.04)	3316.04 (57.59)
Cluster 4				111.91 (10.58)	611.9 (24.74)	1569.09 (39.61)	320.29 (17.90)
Cluster 5					0.00 (0.00)	575.34 (23.99)	1152.37 (33.95)
Cluster 6						0.00 (0.00)	2047.55 (45.25)
Cluster 7							0.00 (0.00)

Figures in parenthesis indicate D values

Figures in bold indicate intra-cluster D² values

from these clusters may be utilized as parents for hybridization which would result in high heterotic expression for physiological and yield components and wider segregation in filial generations. By using such genotypes as parents in hybridization programme, superior recombinants can be obtained. Similar inferences were also suggested by Golakia and Makne (1992), Vijayasekhar (2002) in groundnut. While minimum inter-cluster D^2 value was found between II and V (238.78) indicating that most of the characters had similar values in these clusters.

4.3.1.5 Cluster means for various characters

The cluster means for each of nineteen characters are furnished in Table 4.10. Considerable differences between clusters were observed for most of the characters studied. SCMR at 60 DAS was maximum in cluster II (45.12) and minimum in cluster V (40.13). Cluster VI had maximum SLA at 60 DAS (207.67) while cluster I had minimum SLA at 60 DAS (179.32). Mean values of LAI at 60 DAS ranged from 2.92 (cluster I) to 3.88 (cluster VII). LAI at 80 DAS ranged from 2.29 in cluster V to 5.65 in cluster VI. Cluster VI had maximum mean (290.98) for LAD at 80 DAS and it was minimum in cluster IV (163.24). Mean values of angle between main axis and primary branches at 60 DAS was from 48.67 (cluster VII) to 84 (cluster III).

Angle between main axis and primary branches at 80 DAS was highest in cluster III (85.41) and lowest in cluster VII (48.67). Cluster V and cluster VI showed maximum root length (10.83) whereas in cluster VII it was low (9.70). Mean root dry mass was minimum (0.55) in cluster V and maximum (0.74) in cluster VI. Maximum number of primary branches per plant was identified in cluster VII (7.30) whereas the value was minimum in cluster V (3.75). Cluster VII exhibited maximum number of secondary branches per plant (4.45) and cluster V showed minimum number of secondary branches per plant (0.10).

Table 4.10. Cluster means for physiological, yield and yield attributes in 32 groundnut genotypes (Kharif, 2017)
(Mahalanobis's D² method)

Cluster No.	SCMR	SLA	LAI 60	LAI 80	LAD	Angle 60	Angle 80	RL	RD M	PB	SB	PH	PP	MP	IP	SP	100 SW	HI	PYP
I	44.36	179.32	2.92	2.84	173.80	72.30	73.53	10.38	0.59	4.78	0.82	46.09	24.68	15.34	2.57	70.50	34.80	45.70	10.96
II	45.12	181.74	2.95	2.60	166.52	61.80	64.49	10.02	0.61	4.85	1.02	41.07	21.66	12.46	2.51	70.64	37.71	43.88	10.80
III	43.18	191.48	3.26	3.22	190.92	84.00	85.41	10.25	0.61	4.91	1.00	47.38	20.99	11.25	2.07	69.90	39.45	41.98	10.02
IV	42.59	195.93	3.30	2.53	163.24	52.28	54.03	10.38	0.71	4.75	0.58	46.33	21.39	12.28	2.60	69.83	32.17	38.00	8.90
V	40.13	197.87	3.66	2.29	178.75	61.58	76.25	10.83	0.55	3.75	0.10	55.10	20.63	12.50	2.50	71.50	34.75	41.88	9.70
VI	42.78	207.67	3.50	5.65	290.98	75.00	76.00	10.83	0.74	4.61	1.10	60.60	30.10	24.33	2.95	64.75	32.00	40.16	12.90
VII	44.10	184.97	3.88	3.63	230.89	48.67	50.88	9.70	0.72	7.30	4.45	38.48	39.70	22.45	7.65	68.50	38.00	47.64	17.90

SCMR- SPAD chlorophyll metre reading at 60 DAS; SLA - Specific leaf area at 60 DAS ($\text{cm}^2 \text{g}^{-1}$); LAI 60 - Leaf area index at 60 DAS; LAI 80 - Leaf area index at 80 DAS; LAD - Leaf area duration at 80 DAS ($\text{dm}^2 \text{day}$); Angle 60 - Angle between main axis and first two primary branches at 60 DAS ($^\circ$); Angle 80 - Angle between main axis and first two primary branches at 80 DAS ($^\circ$); RL- Root length (cms); RDM- Root dry mass (g); PB- Number of primary branches per plant; SB- Number of secondary branches per plant; PH= Plant height (cms); PP- Number of pegs per plant; MP- Number of mature pods per plant; IP- Number of immature pods per plant; SP- Shelling percentage (%); 100 SW- 100 seed weight (g); HI- Harvest index (%); PYP- Pod yield per plant (g)

Plant height ranged from 60.60 (cluster VI) to 38.48 (cluster VII). Number of pegs per plant was maximum in cluster VII (39.70) and minimum in clusters V (20.63). Cluster VI had maximum number of mature pods per plant (24.33) while cluster III had minimum number of mature pods per plant (11.25). Number of immature pods per plant ranged from 7.65 in cluster VII to 2.07 in cluster III. Shelling percentage was maximum in cluster V (71.50) and minimum in cluster VI (64.75). Highest 100-seed weight was found cluster III (39.45) while it was lowest in cluster VI (32). Mean value of harvest index ranged from 32.00 (cluster IV) to 47.64 (cluster VII). Pod yield per plant was maximum in cluster VII (17.90) whereas it was minimum in cluster IV (8.90). Intercrossing of the genotypes from these clusters would be useful to generate a wide range of variability for effective selection. Major emphasis has been given by many earlier workers (Vasanthi *et al.*, 2015 and Niveditha *et al.*, 2017) on cluster means for selecting the best parents for crossing programme.

4.2.1.6 Relative contribution of characters towards diversity

The number of times that each of the nineteen characters appeared in first rank and its respective per cent contribution towards diversity is presented in Table 4.11 and Fig 4.2.

Among all the characters studied, angle between main axis and primary branches at 60 DAS contributed maximum (72.58%) to the diversity by taking first rank 360 times, followed by plant height (6.85%) ranking 34 times first, LAI at 80 DAS (5.44%) with 27 times ranking first and angle between main axis and primary branches at 80 DAS (5.44%) with ranking 27 times first. The characters, number of secondary branches per plant, LAI at 60 DAS, SLA at 60 DAS, harvest index, shelling percentage, number of primary branches per plant, SCMR at 60 DAS, number of mature pods per plant, number of immature pods per plant and 100-seed weight contributed 3.43, 2.02, 1.41, 1.01, 0.6, 0.4, 0.2, 0.2, 0.2 and 0.2 per cent respectively to the total genetic divergence. On contrary, LAD at 80 DAS, number of pegs per plant and pod yield per plant did not contribute towards genetic divergence.

Table 4.11. Relative contribution of physiological, yield and yield attributes to genetic diversity in 32 groundnut Genotypes (Kharif, 2017)

Sl. No.	Characters	Times ranked first	Contribution (%)
1.	SCMR at 60 DAS	1	0.20
2.	SLA at 60 DAS	7	1.41
3.	LAI at 60 DAS	10	2.02
4.	LAI at 80 DAS	27	5.44
5.	LAD at 80 DAS	0	0.00
6.	Angle between main axis and primary branches at 60 DAS	360	72.58
7.	Angle between main axis and primary branches at 80 DAS	27	5.44
8.	Root length	0	0.00
9.	Root dry mass	0	0.00
10.	Number of Primary Branches per plant	2	0.40
11.	Number of secondary Branches per plant	17	3.43
12.	Plant height	34	6.85
13.	Number of pegs per plant	0	0.00
14.	Number of mature pods per plant	1	0.20
15.	Number of immature pods per plant	1	0.20
16.	Shelling percentage	3	0.60
17.	100-seed weight	1	0.20
18.	Harvest index	5	1.01
19.	Pod yield per plant	0	0.00

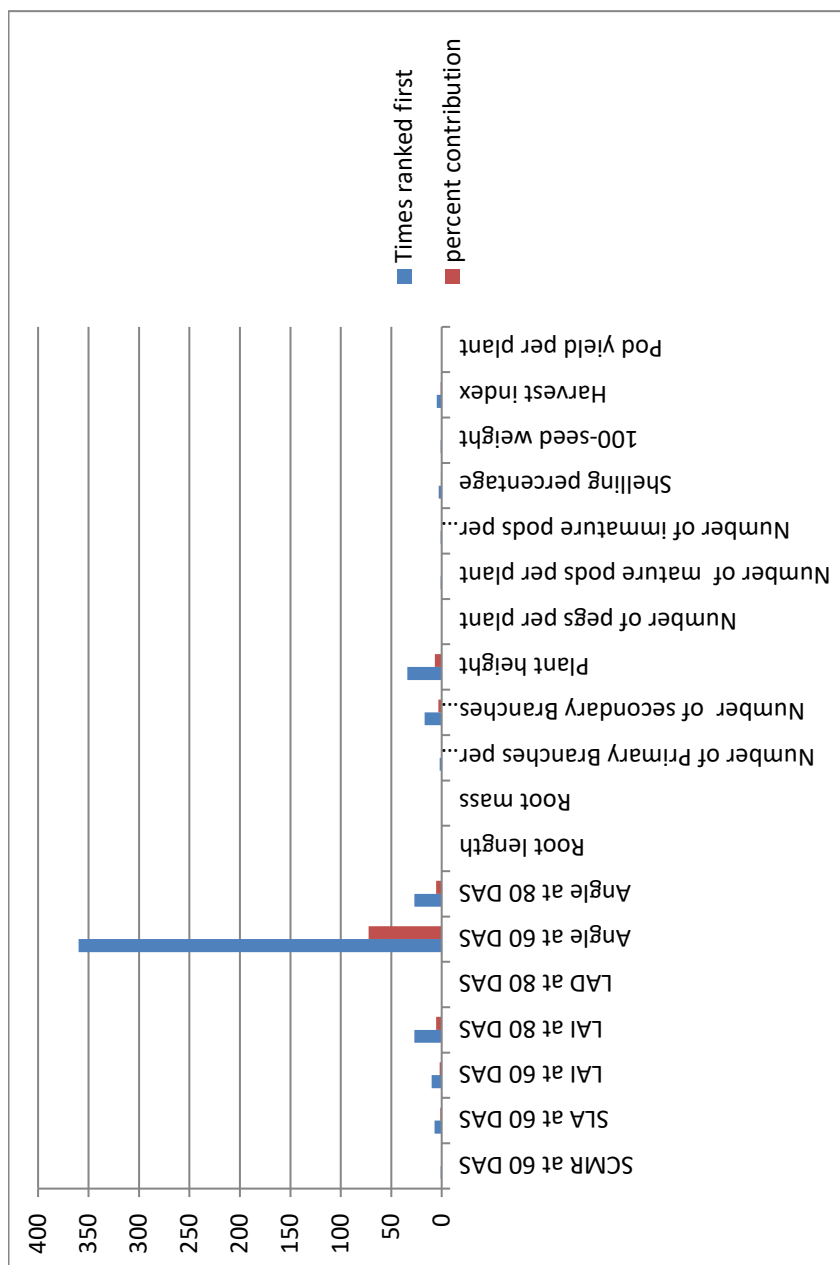


Fig 4.2. Relative contribution of physiological, yield and yield attributes to genetic diversity in 32 groundnut genotypes
(Kharif, 2017)

Suneetha *et al.* (2013) studied divergence among twenty nine released and pre-release cultures of groundnut. Twenty nine genotypes were grouped into nine clusters. Clustering pattern did show relationship with pedigree and place of breeding. Maximum contribution to diversity was by harvest index, days to emergence and length of main axis and minimum contribution was by number of mature pods per plant.

Vasanthi *et al.* (2015) studied genetic diversity among 29 genotypes based on ten physiological attributes- LAD, LAI, CGR, NAR, SLA, SCMR, seedling vigour index, germination percentage, harvest index and pod yield per plant. LAD at 54 DAS contributed maximum (34.48%) followed by LAI at 72 DAS (20.20%), LAD at 72 DAS (12.81%), CGR at 72 DAS (12.32%), CGR at 54 DAS (8.37%), harvest index (4.68%) and SLA at 72 DAS (3.21%). The distribution of genotypes into different clusters was related to the objective with which the genotypes were bred *i.e.* the 11 genotypes in cluster I were derived from WUE breeding programme.

4.3.1.7 Cluster diagram

A cluster diagram was constructed with the help of D^2 values showing the relationship between different populations (Fig 4.3). The highest distance between two clusters was exhibited between cluster III and VII (3316.04) indicating greatest divergence while the least distance was recorded between cluster II and V (238.78) indicating least genetic divergence among the seven clusters formed.

4.3.1.8 Canonical root analysis

In the canonical variate analysis, the number of variables were reduced to a linear expression called the principal components and these accounted for most of the variation produced by these characters. The second and succeeding principal components were formed similarly to account for residual variability. The first and second principal components (Z_1 and Z_2) were used to obtain a scattered distribution of the genotypes on a graph. When

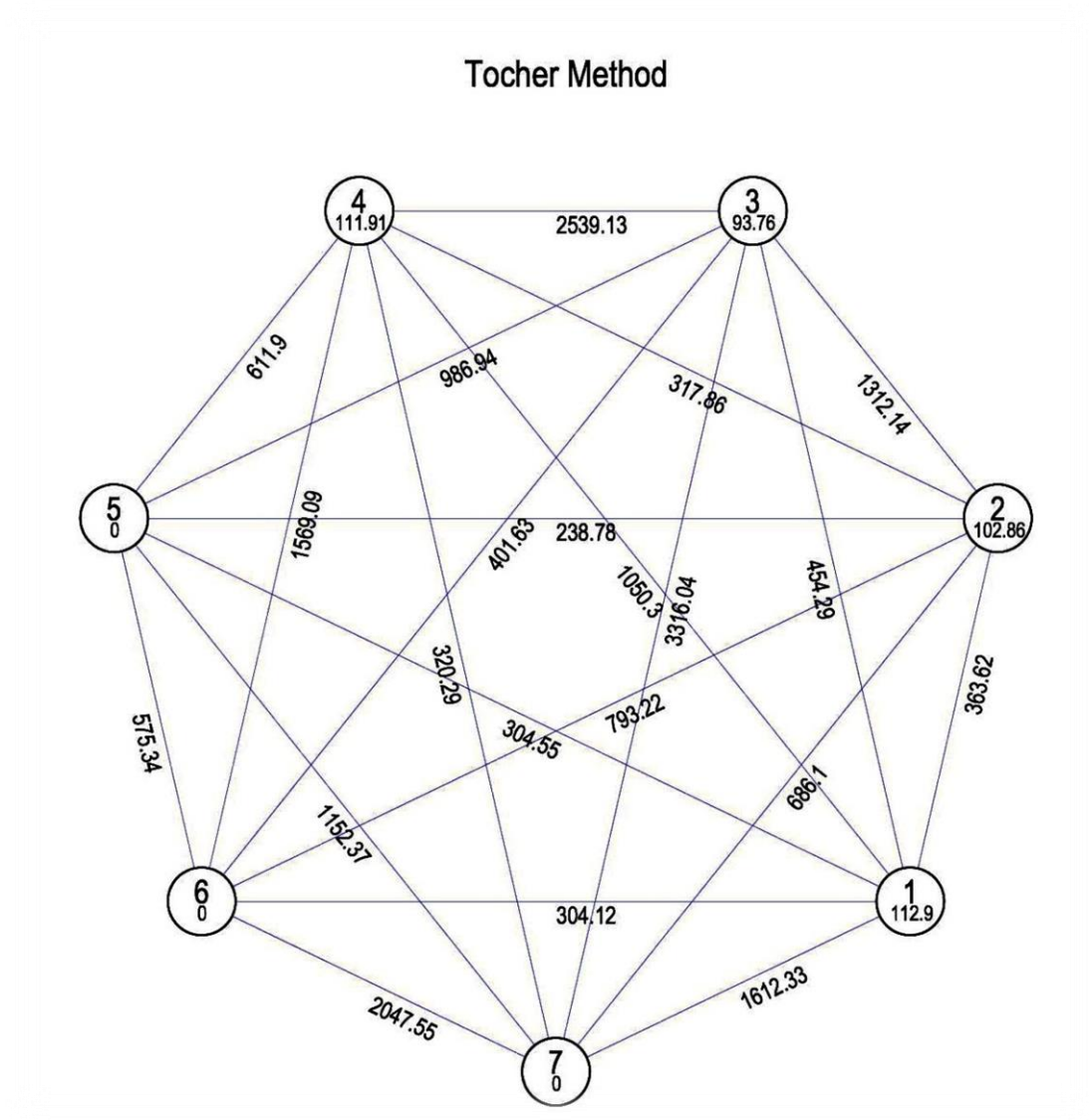


Fig 4.3. Statistical inter-cluster (D) distance among seven clusters of groundnut (Kharif, 2017)

represented graphically considering all the characters together based on genetic divergence, the genotypes differed widely.

4.3.1.9 Canonical roots

Canonical root analysis was carried out in thirty two genotypes of groundnut as per the method suggested by Rao (1952). Values of the six canonical roots and the percentage of variation expressed by them are presented in Table 4.12. First canonical root accounted for 30.51 per cent of variability while second and third roots accounted for 17.85 and 12.19 per cent respectively. Fourth, fifth and sixth vectors accounted for 11.56, 6.96 and 5.14 per cent of total variability respectively. Six canonical roots accounted for 84.21 per cent of total variability. Mean values of the canonical variates for three roots x, y and z are furnished in Table 4.13. The relative distribution of genotypes reflected existence of parallelism between grouping obtained by D^2 analysis and canonical vector analysis.

4.3.1.10 Contribution of vectors towards divergence

For six canonical vectors, the amount of contribution of all the characters towards diversity is presented in Table 4.14. In Z_1 vector, maximum contribution towards genetic divergence was observed by angle between main axis and primary branch at 60 DAS (0.403) followed by angle between main axis and primary branch at 80 DAS (0.389), pod yield per plant (0.368), plant height (0.289), number of primary branches per plant (0.218), shelling percentage (0.171), LAI at 80 DAS (0.113), root mass (0.101), 100-seed weight (0.105), LAD at 80 DAS (0.063), SLA at 60 DAS (0.025), SCMR at 60 DAS (0.024) and number of secondary branches per plant (0.005). Negative contribution to divergence was shown by remaining characters viz., LAI at 60 DAS, root length, number of pegs per plant, number of mature pods per plant, number of immature pods per plant and harvest index.

In Z_2 vector, the characters, number of immature pods per plant (0.457), number of secondary branches per plant (0.340), root dry mass

Table 4.12. Canonical root values, per cent of variation expected and cumulative variation expected for 32 genotypes of groundnut (Kharif, 2017)

Sl. No.	Values of canonical root	Per cent of variation expected	Cumulative total Variation expected
Z₁	5.80	30.51	30.51
Z₂	3.39	17.86	48.36
Z₃	2.32	12.19	60.55
Z₄	2.20	11.56	72.10
Z₅	1.32	6.96	79.06
Z₆	0.98	5.14	84.20

Table 4.13. Mean values of canonical vectors in 32 genotypes of groundnut (*Kharif*, 2017)

Sl. No.	Genotype	‘X’ vector	‘Y’ vector	‘Z’ vector
1	TCGS-1694	88.35	-8.52	-8.03
2	TCGS-1696	88.76	-8.67	-7.83
3	TCGS-1630	87.30	-5.74	-9.30
4	TCGS-1653	96.60	-1.07	-17.63
5	TCGS-1616	93.81	-9.99	-11.58
6	TCGS-1622	71.37	-11.03	-9.47
7	TCGS-1073	95.09	-11.56	-7.73
8	TCGS-1157	81.07	-7.75	-6.36
9	R-2001-2-1	105.31	-7.07	-11.83
10	GPBD-4	70.00	-5.93	-6.72
11	R-2001-3-1	94.32	-6.75	-11.40
12	J 89	75.38	-5.90	-6.19
13	R-2001-3	95.15	-7.47	-10.39
14	SG 99	64.48	2.36	-8.01
15	R-2001-2	91.83	-5.34	-7.52
16	ALG-06-320	86.94	-7.45	-7.38
17	K 1805	91.15	-0.88	-5.24
18	K 1725	82.16	-5.88	-4.81
19	K 9	94.46	-7.15	-3.95
20	K. Harithandra	68.73	-10.21	-9.39
21	K. Anantha	77.01	-10.65	-3.76
22	TCGS-1097	81.15	-8.80	-7.02
23	GG 16	103.95	-7.81	-13.39
24	K 1847	93.59	-7.55	-7.53
25	K 1789	88.26	-6.38	-7.44
26	K 1811	103.26	-8.13	-8.96
27	ICGS 76	108.28	-4.82	-10.00
28	ICG 86325	92.99	-10.65	-11.99
29	Dharani	107.97	-11.85	-11.50
30	Narayani	84.49	-12.67	-13.81
31	GG 20	81.51	-10.90	-7.77
32	K 6	81.08	-10.13	-9.75

Table 4.14. Canonical vectors for physiological, yield and yield attributes contributing to genetic divergence in 32 groundnut genotypes (Kharif, 2017)

Sl. No	Character	Canonical vectors					
		Z ₁	Z ₂	Z ₃	Z ₄	Z ₅	Z ₆
1	SCMR at 60 DAS	0.024	0.002	0.433	0.363	0.020	0.229
2	SLA at 60 DAS	0.025	-0.128	-0.431	0.057	0.172	0.652
3	LAI at 60DAS	-0.008	-0.073	-0.318	0.445	0.304	-0.070
4	LAI at 80DAS	0.113	0.288	-0.249	0.373	-0.169	-0.128
5	LAD at 80DAS	0.063	0.262	-0.370	-0.083	-0.382	0.215
6	Angle between main axis and primary branches at 60 DAS	0.403	0.014	0.004	-0.065	0.039	-0.001
7	Angle between main axis and primary branches at 80 DAS	0.389	-0.062	-0.075	-0.035	0.062	-0.030
8	Root length	-0.399	0.009	-0.032	0.036	-0.080	0.053
9	Root dry mass	0.101	0.327	0.274	-0.096	-0.226	0.295
10	Number of primary branches per plant	0.218	0.247	0.231	-0.164	0.096	0.197
11	Number of secondary branches per plant	0.005	0.340	-0.021	0.428	0.106	-0.021
12	Plant height	0.289	-0.019	-0.298	-0.142	-0.075	-0.120
13	Number of pegs per plant	-0.214	0.133	-0.012	-0.353	0.453	-0.038
14	Number of mature pods per plant	-0.310	0.269	-0.037	-0.156	0.093	0.089
15	Number of immature pods per plant	-0.077	0.457	0.107	0.209	0.111	-0.178
16	Shelling percentage	0.171	-0.227	0.190	0.176	0.428	0.231
17	Harvest Index	-0.207	-0.332	-0.010	0.113	-0.160	-0.281
18	100-seed weight	0.105	0.272	-0.184	-0.197	0.419	-0.283
19	Pod yield per plant	0.368	-0.058	0.138	0.003	-0.064	-0.241

(0.327), LAI at 80 DAS (0.288), 100-seed weight (0.272), number of mature pods per plant (0.269), LAD at 80 DAS (0.262), number of primary branches per plant (0.247), number of pegs per plant (0.133), angle between main axis and primary branch at 60 DAS (0.014), root length (0.009) and SCMR at 60 DAS (0.002) had positive contribution to the total diversity in their decreasing order. On contrary, the characters, SLA at 60 DAS, LAI at 60 DAS, angle between main axis and primary branch at 80 DAS, plant height, shelling percentage, harvest index and pod yield per plant showed negative contribution to diversity.

In Z_3 vector, SCMR at 60 DAS (0.433), root dry mass (0.274), number of primary branches per plant (0.231), shelling percentage (0.190), pod yield per plant (0.138), number of immature pods per plant (0.107) and angle between main axis and primary branch at 60 DAS (0.004) showed positive contribution to total diversity whereas SLA at 60 DAS, LAI at 60 DAS, LAI at 80 DAS, LAD at 80 DAS, angle between main axis and primary branch at 80 DAS, root length, number of secondary branches per plant, plant height, number of pegs per plant, number of mature pods per plant, harvest index and 100-seed weight expressed negative contribution to the diversity.

In vector Z_4 , positive contribution was shown by LAI at 60 DAS (0.445), number of secondary branches per plant (0.428), LAI at 80 DAS (0.373), SCMR at 60 DAS (0.363), number of immature pods per plant (0.209), shelling percentage (0.176), harvest index (0.113), SLA at 60 DAS (0.057), root length (0.036) and pod yield per plant (0.003). On contrary, LAD at 80 DAS, angle between main axis and primary branch at 60 DAS, angle between main axis and primary branch at 80 DAS, root dry mass, number of primary branches per plant, plant height, number of pegs per plant, number of mature pods per plant and 100-seed weight exhibited negative contribution.

In the Z_5 vector, number of pegs per plant (0.453), shelling percentage (0.428), 100-seed weight (0.419), LAI at 60 DAS (0.304), SLA at 60 DAS (0.172), number of immature pods per plant (0.111), number of secondary

branches per plant (0.106), number of primary branches per plant (0.096), number of mature pods per plant (0.093), angle between main axis and primary branch at 80 DAS (0.062), angle between main axis and primary branch at 60 DAS (0.039) and SCMR at 60 DAS (0.020) had positive contribution to the diversity. Negative contribution was reported by LAI at 80 DAS, LAD at 80 DAS, root length, root dry mass, plant height, harvest index and pod yield per plant.

In Z_6 vector, maximum contribution towards genetic divergence was observed by SLA at 60 DAS (0.652), root dry mass (0.295), shelling percentage (0.231), SCMR at 60 DAS (0.229), LAD at 80 DAS (0.215), number of primary branches per plant (0.197), number of mature pods per plant (0.089) and root length (0.053). Negative contribution to divergence was shown by remaining characters viz., LAI at 60 DAS, LAI at 80 DAS, angle between main axis and primary branch at 60 DAS, angle between main axis and primary branch at 80 DAS, number of secondary branches per plant, plant height, number of pegs per plant, number of immature pods per plant, harvest index, 100-seed weight and pod yield per plant.

This was in accordance with the relative contribution of characters as observed through D^2 analysis. Hence, angle between main axis and primary branches, plant height, number of primary and secondary branches per plant, LAI at 60 and 80 DAS and harvest index were important traits contributing towards genetic divergence in groundnut.

A three dimensional plot was illustrated in the Fig4.4 depicting the spacial distribution of thirty two groundnut genotypes using principal component analysis (PCA). Wider distribution of the genotypes was observed indicating the presence of considerable diversity in the genotypes.

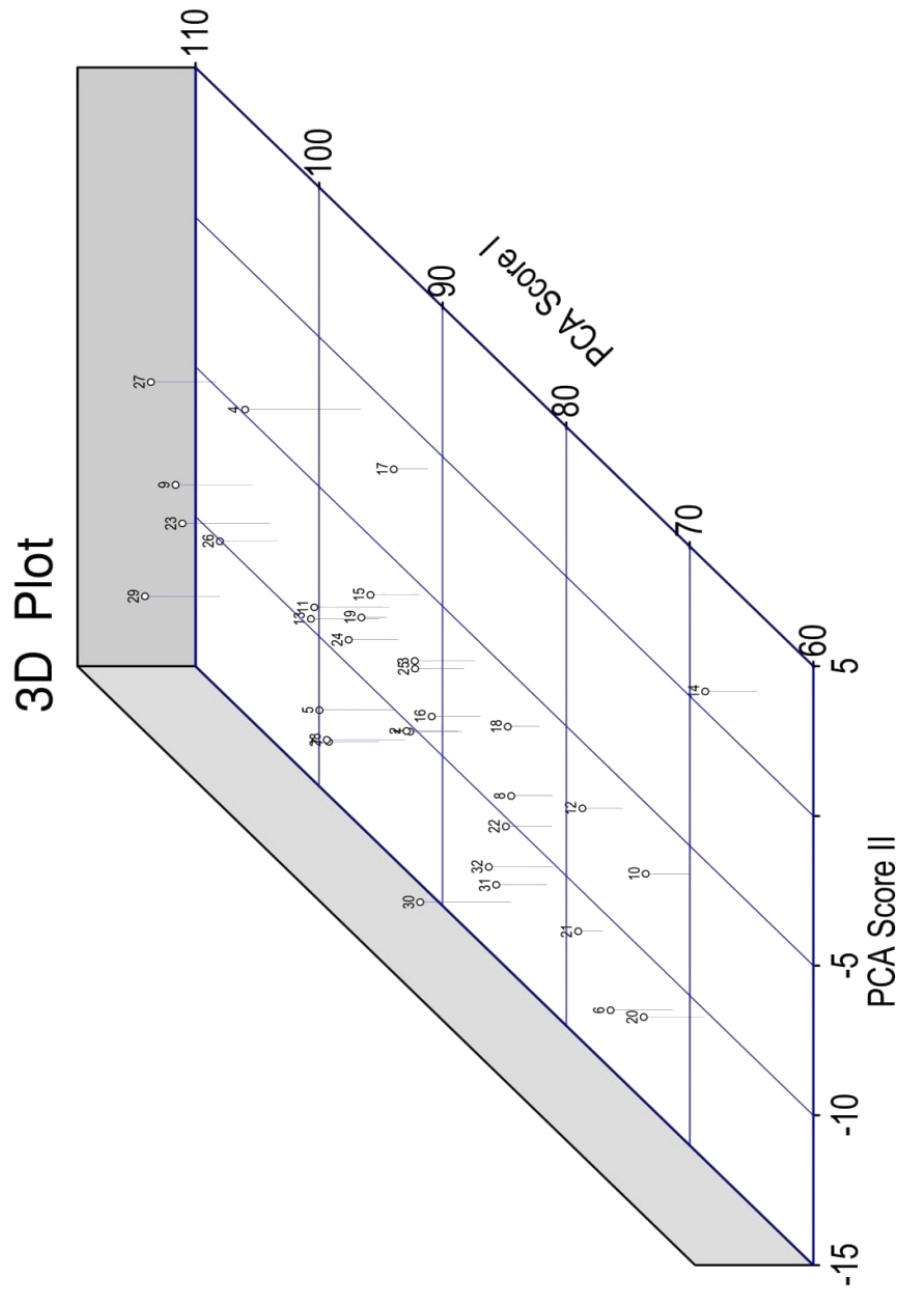


Fig 4.4. Principal component analysis (PCA) of 32 groundnut genotypes as revealed by canonical analysis (Kharif, 2017)

4.3.2 Genetic Divergence using Mahalanobis's D^2 Statistic based on Data of Physiological, Yield and Yield Attributes in *rabi*

Genetic divergence among thirty two genotypes of groundnut was quantitatively assessed by adopting Mahalanobis's D^2 statistic and canonical root analysis based on pod yield and other morphological, physiological characters.

4.3.2.1 Test with wilks criterion and analysis of variance for dispersion of genotypes - *rabi*

Significant differences between genotypes based on the pooled effects of all the traits were tested by Wilks ' λ ' (statistic) criterion. The significance of ' λ ' (statistic) values was tested by ' χ^2 ' at 186 degrees of freedom. The ' λ ' statistic value (51732.59**) was significant indicating that the genotypes differed significantly when all the characters were considered simultaneously. The analysis of variance of dispersion of thirty two genotypes is presented in Table 4.15.

4.3.2.2 Mahalanobis's D^2 values

The mean values of thirty two genotypes $[(x_1)-(x_2)]$ were transformed into standardized uncorrelated mean values $[(y_1)-(y_2)]$. The D^2 values were computed for all the possible 32 $(32-1/2) = 496$ pairs of genotypes. The highest D^2 value of 2031.75 was found between the clusters II and VIII.

4.3.2.3 Grouping of genotypes

All the thirty two genotypes of groundnut were grouped into eight clusters using Tocher's method (Singh and Chaudhary, 1977). The distribution of the genotypes into clusters is presented in Table 4.16 and illustrated in Fig4.5. Cluster II had maximum number of 10 genotypes whereas cluster I comprised 7 genotypes, cluster V had 6 genotypes, cluster IV had 5 genotypes, while cluster III, VI, VII and VIII had one genotype each.

Table 4.15. Analysis of variance for dispersion in 32 genotypes of groundnut for physiological, yield and yield attributes (Rabi, 2017-18)

Source of Variation	Degrees of freedom	Mean sum of squares
Genotype	31	1.6688E02**
Error	30	1.7244E02
Total	61	0.0000E02

** Significant at 1% level

Table 4.16. Distribution of 32 Genotypes of groundnut in different clusters (Tocher's method) (*Rabi*, 2017-18)

Cluster	Number of Genotypes	Genotypes
I	7	J 89, ICGS 76, ALG-06-320, GG 20, K 6, K. Anantha, R 2001-2
II	10	TCGS-1653, Dharani, TCGS-1097, R 2001-3, R-2001-2-1, Narayani, GPBD-4, R-2001-3-1, SG 99, TCGS-1630
III	1	K 9
IV	5	K 1805, K 1811, ICG 86325, K. Harithandra, TCGS-1616
V	6	TCGS-1157, K 1725, TCGS-1694, TCGS-1073, TCGS-1696, TCGS-1622
VI	1	K 1789
VII	1	K 1847
VIII	1	GG 16

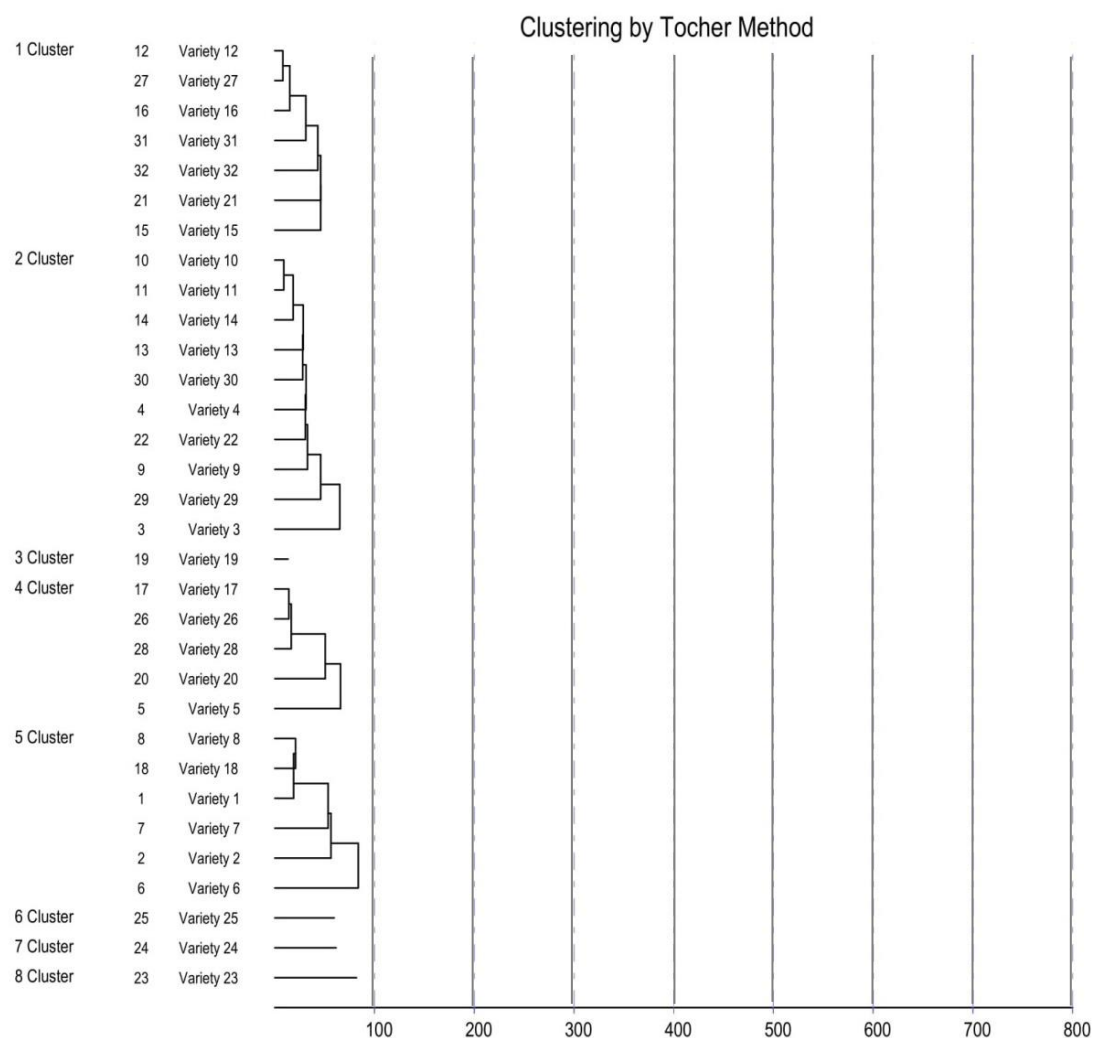


Fig 4.5. Dendrogram of 32 groundnut genotypes obtained through Tocher's method of classification (*Rabi*, 2017-18)

Kumar (2004) observed relationship between clustering pattern and place of breeding of genotypes when clustering was carried out based on physiological attributes. In the present study, there was no correspondence with respect to place of breeding or pedigree in grouping of genotypes.

4.3.2.4 Intra and inter-cluster average distances

The average intra and inter-cluster D^2 and D values of various clusters are furnished in Table 4.17. Maximum intra-cluster D^2 (190.85) and D (13.81) distances were recorded by cluster V while minimum distance was noticed in clusters III, VI, VII and VIII as they included single genotype each. Inter-cluster average D^2 values ranged from 164.21 to 2031.75. Maximum inter-cluster D^2 value was observed between cluster II and VIII (2031.75) indicating the greater diversity between these clusters. In contrast, the minimum inter-cluster D^2 value was found between III and VII (164.21) indicating the close relationship between the genotypes in these clusters.

4.3.2.5 Cluster means for various characters

The cluster means for each of nineteen characters are furnished in Table 4.18. Considerable differences between clusters were observed for most of the characters studied.

SCMR at 60 DAS was maximum in cluster III (54.10) and minimum in clusters VI (45.10). Cluster VIII had maximum SLA at 60 DAS (171.00) while cluster II had minimum SLA at 60 DAS (120.57). Mean values of RWC at 80 DAS ranged from 84.65 (cluster V) to 97.20 (cluster VI). Shelling percentage ranged from 61.00 in cluster VII and VIII to 72.00 in cluster III. Cluster V had maximum mean (47.08) for 100-seed weight and minimum in cluster VII (27.00). Mean values of pod yield per plant ranged from 3.78 (cluster VIII) to 10.16 (cluster V). Intercrossing the elite genotypes from these clusters could be suggested to generate wide range of variability.

Table 4.17. Average intra and inter cluster D² and D values in 32 genotypes of groundnut (*Rabi*, 2017-18)

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	125.92 (11.22)	381.99 (19.54)	221.46 (14.88)	288.38 (16.98)	542.52 (23.29)	308.47 (17.56)	532.63 (23.08)	826.97 (28.76)
Cluster 2		121.42 (11.02)	225.89 (15.03)	966.59 (31.09)	461.68 (21.49)	749.38 (27.37)	585.51 (24.20)	2031.75 (45.07)
Cluster 3			0.00 (0.00)	679.61 (26.07)	721.53 (26.86)	253 (15.91)	164.21 (12.81)	1415.41 (37.62)
Cluster 4				158.54 (12.59)	925.68 (30.42)	449.17 (21.19)	1003.56 (31.68)	335.88 (18.33)
Cluster 5					190.85 (13.81)	1351.43 (36.76)	1494 (38.65)	1768.25 (42.05)
Cluster 6						0.00 (0.00)	181.5 (13.47)	813.19 (28.52)
Cluster 7							0.00 (0.00)	1702.17 (41.26)
Cluster 8								0.00 (0.00)

Figures in parenthesis indicate D values

Figures in bold indicate intra-cluster D² values

**Table 4.18. Cluster means for physiological, yield and yield attributes in 32 groundnut genotypes
(Mahalanobis's D² method) (Rabi, 2017-18)**

Cluster No.	SCMR at 60 DAS	SLA at 60 DAS	RWC at 80 DAS	Shelling percentage	100 seed weight	Pod yield per plant
I	48.73	140.65	90.57	64.57	37.93	7.71
II	47.29	120.57	86.80	65.20	34.00	8.48
III	54.10	123.99	94.05	72.00	35.50	9.38
IV	48.72	160.71	90.48	65.60	39.80	7.18
V	50.12	126.56	84.65	68.33	47.08	10.16
VI	45.10	143.32	97.20	63.00	31.00	6.18
VII	52.70	125.54	96.85	61.00	27.00	7.59
VIII	52.90	171.00	97.00	61.00	47.00	3.78

4.2.2.6 Relative contribution of characters towards diversity

The number of times that each of the six characters appeared in first rank and its respective per cent contribution towards diversity is presented in Table 4.19 and Fig4.6.

Among all the characters studied, SLA at 60 DAS contributed maximum (33.67%) to the diversity by taking first rank 167 times, followed by 100-seed weight (33.06%) ranking 164 times first and RWC at 80 DAS (32.26%) with 160 times ranking first. These three characters contribution was almost equal. The characters, pod yield per plant, shelling percentage and SCMR at 60 DAS contributed 0.6, 0.2 and 0.2 per cent respectively to the total genetic divergence.

Maximum contribution of SLA to genetic diversity is in accordance to the reports of Venkataravana (2010). Least contribution of pod yield per plant towards diversity was reported earlier by Venkateswarlu *et al.* (2011).

4.3.2.7 Cluster diagram

A cluster diagram was constructed with the help of D^2 values showing the relationship between different populations (Fig 4.7). The highest distance between two clusters was exhibited between cluster II and VIII (2031.75) indicating greatest divergence while the least distance was recorded between cluster III and VII (164.21) indicating least genetic divergence among the genotypes in these clusters.

4.3.2.8 Canonical root analysis

In the canonical variate analysis, the number of variables were reduced to a linear expression called the principal components and these accounted for most of the variation produced by these characters. The second and succeeding principal components were formed similarly to account for residual variability. The first and second principal components (Z_1 and Z_2) were used to obtain a scattered distribution of the genotypes on a graph. When

Table 4.19. Relative contribution of physiological, yield and yield attributes to genetic diversity in 32 groundnut genotypes (*Rabi*, 2017-18)

Sl. No.	Characters	Times ranked first	Contribution (%)
1.	SCMR at 60 DAS	1	0.20
2.	SLA at 60 DAS	167	33.67
3.	RWC at 80DAS	160	32.26
4.	Shelling percentage	1	0.20
5.	100-seed weight	164	33.06
6.	Pod yield per plant	3	0.60

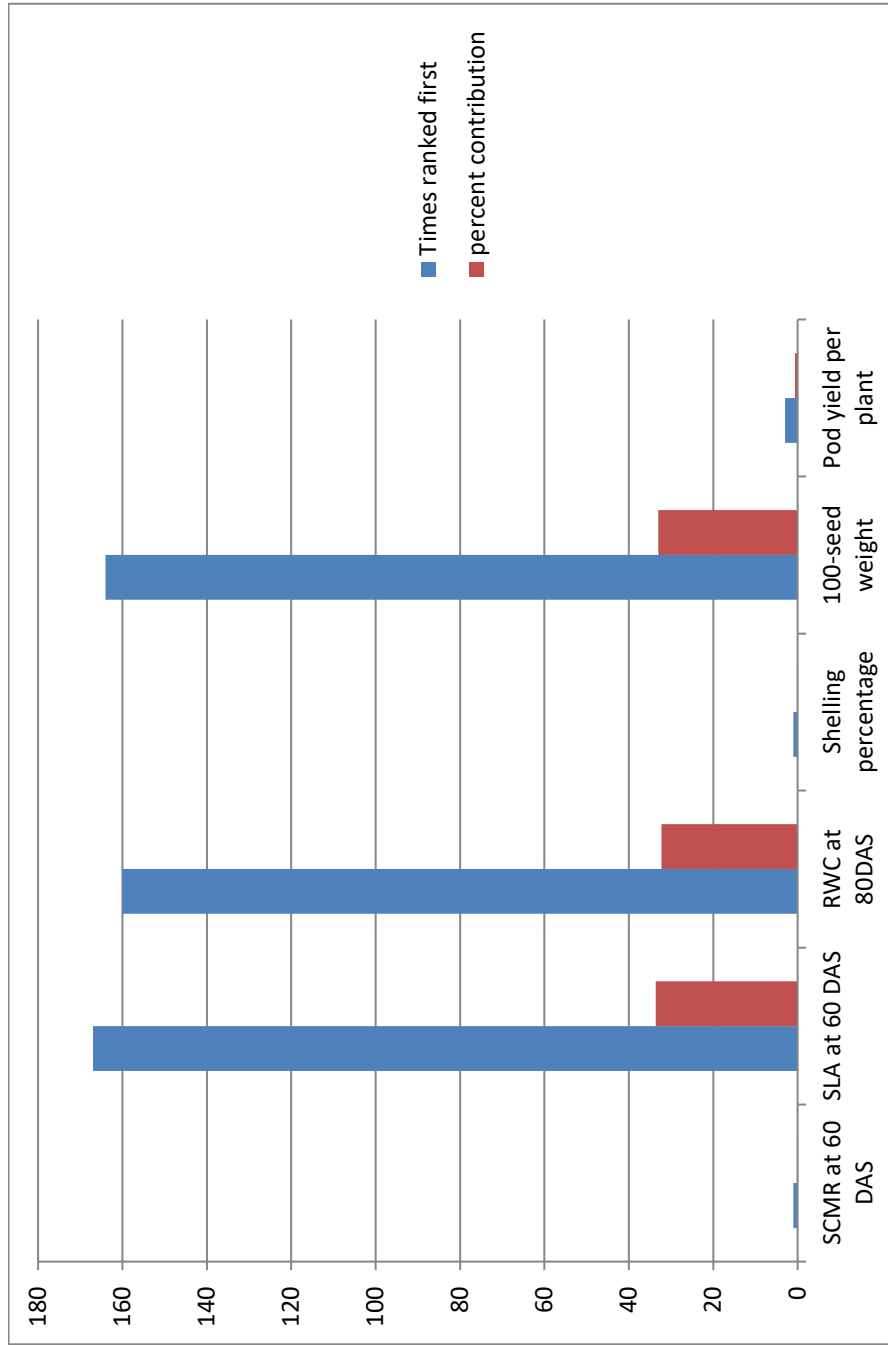


Fig 4.6. Relative contribution of physiological, yield and yield attributes to genetic diversity in 32 groundnut genotypes (Rabi, 2017-18)

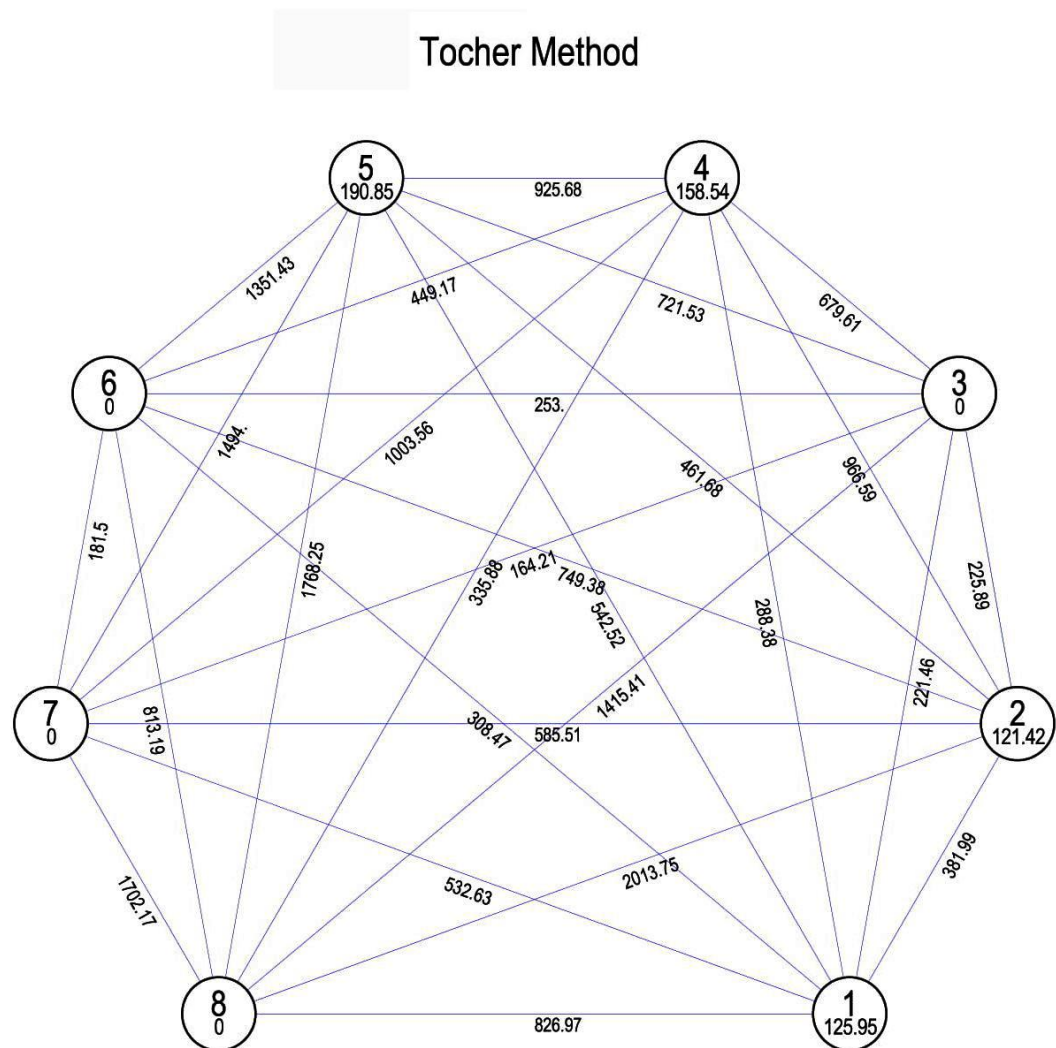


Fig 4.7. Statistical inter-cluster (D) distance among eight clusters of groundnut (*Rabi*, 2017-18)

represented graphically considering all the characters together based on genetic divergence, the genotypes differed widely.

4.3.2.9 Canonical roots

Canonical root analysis was carried out in thirty two genotypes of groundnut as per the method suggested by Rao (1952). Values of the three canonical roots and the percentage of variation expressed by them are presented in Table 4.20. First canonical root accounted for 54.03 per cent of variability while second and third roots accounted for 23.60 and 14.42 per cent respectively. Three canonical roots accounted for 92.05 per cent of total variability. Mean values of the canonical variates for three roots x, y and z are furnished in Table 4.21.

4.3.2.10 Contribution of vectors towards divergence

For three canonical vectors, the amount of contribution of all the characters towards diversity is presented in Table 4.22. In Z_1 vector, maximum contribution towards genetic divergence was observed by RWC at 80 DAS (0.518), SLA at 60 DAS (0.456) and SCMR at 60 DAS (0.143). Negative contribution to divergence was shown by remaining characters viz., shelling percentage, 100-seed weight and pod yield per plant. In Z_2 vector, the characters, 100-seed weight (0.745), SCMR at 60 DAS (0.411), shelling percentage (0.346) and SLA at 60 DAS (0.327) had positive contribution to the total diversity in their decreasing order. On contrary, the characters, RWC at 80 DAS and pod yield per plant showed negative contribution to diversity. In Z_3 vector, SCMR at 60 DAS (0.895), pod yield per plant (0.141) and RWC at 80 DAS (0.085) showed positive contribution to total diversity whereas SLA at 60 DAS, shelling percentage and 100-seed weight showed negative contribution to the diversity.

A three dimensional plot was illustrated in the Fig 4.8 depicting the spacial distribution of thirty two groundnut genotypes using principal

Table 4.20. Canonical root values, per cent of variation expected and cumulative variation expected for 32 genotypes of groundnut (*Rabi*, 2017-18)

Sl. No.	Values of canonical root	Per cent of variation expected	Cumulative total Variation expected
Z ₁	3.24152	54.02530	54.02530
Z ₂	1.41600	23.59991	77.62521
Z ₃	0.86534	14.42236	92.04757

Table 4.21. Mean values of canonical vectors in 32 genotypes of groundnut (*Rabi*, 2017-18)

Sl. No.	Genotype	‘X’ vector	‘Y’ vector	‘Z’ vector
1	TCGS-1694	227.032	-44.778	19.151
2	TCGS-1696	224.401	-53.937	23.516
3	TCGS-1630	235.911	-61.749	24.816
4	TCGS-1653	233.116	-64.208	26.476
5	TCGS-1616	245.938	-45.088	16.046
6	TCGS-1622	224.393	-38.968	16.310
7	TCGS-1073	234.794	-51.003	22.838
8	TCGS-1157	231.658	-50.195	22.044
9	R-2001-2-1	232.779	-60.007	23.734
10	GPBD-4	224.668	-60.213	24.204
11	R-2001-3-1	226.650	-58.855	23.625
12	J 89	244.680	-58.063	20.597
13	R 2001-3	228.477	-65.999	27.939
14	SG 99	224.758	-60.227	25.680
15	R 2001-2	241.031	-58.633	21.523
16	ALG-06-320	244.533	-53.414	20.069
17	K 1805	254.946	-55.696	18.047
18	K 1725	235.464	-45.383	19.820
19	K 9	238.712	-65.281	29.119
20	K Harithandra	251.878	-43.802	15.719
21	K. Anantha	242.138	-62.938	25.349
22	TCGS-1097	232.726	-63.949	27.718
23	GG 16	266.749	-45.195	15.135
24	K 1847	244.461	-74.874	31.756
25	K 1789	252.208	-67.220	24.033
26	K 1811	256.806	-55.499	18.424
27	ICGS 76	247.642	-56.029	23.101
28	ICG 86325	256.865	-50.474	17.350
29	Dharani	235.826	-64.424	26.894
30	Narayani	225.715	-66.986	28.669
31	GG 20	243.202	-48.753	19.853
32	K 6	243.994	-59.614	22.650

Table 4.22. Canonical vectors for physiological, yield and yield attributes contributing to genetic divergence in 32 groundnut genotypes (*Rabi*, 2017-18)

Sl. No	Character	Canonical vectors		
		Z ₁	Z ₂	Z ₃
1	SCMR at 60 DAS	0.14290	0.41056	0.89499
2	SLA at 60 DAS	0.45616	0.32748	-0.28352
3	RWC at 80DAS	0.51752	-0.19151	0.08464
4	Shelling percentage	-0.46923	0.34585	-0.06465
5	100-seed weight	-0.00832	0.74526	-0.29552
6	Pod yield per plant	-0.53238	-0.11184	0.14117

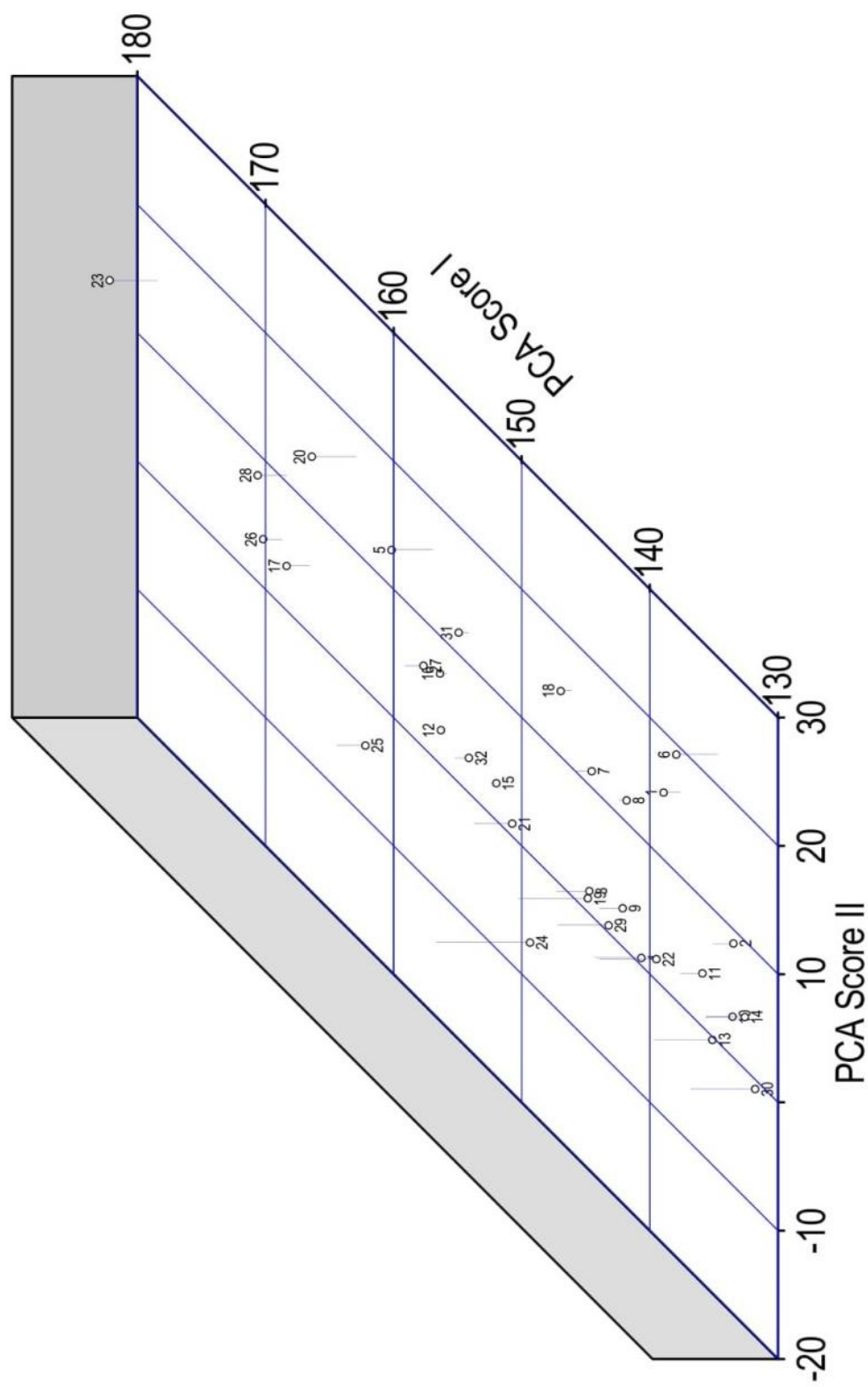


Fig 4.8. Principal component analysis (PCA) of 32 groundnut genotypes as revealed by canonical analysis (Rabi, 2017-18)

component analysis (PCA). Wider distribution of the genotypes was observed indicating the presence of considerable diversity in the genotypes.

The group constellations formulated on the basis of Mahalanobis's D^2 statistic were confirmed by canonical root analysis. The three canonical roots were responsible for 92.05 per cent of total variance of uncorrelated (y) variables for 6 physiological, yield and yield attributes in *rabi*, which indicated that differentiation of these traits was nearly complete in these genotypes in 3 phases (Table 4.20.). The relative distribution of genotypes reflected existence of parallelism between grouping obtained by D^2 analysis and canonical vector analysis.

The three vectors as a whole contributed 92.05 per cent towards genetic divergence because of which discernible overlapping was observed in group constellation of canonical vectors. The character, RWC at 80DAS and SLA at 60 DAS in the first vector, 100-seed weight in the second vector, SCMR at 60 DAS and pod yield per plant in the third vector contributed the maximum towards divergence. This was in accordance with the relative contribution of characters as observed through D^2 analysis. Hence, RWC at 80 DAS, SLA at 60 DAS, SCMR at 60 DAS and pod yield per plant were important traits contributing towards genetic divergence in groundnut.

4.3.3 Genetic Divergence at Molecular Level using SSR Markers

The molecular tools such as DNA markers are becoming increasingly important as effective tools in crop breeding programmes. Molecular markers are useful in the assessment of genetic diversity for (i) the identification and removal of duplicates (ii) production of core collections (iii) evaluating genetic relationships between taxa (iv) selecting diverse parental genotypes required for (a) studying QTLs for complex traits (b) developing mapping populations (Tanksley *et al.*, 1989). Their application in genetic enhancement of groundnut is lagging behind due to limited knowledge of the genome. Wide variation for morphological and physiological characteristics exists in both

wild and cultivated groundnut (Halward *et al.*, 1993) but low DNA polymorphism has been observed in cultivated species (Kochert *et al.*, 1991 and Halward *et al.*, 1993), this can be attributed due to its recent evolution, tetraploid nature and narrow genetic base.

Studies using RFLP, RAPD, AFLP and SSR techniques have revealed the presence of DNA polymorphism in cultivated groundnuts (Dwivedi and Varma, 2002). SSRs have been widely useful in detection of polymorphism among cultivated accessions. SSR markers are preferred due to their co-dominance, simplicity, high polymorphism, repeatability, multi-allelic nature and transferability within the genus *Arachis* (Kanyika *et al.*, 2015). Microsatellites have been recognized as useful molecular markers in marker assisted selection (MAS) and analysis of genetic divergence (Krishna *et al.*, 2004).

4.3.3.1 SSR marker screening

Out of 32 genotypes, ten genotypes with contrasting drought characteristics like SCMR, SLA and RWC were included for molecular analysis. 27 SSR markers which include drought specific markers (Gautami *et al.*, 2012, Varshney *et al.*, 2009) were employed for screening 10 selected groundnut genotypes. Among 27 SSR markers, eleven showed polymorphism (Table 4.23). Hence, these eleven markers were employed for assessment of diversity.

4.3.3.2 SSR markers polymorphism in groundnut genotypes

The ten genotypes showed different banding pattern with eleven polymorphic SSR markers. In the present study, a total of 60 alleles were detected across ten genotypes by eleven polymorphic SSR markers, on an average 5.45 alleles per marker, out of which five alleles per marker were polymorphic.

Table 4.23. Details of alleles amplified and PIC values of primers

S. No	SSR Marker	Total No.of alleles	No.of polymorphic alleles	Size of the fragment (bp)	PIC	Annealing temperature (° C)
1	IPAHM 105	7	6	250-320	0.70	58.5
2	IPAHM 123	5	4	140-180	0.72	58.7
3	IPAHM 689	4	4	315-340	0.72	58.9
4	PM 3	7	7	170-220	0.70	56.8
5	PM 375	5	5	100-120	0.74	59.8
6	PM 418	5	5	120-140	0.61	57.1
7	PM 45	7	5	75-125	0.95	58.5
8	PM 50	4	4	90-110	0.74	56.8
9	SEQ2G4	5	4	255-350	0.58	58.4
10	SEQ3A1	4	4	230-280	0.72	58.5
11	SEQ5D05	7	7	230-300	0.75	58.8
12	AH 191	1	0	145	0	62.9
16	AH 229	1	0	200	0	61.6
14	AH 41	2	0	250	0	62.4
15	AH 522	1	0	160	0	62.8
16	GM2350	2	0	140	0	58.6
17	GM 2724	2	0	100	0	57.6
18	IPAHM 103	1	0	130	0	58.7
19	IPAHM 108	2	0	170	0	57.2
20	IPAHM 165	1	0	250	0	59.8
21	IPAHM 406	1	0	300	0	59.1
22	TC3E05	1	0	300	0	61.0
23	TC4H02	3	0	180	0	59.0
24	TC9F04	1	0	120	0	61.0
25	PM 106	2	0	170	0	58.6
26	SEQ2G3	1	0	200	0	58.7
27	SEQ3A06	1	0	200	0	61.0

Amplification allele size with SSR markers varied from 75bp (PM 45) to 350bp (SEQ2G4) (Table 4.23). IPAHM 105 amplified three loci out of which 500bp allele was monomorphic and other two loci are polymorphic (Fig 4.9). It is located on two chromosomes viz., A05 and B04 at 57.475 and 77.186 cM respectively. An allele of 250 bp size was amplified in Dharani, TCGS-1622, K 1725, TCGS-1694 and TCGS-1073. K 9 showed an unique allele of high molecular weight i.e. 320 bp. In it six polymorphic alleles were amplified. Cuc *et al.* (2008) reported among 32 germplasm lines of groundnut IPAHM 105 amplified three alleles. Ravi *et al.* (2010) reported that 18 alleles were amplified by IPAHM 105.

IPAHM 123 amplified four alleles among ten groundnut genotypes studied. The size of the alleles ranged from 140bp (TCGS-1622) to 180bp (GG-20, K 9, Dharani, TCGS-1694, K 1725 and TCGS-1073). A specific allele of 140 bp was amplified in TCGS-1622(Fig 4.10). Cuc *et al.* (2008) reported among 32 germplasm lines of groundnut IPAHM 123 amplified four alleles.

The size of the alleles amplified by IPAHM 689 ranged from 315 bp (Narayani, TCGS-1157 and GG-20) to 340 bp (Fig 4.11). The 340bp allele of IPAHM 689 was specific to drought tolerant genotype, K 1725. Most probably this allele may be linked to drought tolerance. It amplified four polymorphic alleles. Cuc *et al.* (2008) identified that two alleles were amplified by IPAHM 689 among 32 germplasm lines of groundnut.

In all the genotypes two loci were amplified with PM 3 marker. 170 bp allele of PM 3 was specific to Narayani. The range of amplified alleles size was 170 bp (Narayani) to 220 bp (K 1725 and TCGS-1694). The total number of alleles amplified was seven. Naito *et al.* (2008) detected 15 alleles of PM 3 marker with size ranging from 192 to 225bp among 214 groundnut accessions (Fig 4.12). He *et al.* (2003) reported seven alleles with size ranging from 200 to 222bp with PM 3 marker. PM 3 marker have two alleles which might have been amplified from loci in both genomes of *A. hypogaea* (Gimenes *et al.*,

Fig 4.9. SSR gel profile of 10 groundnut genotypes using IPAHM 105 primer

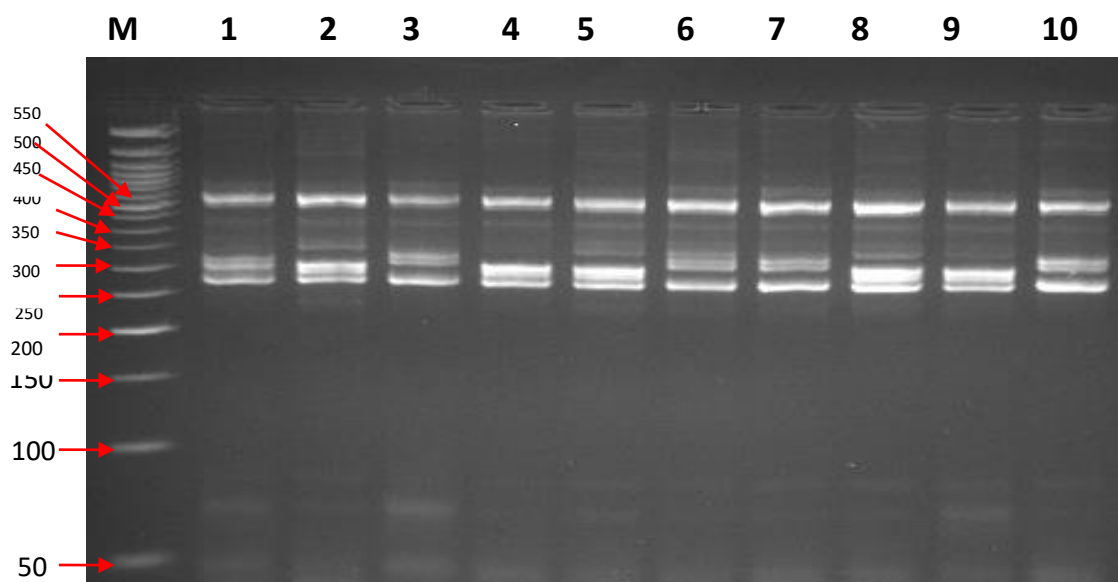
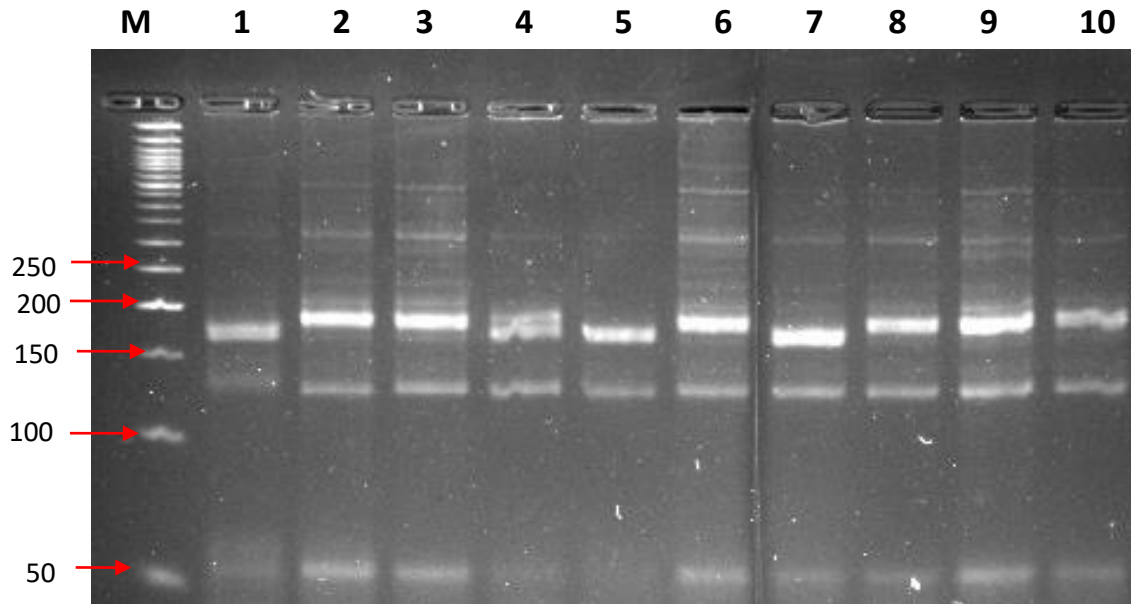


Fig 4.10. SSR gel profile of 10 groundnut genotypes using IPAHM 123 primer



Lane M = Marker

- | | |
|--------------|---------------|
| 1. Narayani | 6. Dharani |
| 2. GG-20 | 7. TCGS-1622 |
| 3. K 9 | 8. K 1725 |
| 4. TCGS-1157 | 9. TCGS-1694 |
| 5. TCGS-1616 | 10. TCGS-1073 |

Fig 4.11 SSR gel profile of 10 groundnut genotypes using IPAHM 689 primer

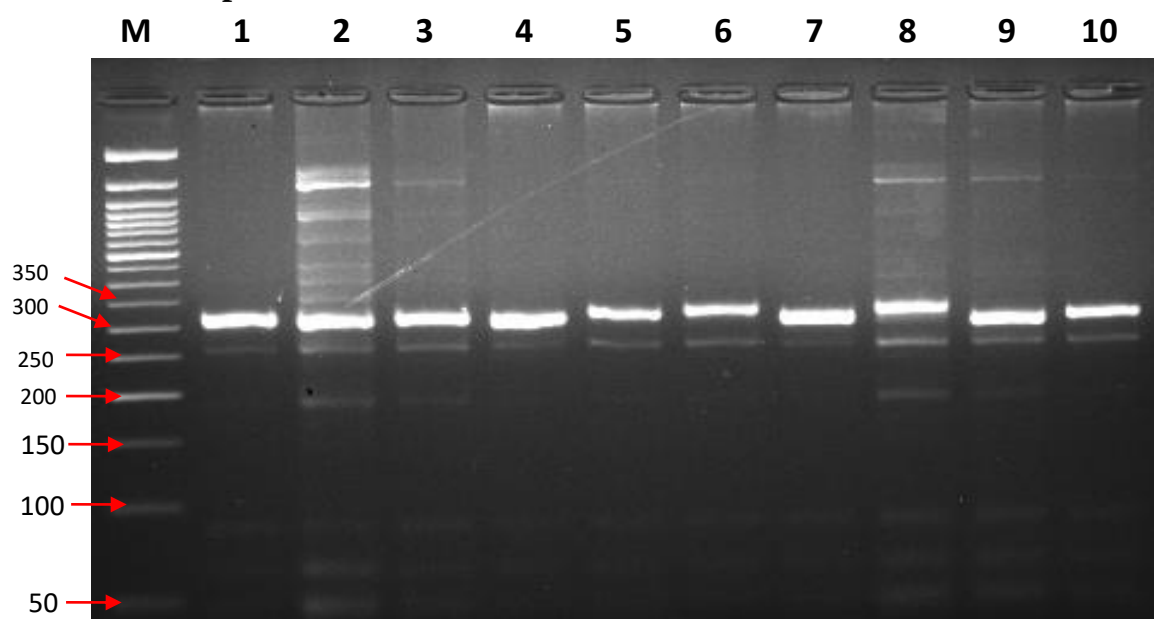
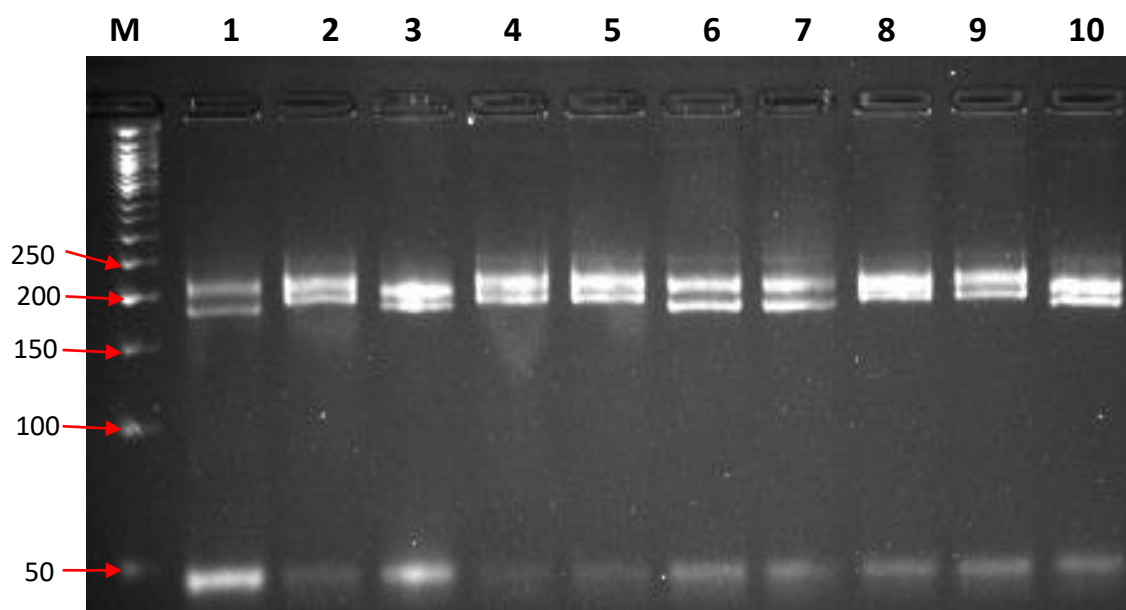


Fig 4.12. SSR gel profile of 10 groundnut genotypes using PM 3 primer



Lane M = Marker

- | | |
|--------------|---------------|
| 1. Narayani | 6. Dharani |
| 2. GG-20 | 7. TCGS-1622 |
| 3. K 9 | 8. K 1725 |
| 4. TCGS-1157 | 9. TCGS-1694 |
| 5. TCGS-1616 | 10. TCGS-1073 |

2007). PM 3 is located on two chromosomes viz., A03 and B03 at 99.899 and 58.833 cM respectively.

PM 375 is a single locus marker with five alleles with very clear allelic separation, amplified 100 bp allele in Dharani, TCGS-1622, TCGS-1694, TCGS-1073 and Narayani with a upper range of 120 bp in the genotypes, K 9, TCGS-1157 and TCGS-1616(Fig 4.13). Naito *et al.* (2008) reported PM 375 amplified three alleles with size ranging from 120 to 134 bp among 214 groundnut accessions.

Five alleles were detected on scoring bands of PM 418 with size ranging from 120 bp (TCGS-1616 and TCGS-1157) to 140 bp (Dharani and K 1725). In K 9, a specific allele of 135 bp was amplified (Fig 4.14).

PM 45 marker amplified three to four alleles, out of which 75 and 80 bp alleles are monomorphic and two are scorable and polymorphic. All the genotypes studied showed small differences with respect to third allele (100-110 bp) (Fig 4.15). Fourth allele was amplified in three genotypes, out of which GG-20 and TCGS-1694 amplified 115 bp allele whereas TCGS-1157 produced a unique allele of molecular weight 125 bp. PM 45 is located at two positions on a single chromosome viz., A05 at 51.567 and 54.003 cM respectively. He *et al.* (2003) reported that PM 45 marker amplified three alleles with size ranging from 101 to 111bp.

PM 50 amplified 4 alleles. The size of the alleles amplified by PM 50 ranged from 95 bp (K 1725 and Dharani) to 110 bp (TCGS-1616, TCGS-1157 and Narayani) (Fig 4.16). Naito *et al.* (2008) reported amplification of 11 alleles of size ranging from 103 to 123bp among 214 groundnut accessions. Molla *et al.* (2010) reported that PM 50 amplified six alleles with size ranging from 109 to 139bp among ten groundnut varieties.

SEQ2G4 amplified two alleles in all the genotypes studied, of which 350 bp allele of first allele is monomorphic and other allele showed polymorphism (Fig 4.17). The size of the amplified alleles ranged from 255

Fig4.13 SSR gel profile of 10 groundnut genotypes using PM 375 primer

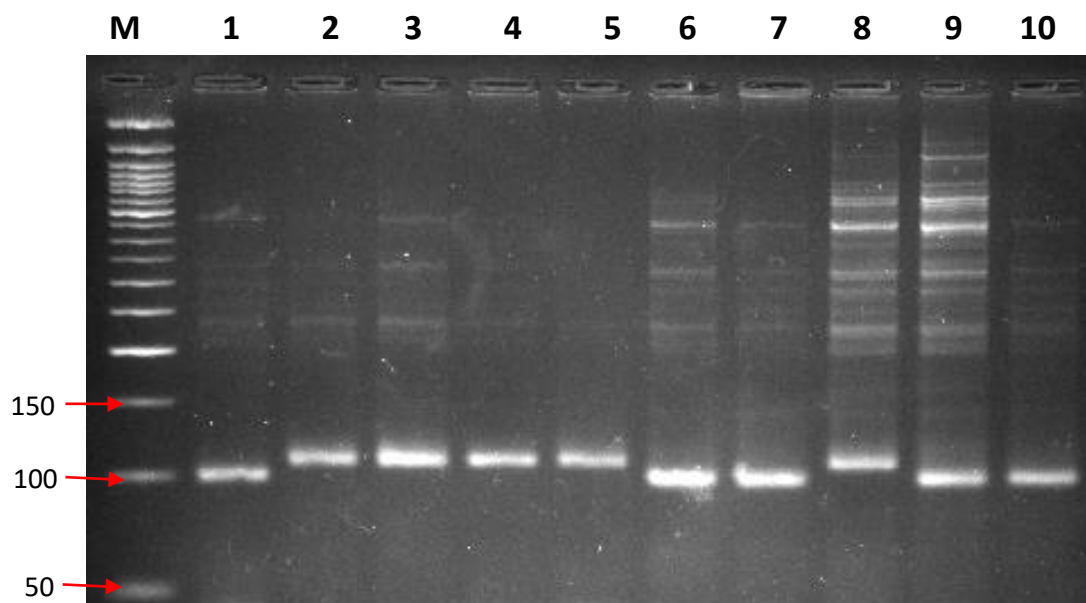
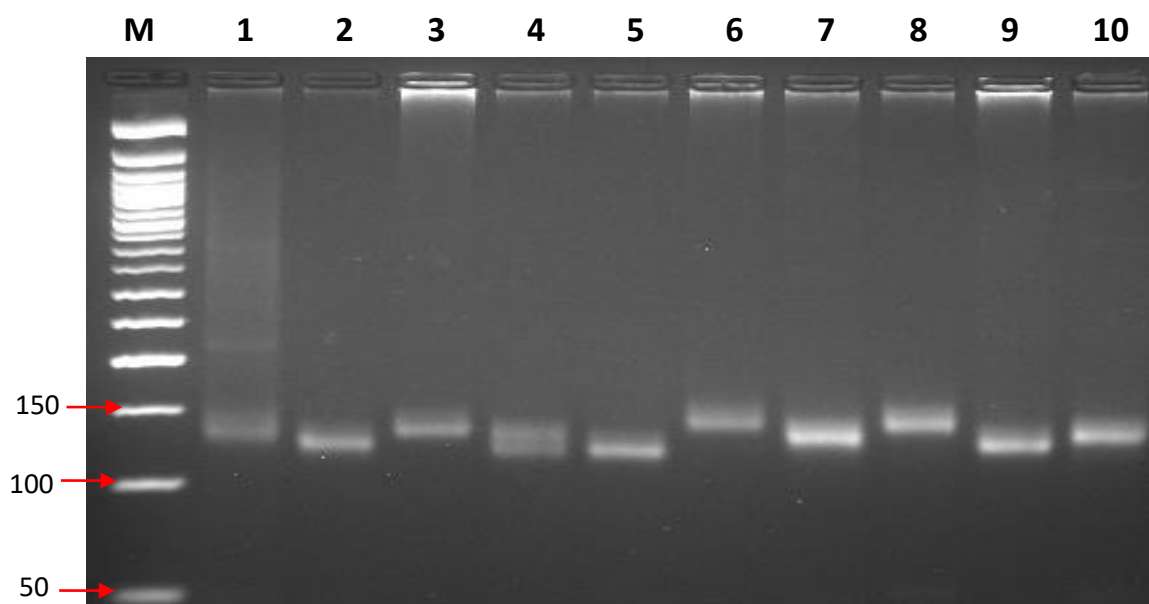


Fig 4.14 SSR gel profile of 10 groundnut genotypes using PM 418 primer



Lane M = Marker

- | | |
|--------------|---------------|
| 1. Narayani | 6. Dharani |
| 2. GG-20 | 7. TCGS-1622 |
| 3. K 9 | 8. K 1725 |
| 4. TCGS-1157 | 9. TCGS-1694 |
| 5. TCGS-1616 | 10. TCGS-1073 |

Fig 4.15. SSR gel profile of 10 groundnut genotypes using PM 45 primer

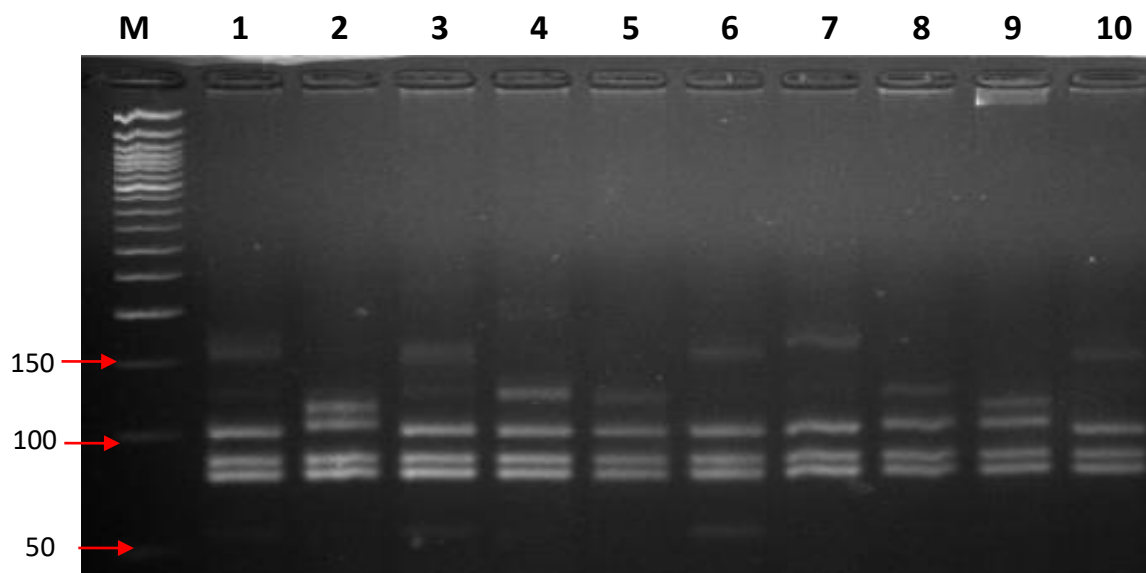
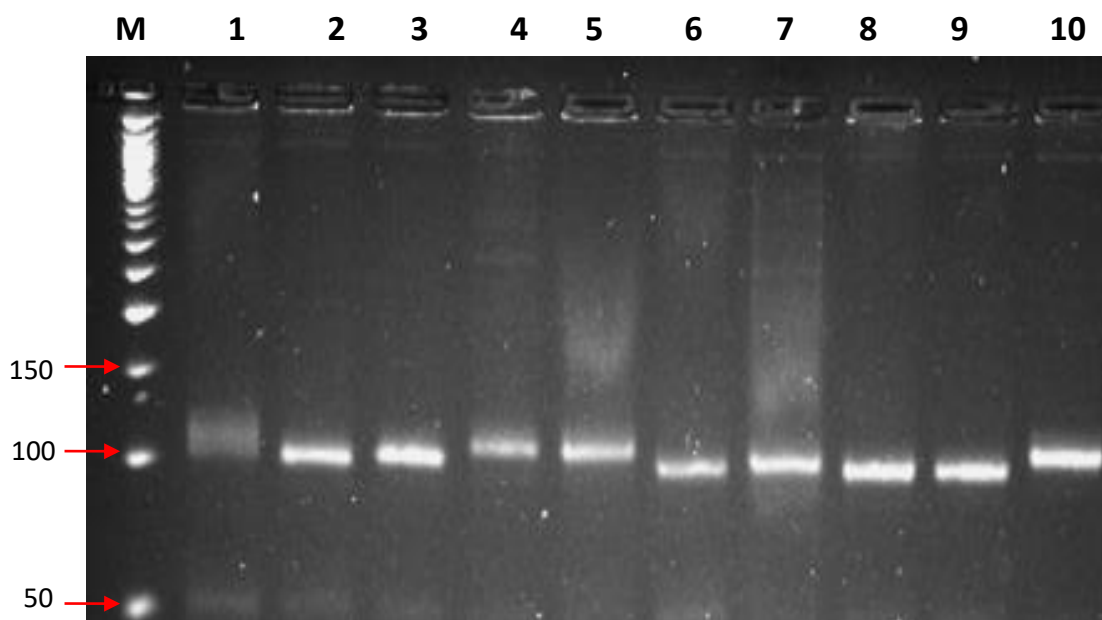


Fig 4.16. SSR gel profile of 10 groundnut genotypes using PM 50 primer



Lane M = Marker

- | | |
|--------------|---------------|
| 1. Narayani | 6. Dharani |
| 2. GG-20 | 7. TCGS-1622 |
| 3. K 9 | 8. K 1725 |
| 4. TCGS-1157 | 9. TCGS-1694 |
| 5. TCGS-1616 | 10. TCGS-1073 |

Fig 4.17. SSR gel profile of 10 groundnut genotypes using SEQ2G4 primer

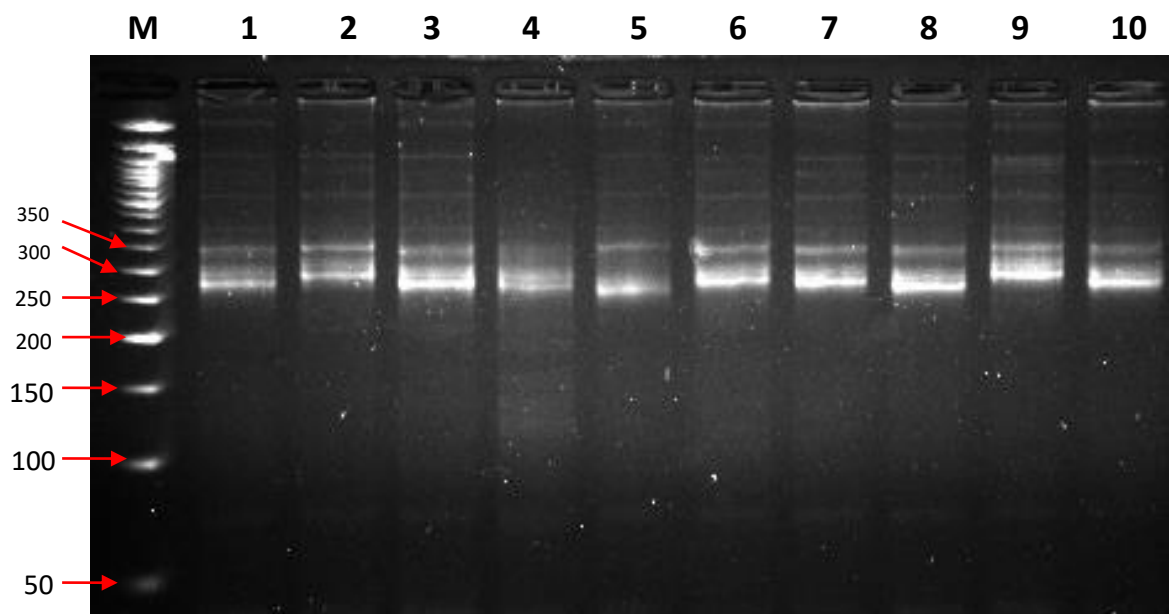
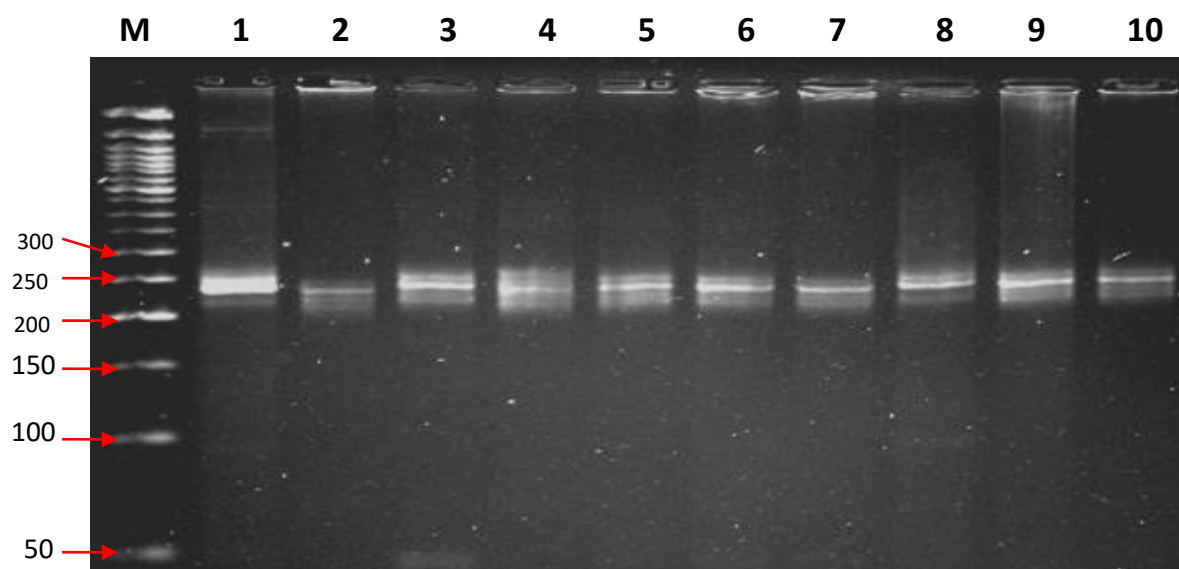


Fig 4.18. SSR gel profile of 10 groundnut genotypes using SEQ3A1 primer



Lane M = Marker

- | | |
|--------------|---------------|
| 1. Narayani | 6. Dharani |
| 2. GG-20 | 7. TCGS-1622 |
| 3. K 9 | 8. K 1725 |
| 4. TCGS-1157 | 9. TCGS-1694 |
| 5. TCGS-1616 | 10. TCGS-1073 |

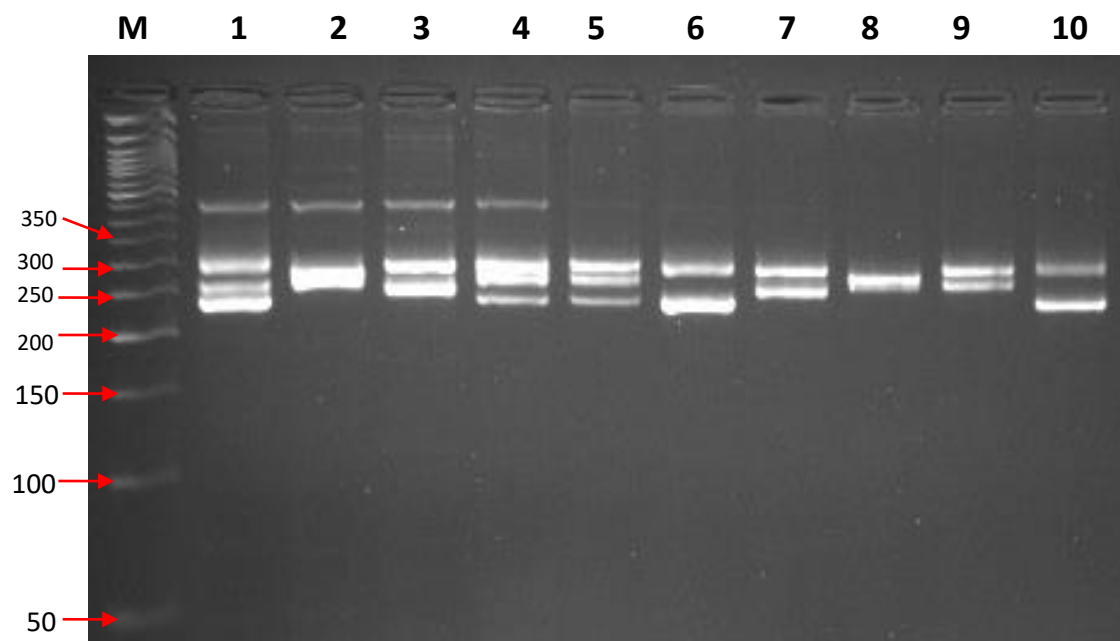
bp (TCGS-1616) to 290 bp (GG-20) SEQ3A1 marker amplified specific alleles of size 230 bp and 270 bp in GG-20 and TCGS-1073 respectively (Fig 4.18).

SEQ5D05 produced unique banding pattern among genotypes studied, it produced multiple bands (1-3) (Fig 4.19). Marker SEQ5D05 is located on two chromosomes viz., A07 at 49.124 and 26.025 cM respectively and on B07 at three different positions (50.184, 55.56 and 79.141 cM respectively). The size of the alleles ranged from 230 bp to 295 bp. Only single specific allele of molecular weight 270 was observed in K 1725 and GG-20. In Narayani three alleles of 295, 250 and 230 bp were amplified. Seven alleles were detected on scoring bands of SEQ5D05. Gaikpa *et al.* (2015) reported that SEQ5D05 amplified 6 alleles with PIC of 0.66 among 18 groundnut varieties.

In this study, we found unique alleles with IPAHM 105 (K 9), IPAHM 123 (TCGS-1622), IPAHM 689 (K 1725), PM 3 (Narayani), PM 418 (K 9), PM 45 (TCGS-1157), SEQ2G4 (TCGS-1616 and GG-20) and SEQ5D05 (Narayani) markers. Thus, genotype specific banding patterns observed with specific markers would help in the identification of the genotypes. Amaravathi *et al.* (2014) found eight unique alleles with markers, Seq16G8, Seq5D5, GM 1489, PM377, PM36 and TC5A06 specific to six groundnut varieties. If these alleles were confirmed as unique over a broader range of groundnut genotypes, then these genotype specific unique alleles can be used for identification of these varieties directly.

PIC value is an important primary data which determines informativeness of a genetic marker. Analysis for PIC with 27 SSR markers across ten genotypes revealed that the PIC values of SSR markers in the present study ranged from zero (monomorphic) to 0.95 (PM 45) (Table 4.23). Highest number of alleles (7) were amplified by SSR marker PM 3 and SEQ5D05 while the lowest by IPAHM 689, PM 50 and SEQ3A1 marker (4). Nine SSR markers displayed PIC more than 0.70 and were highly informative

Fig 4.19. SSR gel profile of 10 groundnut genotypes using SEQ5D05 primer



Lane M = Marker

- | | |
|--------------|---------------|
| 1. Narayani | 6. Dharani |
| 2. GG-20 | 7. TCGS-1622 |
| 3. K 9 | 8. K 1725 |
| 4. TCGS-1157 | 9. TCGS-1694 |
| 5. TCGS-1616 | 10. TCGS-1073 |

and remaining two markers were found moderately informative. 16 markers are monomorphic and least informative (Table 4.23).

The most polymorphic markers of PIC value greater than 0.70 had allele values ranging from 5 to 11 (Hildebrand *et al.*, 1992). Thus, the number of alleles was directly proportional to the PIC (Tantasawat *et al.*, 2011). The polymorphism of these markers was high in comparison with other studies in groundnut (He *et al.*, 2003; Moretzsohn *et al.*, 2004). Molecular markers with high PIC values are described as highly polymorphic and detect higher level of genetic variation in an organism (Gaikpa *et al.*, 2015).

Mace *et al.* (2004) screened twenty three SSRs across 22 groundnut genotypes with differing levels of resistance to rust and LLS and reported that twelve of the 23 SSRs (52 per cent) showed a high level of polymorphism with PIC values ≥ 0.5 .

4.3.3.3 Jaccard's similarity index

Banding profiles obtained with 27 markers for ten groundnut genotypes were analyzed on the basis of presence or absence of SSR allele at a particular position. The Jaccard's similarity co-efficients are directly proportional to the genetic distance of genotypes under consideration (Perrier *et al.*, 2003) and are expressed as a proportion of the total polymorphic markers respective to each pair-wise comparison. Hence, this aided in determining the most appropriate parental genotypes for breeding programmes.

Jaccard's similarity co-efficients among ten genotypes were calculated to establish the genetic relationship and are presented in Table 4.24. The similarity index values ranged from 0.34 to 0.703 indicating the presence of wide range of genetic diversity at molecular level among the ten genotypes. The maximum genetic similarity was found between the genotypes, TCGS-1616 and TCGS-1157 (0.703). The genotypes, Dharani and TCGS-1073 (0.667), K 1727 and TCGS-1694 (0.622), TCGS-1622 and Dharani (0.622), GG-20 and TCGS-1157 (0.59), Narayani and K 9 (0.564), Narayani and

Table 4.24. Similarity matrix of ten groundnut genotypes using Jaccard's coefficient of similarity

Sl. No.	Genotype	1	2	3	4	5	6	7	8	9	10
1	TCGS-1694	1									
2	TCGS-1073	0.419	1								
3	TCGS-1157	0.340	0.550	1							
4	K 1725	0.622	0.475	0.386	1						
5	K 9	0.419	0.500	0.476	0.405	1					
6	Dharani	0.419	0.667	0.476	0.553	0.463	1				
7	Narayani	0.348	0.488	0.537	0.395	0.564	0.564	1			
8	GG-20	0.525	0.500	0.590	0.439	0.500	0.395	0.419	1		
9	TCGS-1616	0.378	0.525	0.703	0.429	0.419	0.525	0.476	0.488	1	
10	TCGS-1622	0.452	0.538	0.476	0.439	0.538	0.622	0.488	0.429	0.419	1

Dharani (0.564), Dharani and K 1725 (0.553), TCGS-1157 and TCGS-1073 (0.55), TCGS-1622 and K 9 (0.538), TCGS-1157 and Narayani (0.537), TCGS- 1694 and GG-20 (0.525), TCGS-1616 and TCGS-1073 (0.525), Dharani and TCGS-1616 (0.525), GG-20 and TCGS-1073 (0.50), GG-20 and K 9 (0.50) had moderate similarity whereas minimum similarity was found between TCGS-1157 and TCGS-1694 (0.34), Narayani and TCGS-1694 (0.348) and TCGS-1616 and TCGS-1694 (0.378). In general, the genotypes TCGS-1694 and GG-20 exhibited least similarity with other genotypes and appear to be genetically more distinct and diverse.

4.3.3.4 Cluster analysis

The abundant phenotypic variation in groundnut was reflected at the DNA level also. Similarity co-efficients were subjected to Unweighted Pair Group method on Arithmetic Average (UPGMA) using paired matrix values. The dendrogram (Fig 4.20) exhibited variable degree of relationships among the genotypes studied and consisted of three clusters at 80% similarity index.

S. No.	Clusters	Genotypes
1	Cluster I	TCGS-1694 and K 1725
2	Cluster II	TCGS-1073, K 9, Dharani, Narayani and TCGS-1622
3	Cluster III	TCGS-1157, TCGS-1616 and GG-20

Cluster I consisted of two genotypes viz., TCGS-1694 and K 1725 and these were also grouped as highly drought tolerant based on physiological characters. Cluster II consisted of five genotypes which were further sub-clustered into IIA and IIB. The sub-cluster IIA had three genotypes, TCGS-1073, Dharani and TCGS-1622. K 9 and Narayani were grouped in sub-cluster IIB. Sub-clustering pattern indicated low variation within the cluster and high variation between the clusters. Cluster III had three genotypes which were further sub-clustered into IIIA and IIIB. The sub-cluster IIIA had two genotypes, TCGS-1157 and TCGS-1616. GG-20 was grouped in sub-cluster IIIB. GG-20 was diverse from TCGS-1157 and TCGS-1616 at 85% similarity

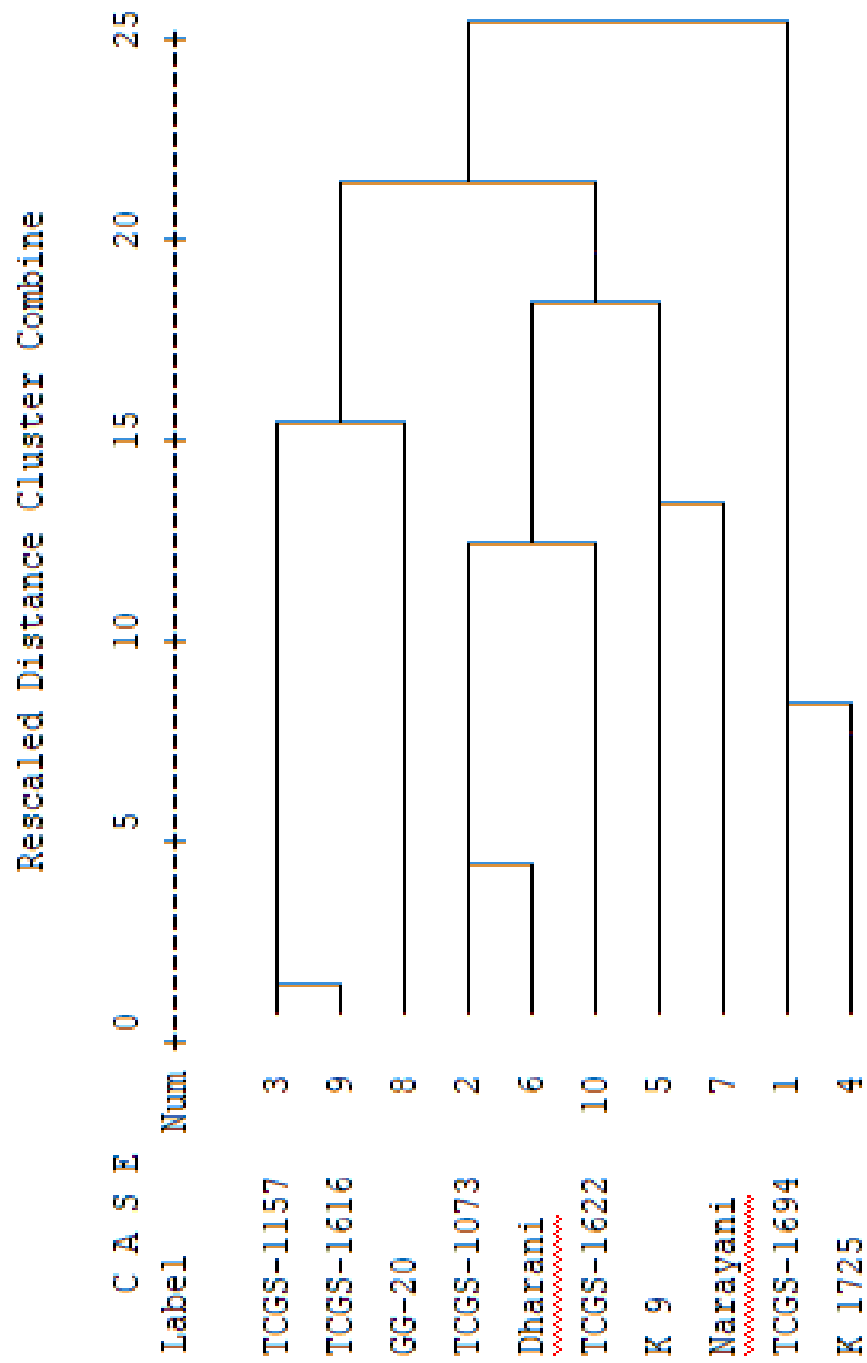


Fig 4.20. Dendrogram generated using UPGMA analysis showing relationship between 10 groundnut genotypes using SSR markers

index. It is a Virginia bunch variety released for the state of Gujarat. Genotypes clustered together irrespective of their unrelated pedigree. The similar findings of grouping of groundnut genotypes together irrespective of pedigree were reported by Mondal and Badigannavar (2010).

The grouping was based on 27 SSR markers and more number of markers covering the entire genome are required to relate the genotypes from the genotype with the corresponding phenotype. Gautami *et al.* (2009) and Oteng-Frimpong *et al.* (2015) reported grouping of susceptible and resistant genotypes under the same cluster.

Genetic diversity studies in cultivated groundnut using SSR markers were reported by various authors. Tang *et al.* (2007) assessed the genetic variation of four sets of twenty-four accessions each from the four botanical varieties of the cultivated peanut by thirty four SSR markers. Among the 34 pairs of SSR markers ten, thirteen, fifteen and sixteen pairs of SSR markers showed polymorphisms in var. *vulgaris*, var. *hirsuta*, var. *hypogaea* and var. *fastigiata* respectively. The dendrograms based on genetic distances were constructed for the four botanical varieties which revealed the existence of different clusters. To get an objective discrimination of genetic diversity of cultivated peanut and make a correct classification of them, substantially more DNA markers and more genotypes would be needed.

Shoba *et al.* (2010) reported that among 17 SSR primer pairs used for assessing the genetic diversity, six primer pairs (24.0 per cent) were polymorphic and Jaccard's similarity co-efficient estimate for the 11 groundnut genotypes ranged from 0.54 to 1.00. Based on the dendrogram 11 genotypes of groundnut were grouped into six clusters at 0.92 similarity coefficient.

Roomi *et al.* (2014) explored the genetic diversity among seventy Pakistani accessions of *Arachis hypogaea*. The dendrogram was constructed on the basis of allelic data from fifteen SSR markers across the selected

accessions. At 0.67 coefficients of similarity, all the accessions were grouped into six clusters. The selected accessions were grouped mainly according to their place of breeding /research stations.

Our results indicate that sufficient polymorphism exists among the genotypes and it can be exploited for developing genetic linkage map of cultivated groundnut using sufficient SSR markers which facilitates increased breeding efficiency through marker assisted selection.

Based on genetic diversity studies in *kharif* cross combinations proposed are SG 99 (cluster VII) × Dharani (cluster III); SG 99 (cluster VII) × R 2001-2-1 (cluster III) in order to get transgressive segregants for physiological, yield and yield parameters since these genotypes showed maximum diversity among themselves with desirable yield parameters. Similarly, the cross between genotypes SG 99 (cluster VII) × K 9 (cluster I) could be suggested for the exploitation of transgressive segregants for high yield coupled with drought tolerance. In the same way, based on genetic diversity studies in *rabi*, cross combinations proposed are GPBD-4 (cluster II) × GG-16 (cluster VIII); GG-16 (cluster VIII) × TCGS-1694 (cluster V) in order to get transgressive segregants for yield and yield parameters. Similarly, the crosses between genotypes, GG-16 (cluster VIII) × K 9 (cluster III); GG-16 (cluster VIII) × Narayani (cluster II) could be suggested for the exploitation of transgressive segregants for high yield coupled with drought tolerance.

The clustering pattern was different in different methods used. Genotypes with dissimilar pedigrees were grouped into the same cluster while genotypes with same pedigrees are farther apart. Likewise certain genotypes were grouped together in either of the ways *i.e.* grouping through *kharif*/SSR data or *rabi*/SSR data or *kharif/rabi* data. TCGS-1694 and K 1725 were grouped in one cluster when grouping of genotypes was done in both ways *i.e.* based on *kharif* data and SSR based analysis. While GG-20, Anantha, K 6 and J 89 were grouped in one cluster when grouping of genotypes was done in

both ways *i.e.* based on *kharif* data and *rabi* data. Similarly R-2001-2-1 and Dharani appeared together in one cluster, while R-2001-3, TCGS-1630 and R-2001-3-1 were grouped in one cluster; K 1805, ICG 86325 and TCGS-1616 formed a cluster; TCGS-1157 and K 1725 were grouped in one cluster; TCGS-1694, TCGS-1073 and TCGS-1696 appeared together in one cluster when grouping was carried out based on physiological, yield and yield attributes data influencing yield in *kharif* and *rabi*. However, the diversity analysed was based on 19 characters in *kharif* while in *rabi*, it was based on only six characters. Hence, diversity observed in these two situations cannot be compared.

4.4 CHARACTER ASSOCIATION

Correlation studies provide reliable information on nature and extent of relationship between different characters. The information on the association between traits of economic worth is of great value to plant breeders as it will help in assessing the scope of simultaneous improvement of two or more characters. Yield is a highly complex character and polygenic in nature which is influenced by the environment. Hence, the study of inter-association is essential to understand the relationship of simple traits with complex yield contributing traits. These relationships may be positive or negative. Negative associations are limiting factors in selection for higher yield. The study of genetic correlations gives an idea about the extent to which the characters are under the control of same set of genes. Pleiotropy assumes importance if the correlation is high whereas the independent inheritance of traits may be perceived if the correlation is low.

In the present study, both phenotypic and genotypic correlation coefficient were computed in order to assess the degree and direction of relationship present between pod yield and other component characters in both *kharif* and *rabi* seasons and the results were presented in Table 4.25 and 4.26 respectively.

4.4.1 Correlation between Pod Yield and its Component Traits in *Kharif*

In general, the genotypic correlation co-efficients were higher than the phenotypic correlation co-efficients, indicating inherent association of traits. The correlation between pod yield per plant with SCMR at 60 DAS, SLA at 60 DAS, LAI at 60 and 80 DAS, LAD at 80 DAS, angle between main axis and primary branches at 60 and 80 DAS, root length, root dry mass, number of primary branches per plant, number of secondary branches per plant, plant height, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, shelling percentage, harvest index, 100-seed weight, and among themselves were presented in Table 4.25.

Pod yield per plant showed highly significant and positive correlation with number of pegs per plant ($r_p = 0.663^{**}$, $r_g = 0.840$), number of mature pods per plant ($r_p = 0.593^{**}$, $r_g = 0.701$), harvest index ($r_p = 0.543^{**}$, $r_g = 0.702$), number of immature pods per plant ($r_p = 0.429^{**}$, $r_g = 0.658$), number of primary branches per plant ($r_p = 0.295^{**}$, $r_g = 0.389$) and number of secondary branches per plant ($r_p = 0.288^{**}$, $r_g = 0.389$).

Results of significant positive association of pod yield per plant with number of mature pods per plant and number of primary branches per plant was reported by Vasanthi *et al.* (2015), Shreya *et al.* (2015), Kumar and Sekhar (2016), Kamdi *et al.* (2017), Nirmala and Jayalakshmi (2015) and Pavankumar *et al.* (2014). Significant and positive correlation of pod yield per plant with number of secondary branches per plant and harvest index was registered Alam (2014), Kumar and Sekhar (2016), Nirmala and Jayalakshmi (2015) and Pavankumar *et al.* (2014). The results of significant and positive association for number of immature pods per plant and number of pegs per plant were in accordance with the reports of Shreya *et al.* (2015).

Pod yield per plant exhibited non-significant positive correlation with number of SLA at 60 DAS ($r_p = 0.013$, $r_g = -0.009$), LAI at 60 DAS ($r_p = 0.021$, $r_g = 0.042$), LAI at 80 DAS ($r_p = 0.132$, $r_g = 0.170$), LAD at 80 DAS (r_p

Table 4.25. Genotypic and phenotypic correlation coefficient analysis for pod yield per plant and its components in groundnut (Kharif, 2017)

Character	SLA at 60 DAS	LAI at 60 DAS	LAI at 80 DAS	LAD at 80 DAS	Angle at 60 DAS	Angle at 80 DAS	RL	RDM	PB	SB	PH	PP	MP	IP	SP	100 SW	HI	PYP
SCMRat	-																	
60DAS	0.323**	0.005	0.256**	0.248**	0.050	-0.015	-0.172	-0.000	0.186*	0.265**	-0.432**	-0.158	-0.217*	-0.114	0.120	0.377**	-0.150	-0.048
r _g	-	-0.002	0.261**	0.261**	0.052	-0.017	-0.319**	0.008	0.192*	0.282**	-0.468**	-	0.246**	-0.119	0.194*	0.415**	-0.185*	-0.088
SLA at 60 DAS		0.290**	-0.046	-0.017	0.021	0.086	-0.015	0.061	-0.052	-0.138	0.339**	0.081	0.140	-0.100	0.055	-0.052	0.040	0.013
r _p		0.319**	-0.047	-0.001	0.023	0.091	0.005	0.055	-0.059	-0.147	0.354**	0.090	0.142	-0.146	0.072	-0.070	0.047	-0.009
60 DAS																		
LAI at 60 DAS			0.296**	0.525**	-0.081	-0.010	-0.305**	-0.010	0.084	0.174	0.134	-0.042	-0.164	-0.066	0.086	0.133	-0.166	0.021
r _p			0.317**	0.569**	-0.086	-0.009	-0.526**	-0.022	0.082	0.192*	0.134	-0.050	-0.181*	-0.061	0.113	0.162	-0.181*	0.042
60 DAS																		
LAI at 80 DAS				0.881**	0.255**	0.207*	-0.029	0.120	0.219*	0.366**	0.083	0.124	0.141	0.072	0.287**	0.182*	0.256**	0.132
r _p				0.972**	0.259**	0.210*	-0.055	0.139	0.230**	0.381**	0.086	0.134	0.147	0.088	0.330**	0.190*	-	0.170
80 DAS																		
LAD at 80 DAS					0.157	0.149	-0.096	0.096	0.226*	0.380**	0.086	0.071	0.051	0.070	-0.189*	0.223*	0.252**	0.116
r _p					0.172	0.163	-0.216*	0.132	0.269**	0.436**	0.092	0.081	0.076	0.106	0.250**	0.260**	-	0.165
80 DAS																	0.319**	
Angle at 60 DAS						0.959**	0.040	-0.188*	-0.099	-0.168	0.211*	-0.131	-0.094	0.317**	0.012	0.148	0.040	-0.126
r _p						0.961**	0.062	-0.208*	-0.106	-0.172	0.215*	-0.153	-0.101	-	0.015	0.157	0.042	-0.167
60 DAS														0.357**				
Angle at 80 DAS							0.060	-	-0.173	-0.219*	0.305**	-0.163	-0.146	-	0.068	0.201*	0.044	-0.128
r _p							0.093	-	-	-0.222*	0.310**	-	-0.154	-	0.077	0.219*	0.044	-0.182*
80 DAS								0.271**	0.190*	-		0.190*		0.396**				
Root Length								0.069	-0.033	-0.079	0.057	-0.013	0.114	0.056	-0.102	-0.021	0.083	-0.030
r _p								0.080	-	-0.134	0.087	-0.134	0.160	0.076	-0.198*	0.009	0.062	-0.076
80 DAS									0.223*									
Root Mass									0.339**	0.205*	-0.113	0.209*	0.240**	0.423**	-0.171	0.208*	-	0.038
r _p									0.420**	0.243**	-0.121	0.274**	0.285**	0.528**	-0.226*	-	0.339**	0.034
80 DAS																0.260**	0.391**	

Cont.....

Table 4.25. cont...

Character	SLA at 60 DAS	LAI at 60 DAS	LAI at 80 DAS	LAD at 80 DAS	Angle at 60 DAS	Angle at 80 DAS	RL	RDM	PB	SB	PH	PP	MP	IP	SP	100 SW	HI	PYP
No. of PB r _p r _g										0.707** 0.773**	-0.317** -0.346**	0.358** 0.403**	0.090 0.087	0.510** 0.599**	-0.306** -0.356**	-0.044 -0.056	-0.157 -0.179*	0.295** 0.389**
No. of SB r _p r _g											-0.257** -0.263**	0.297** 0.344**	0.085 0.093	0.506** 0.593**	-0.222* -0.249**	0.135 0.128	-0.237** -0.253**	0.288** 0.389**
Height r _p r _g												0.004 0.001	0.093 0.096	-0.165 -0.188*	0.138 0.157	-0.009 -0.007	-0.031 -0.031	-0.009 -0.010
No. of PG r _p r _g													0.776** 0.845**	0.608** 0.770**	-0.188* -0.216*	-0.440** -0.544**	0.286** 0.342**	0.663** 0.840**
No. of MP r _p r _g														0.450** 0.542**	-0.149 -0.169	-0.523** -0.586**	0.404** 0.439**	0.593** 0.701**
No. of IP r _p r _g															-0.182* -0.242**	-0.311** -0.357**	-0.006 0.026	0.429** 0.658**
Shelling % r _p r _g																0.205* 0.241**	0.268** 0.302**	0.029 0.029
100-seed Weight r _p r _g																	-0.120 -0.148	-0.141 -0.245**
Harvest Index r _p r _g																		0.543** 0.702**

** - Significant at 1% level * - Significant at 5% level

SCMR at 60 DAS- SPAD chlorophyll metre reading at 60 DAS; SLA at 60 DAS- Specific leaf area at 60 DAS (cm² g⁻¹); LAI at 60 DAS- Leaf area index at 60 DAS; LAD at 80 DAS- Leaf area duration at 80 DAS(dm² day); Angle at 60 DAS- Angle between main axis and first two primary branches at 60 DAS (°); Angle at 80 DAS- Angle between main axis and first two primary branches at 80 DAS (°); RL- Root length (cm); RDM- Root dry mass (g); PB- Number of primary branches per plant; SB- Number of secondary branches per plant; PH= Plant height (cm); PP- Number of pegs per plant; MP- Number of mature pods per plant; IP- Number of immature pods per plant; SP- Shelling percentage (%); 100 SW- 100 seed weight (g); HI- Harvest index (%); PYP- Pod yield per plant (g)

= 0.116 , $r_g = 0.165$), root dry mass ($r_p = 0.038$, $r_g = 0.034$), shelling percentage ($r_p = 0.029$, $r_g = 0.029$). Non-significant positive correlation of pod yield per plant with SLA at 60 DAS was in accordance with the reports of John and Reddy (2016) and Nirmala and Jayalakshmi (2015). Junjittakarn *et al.* (2014) reported non-significant positive correlation of pod yield per plant with root dry mass. Reddy *et al.* (2017) and Bhakal and Lal (2017) reported non-significant positive correlation of pod yield per plant with shelling percentage.

Pod yield per plant showed non-significant negative correlation with SCMR at 60 DAS ($r_p = -0.048$, $r_g = -0.088$), angle between main axis and primary branches at 60 DAS ($r_p = -0.126$, $r_g = -0.167$), angle between main axis and primary branches at 80 DAS ($r_p = -0.128$, $r_g = -0.182$), root length ($r_p = -0.030$, $r_g = -0.076$), plant height ($r_p = -0.009$, $r_g = -0.010$), 100-seed weight ($r_p = -0.141$, $r_g = -0.245$).

Nirmala and Jayalakshmi (2015) and Alam *et al.* (2014) reported non-significant negative correlation of pod yield per plant with SCMR at 60 DAS. Similar results of pod yield per plant with plant height were reported by Satish (2014) and Kamdi *et al.* (2017). John and Reddy (2016) reported non-significant negative correlation of pod yield per plant with root length. Non-significant negative correlation of pod yield per plant with 100-seed weight was in accordance with the reports of Rasheed *et al.* (2015).

4.4.1.1 Inter-correlation among Traits

4.4.1.1.1 SCMR at 60 DAS :

SCMR at 60 DAS showed significant and positive correlation with LAI at 80 DAS ($r_p = 0.256^{**}$, $r_g = 0.261$), LAI at 80 DAS ($r_p = 0.248^{**}$, $r_g = 0.261$), number of primary branches per plant ($r_p = 0.186^*$, $r_g = 0.192$), number of secondary branches per plant ($r_p = 0.265^{**}$, $r_g = 0.282$) and 100-seed weight ($r_p = 0.377^{**}$, $r_g = 0.415$). It exhibited significant and negative correlation with SLA at 60 DAS ($r_p = -0.323^{**}$, $r_g = -0.341$), plant height ($r_p = -0.432^{**}$, $r_g = -0.468$) and number of mature pods per plant ($r_p = -0.217^*$, $r_g = -0.246$). Non-

significant positive association of SCMR at 60 DAS was observed for LAI at 60 DAS ($r_p = 0.005$, $r_g = -0.002$), angle between main axis and primary branches at 60 DAS ($r_p = 0.050$, $r_g = 0.052$) and shelling percentage ($r_p = 0.120$, $r_g = 0.194$). It exhibited non-significant negative correlation with angle between main axis and primary branches at 80 DAS ($r_p = -0.015$, $r_g = -0.017$), root length ($r_p = -0.172$, $r_g = -0.319$), root dry mass ($r_p = -0.00$, $r_g = -0.008$), number of pegs per plant ($r_p = -0.158$, $r_g = -0.208$), number of immature pods per plant ($r_p = -0.114$, $r_g = -0.119$) and harvest index ($r_p = -0.150$, $r_g = -0.185$).

Kumar *et al.* (2012) reported significant positive correlation of SCMR with 100-seed weight, significant negative correlation with plant height and number of mature pods per plant and non-significant negative correlation with harvest index. Significant negative correlation of SCMR with SLA was in accordance with the reports of Mallikarjun and Savithramma (2017). Non-significant negative correlation of SCMR with harvest index was observed by Pavankumar *et al.* (2014) and Nirmala and Jayalakshmi (2015). Hugar and Savithramma (2017), reported significant positive correlation with number of primary branches per plant. Non-significant negative correlation with number of immature pods per plant was observed by Sirisha (2005).

4.4.1.1.2 SLA at 60 DAS :

SLA at 60 DAS exhibited significant and positive association with LAI at 60 DAS ($r_p = 0.290^{**}$, $r_g = 0.319$) and plant height ($r_p = 0.339^{**}$, $r_g = 0.354$). It exhibits non-significant negative correlation with LAI at 80 DAS ($r_p = -0.046$, $r_g = -0.047$), LAD at 80 DAS ($r_p = -0.017$, $r_g = -0.001$), root length ($r_p = -0.015$, $r_g = 0.005$), number of primary branches per plant ($r_p = -0.052$, $r_g = -0.059$), number of secondary branches per plant ($r_p = -0.138$, $r_g = -0.147$), number of immature pods per plant ($r_p = -0.100$, $r_g = -0.146$) and 100-seed weight ($r_p = -0.052$, $r_g = -0.070$). Non-significant positive association of SLA at 60 DAS was observed for angle between main axis and primary branches at 60 DAS ($r_p = 0.021$, $r_g = 0.023$), angle between main axis and primary branches at 80 DAS ($r_p = 0.086$, $r_g = 0.091$), root dry mass ($r_p = 0.061$, $r_g =$

0.055), number of pegs per plant ($r_p = 0.081$, $r_g = 0.090$), number of mature pods per plant ($r_p = 0.140$, $r_g = 0.142$), shelling percentage ($r_p = 0.055$, $r_g = 0.072$) and harvest index ($r_p = 0.040$, $r_g = 0.047$).

Non- significant positive association of SLA with shelling percentage was reported by Mallikarjun and Savithramma (2017) and Nirmala and Jayalakshmi (2015). The result of non-significant negative correlation number of primary branches per plant with SLA was in accordance with the reports of Nirmala and Jayalakshmi (2015), Pavankumar *et al.* (2014) and Hugar and Savithramma (2017). Nirmala and Jayalakshmi (2015) reported significant positive association of SLA with plant height and exhibits non-significant negative correlation with 100-seed weight. Non-significant positive association of SLA with harvest index was reported by Nirmala and Jayalakshmi (2015), Pavankumar *et al.* (2014) and Sirisha (2005). Non-significant positive association of SLA with number of mature pods per plant and non-significant negative correlation with number of immature pods per plant were similar to the reports of Pavankumar *et al.* (2014) and Sirisha (2005) respectively. Non-significant negative correlation of SLA with root length was reported by Thakur *et al.* (2013).

4.4.1.1.3 LAI at 60 DAS :

Significant positive relationship of LAI at 60 DAS was observed for LAI at 80 DAS ($r_p = 0.296^{**}$, $r_g = 0.317$) and LAD at 80 DAS ($r_p = 0.525^{**}$, $r_g = 0.569$). LAI at 60 DAS also exhibited significant negative correlation with root length ($r_p = -0.305^{**}$, $r_g = -0.526$). It exhibited non- significant positive association with number of primary branches per plant ($r_p = 0.084$, $r_g = 0.082$), number of secondary branches per plant ($r_p = 0.174$, $r_g = 0.192$), plant height ($r_p = 0.134$, $r_g = 0.134$), shelling percentage ($r_p = 0.086$, $r_g = 0.113$) and 100-seed weight ($r_p = 0.133$, $r_g = 0.162$). Non- significant negative correlation of LAI at 60 DAS with angle between main axis and primary branches at 60 DAS ($r_p = -0.081$, $r_g = -0.086$), angle between main axis and primary branches at 80 DAS ($r_p = -0.010$, $r_g = -0.009$), root dry mass ($r_p = -0.010$, $r_g =$

-0.022), number of pegs per plant ($r_p = -0.042$, $r_g = -0.050$), number of mature pods per plant ($r_p = -0.164$, $r_g = -0.181$), number of immature pods per plant ($r_p = -0.066$, $r_g = -0.061$) and harvest index ($r_p = -0.166$, $r_g = -0.181$). Patra *et al.* (1995) reported non-significant positive association of leaf area index with plant height and 100-seed weight

4.4.1.1.4 LAI at 80 DAS :

Significant positive correlation of LAI at 80 DAS was observed for LAD at 80 DAS ($r_p = 0.881^{**}$, $r_g = 0.972$), angle between main axis and primary branches at 60 DAS ($r_p = 0.255^{**}$, $r_g = 0.259$), angle between main axis and primary branches at 80 DAS ($r_p = 0.207^{**}$, $r_g = 0.210$), number of primary branches per plant ($r_p = 0.219^{**}$, $r_g = 0.230$), number of secondary branches per plant ($r_p = 0.366^{**}$, $r_g = 0.381$) and 100-seed weight ($r_p = 0.182^{**}$, $r_g = 0.190$). Whereas shelling percentage ($r_p = -0.287^{**}$, $r_g = -0.330$) and harvest index ($r_p = -0.256^{**}$, $r_g = -0.273$) showed significant negative association. It also exhibited non-significant negative relationship with root length ($r_p = -0.029$, $r_g = -0.055$). It exhibited non-significant positive association with root dry mass ($r_p = 0.120$, $r_g = 0.139$), plant height ($r_p = 0.083$, $r_g = 0.086$), number of pegs per plant ($r_p = 0.124$, $r_g = 0.134$), number of mature pods per plant ($r_p = 0.141$, $r_g = 0.147$) and number of immature pods per plant ($r_p = 0.072$, $r_g = 0.088$).

4.4.1.1.5 LAD at 80 DAS :

LAD at 80 DAS exhibited significant positive relationship with number of primary branches per plant ($r_p = 0.226^*$, $r_g = 0.269$), number of secondary branches per plant ($r_p = 0.380^{**}$, $r_g = 0.436$) and 100-seed weight ($r_p = 0.223^*$, $r_g = 0.260$). It also exhibited significant negative relationship with shelling percentage ($r_p = -0.189^*$, $r_g = -0.250$) and harvest index ($r_p = -0.252^{**}$, $r_g = -0.319$). Whereas its correlation with angle between main axis and primary branches at 60 DAS ($r_p = 0.157$, $r_g = 0.172$), angle between main axis and primary branches at 80 DAS ($r_p = 0.149$, $r_g = 0.163$), root dry mass ($r_p = 0.096$,

$r_g = 0.132$), plant height ($r_p = 0.086$, $r_g = 0.092$), number of pegs per plant ($r_p = 0.071$, $r_g = 0.081$), number of mature pods per plant ($r_p = 0.051$, $r_g = 0.076$) and number of immature pods per plant ($r_p = 0.070$, $r_g = 0.106$) was non-significant and positive. While root length ($r_p = -0.096$, $r_g = -0.216$) registered non-significant negative association.

4.4.1.1.6 Angle between main axis and primary branches at 60 DAS :

Significant positive relationship of angle between main axis and primary branches at 60 DAS was observed for angle between main axis and primary branches at 80 DAS ($r_p = 0.959^{**}$, $r_g = 0.961$) and plant height ($r_p = 0.211^*$, $r_g = 0.215$). It also exhibited significant negative correlation with root dry mass ($r_p = -0.188^*$, $r_g = -0.208$) and number of immature pods per plant ($r_p = -0.317^{**}$, $r_g = -0.357$). It exhibited non-significant positive correlation with root length ($r_p = 0.040$, $r_g = 0.062$), shelling percentage ($r_p = 0.012$, $r_g = 0.015$), 100-seed weight ($r_p = 0.148$, $r_g = 0.157$) and harvest index ($r_p = 0.040$, $r_g = 0.042$). It exhibited non-significant and negative relationship with number of primary branches per plant ($r_p = -0.099$, $r_g = -0.106$), number of secondary branches per plant ($r_p = -0.168$, $r_g = -0.172$), number of pegs per plant ($r_p = -0.131$, $r_g = -0.153$) and number of mature pods per plant ($r_p = -0.094$, $r_g = -0.101$).

4.4.1.1.7 Angle between main axis and primary branches at 80 DAS :

Angle between main axis and primary branches at 80 DAS shows significant positive correlation with plant height ($r_p = 0.305^{**}$, $r_g = 0.310$) and 100-seed weight ($r_p = 0.201^*$, $r_g = 0.219$). It exhibited significant negative correlation with root dry mass ($r_p = -0.237^{**}$, $r_g = -0.271$), number of secondary branches per plant ($r_p = -0.219^*$, $r_g = -0.222$) and number of immature pods per plant ($r_p = -0.349^{**}$, $r_g = -0.396$). It registered non-significant positive association with root length ($r_p = 0.069$, $r_g = 0.093$), shelling percentage ($r_p = 0.068$, $r_g = 0.077$) and harvest index ($r_p = 0.044$, $r_g = 0.044$). It exhibited non-significant negative correlation with number of

primary branches per plant ($r_p = -0.173$, $r_g = -0.190$), number of pegs per plant ($r_p = -0.163$, $r_g = -0.190$) and number of mature pods per plant ($r_p = -0.146$, $r_g = -0.154$).

4.4.1.1.8 Root length :

Non-significant negative association of root length was observed for number of primary branches per plant ($r_p = -0.033$, $r_g = -0.223$), number of secondary branches per plant ($r_p = -0.079$, $r_g = -0.134$), number of pegs per plant ($r_p = -0.013$, $r_g = -0.134$), shelling percentage ($r_p = -0.102$, $r_g = -0.198$) and 100-seed weight ($r_p = -0.021$, $r_g = -0.009$). Whereas non-significant positive association was observed with root dry mass ($r_p = 0.069$, $r_g = 0.080$), plant height ($r_p = 0.57$, $r_g = 0.087$), number of mature pods per plant ($r_p = 0.114$, $r_g = 0.160$), number of immature pods per plant ($r_p = 0.056$, $r_g = 0.076$) and harvest index ($r_p = 0.083$, $r_g = 0.062$). Thakur *et al.* (2013) reported non-significant negative association of root length with 100-seed weight.

4.4.1.1.9 Root dry mass:

Root dry mass show significant positive correlation with number of primary branches per plant ($r_p = 0.339^{**}$, $r_g = 0.420$), number of secondary branches per plant ($r_p = 0.205^*$, $r_g = 0.243$), number of pegs per plant ($r_p = 0.209^*$, $r_g = 0.274$), number of mature pods per plant ($r_p = 0.240^{**}$, $r_g = 0.285$) and number of immature pods per plant ($r_p = 0.423^{**}$, $r_g = 0.528$). It exhibited significant negative correlation with 100-seed weight ($r_p = -0.208^*$, $r_g = -0.260$) and harvest index ($r_p = -0.339^{**}$, $r_g = -0.391$). Non-significant negative correlation of root dry mass was observed for plant height ($r_p = -0.113$, $r_g = -0.121$) and shelling percentage ($r_p = -0.171$, $r_g = -0.226$).

4.4.1.1.10 Number of primary branches per plant :

Significant positive relationship of number of primary branches per plant was observed with number of secondary branches per plant ($r_p = 0.707^{**}$, $r_g = 0.773$), number of pegs per plant ($r_p = 0.358^{**}$, $r_g = 0.403$) and

number of immature pods per plant ($r_p = 0.510^{**}$, $r_g = 0.599$). Number of primary branches per plant also exhibited significant negative correlation with plant height ($r_p = -0.317^{**}$, $r_g = -0.346$) and shelling percentage ($r_p = -0.306^{**}$, $r_g = -0.356$). It exhibited non-significant positive correlation with number of mature pods per plant ($r_p = 0.090$, $r_g = 0.087$). Whereas it exhibited non-significant negative relationship with 100-seed weight ($r_p = -0.044$, $r_g = -0.056$) and harvest index ($r_p = -0.157$, $r_g = -0.179$).

Significant negative correlation of number of primary branches per plant with plant height was reported by Gupta *et al.* (2015). Significant positive relationship of number of primary branches per plant with number of secondary branches per plant was in accordance with the results of Korat *et al.* (2010) and Pavankumar *et al.* (2014). Non-significant negative relationship of number of primary branches per plant with harvest index and significant negative correlation with shelling percentage was in accordance with reports of Korat *et al.* (2010) and Pavankumar *et al.* (2014).

4.4.1.1.11 Number of secondary branches per plant :

Number of secondary branches per plant exhibited significant positive relationship with number of pegs per plant ($r_p = 0.297^{**}$, $r_g = 0.344$) and number of immature pods per plant ($r_p = 0.506^{**}$, $r_g = 0.593$). It also exhibited significant negative relationship with plant height ($r_p = -0.257^{**}$, $r_g = -0.263$), shelling percentage ($r_p = -0.222^{**}$, $r_g = -0.249$) and harvest index ($r_p = -0.237^{**}$, $r_g = -0.253$). While number of mature pods per plant ($r_p = 0.085$, $r_g = 0.093$) and 100-seed weight ($r_p = 0.135$, $r_g = 0.128$) registered non-significant positive association.

Korat *et al.* (2010) reported non-significant positive association of number of secondary branches per plant with 100-seed weight, whereas Pavankumar *et al.* (2014) reported significant negative relationship with shelling percentage and harvest index.

4.4.1.1.12 Plant height :

Non-significant negative correlation of plant height was observed with number of immature pods per plant ($r_p = -0.165$, $r_g = -0.188$), 100-seed weight ($r_p = -0.009$, $r_g = -0.007$) and harvest index ($r_p = -0.031$, $r_g = -0.031$). While number of pegs per plant ($r_p = 0.004$, $r_g = 0.001$), number of mature pods per plant ($r_p = 0.093$, $r_g = 0.096$) and shelling percentage ($r_p = 0.138$, $r_g = 0.157$) registered non-significant positive association.

Reddy *et al.* (2017) reported non-significant positive association of plant height with number of pegs per plant. Non-significant positive association of plant height with number of mature pods per plant was in accordance with the results of Reddy *et al.* (2017), Kumar *et al.* (2012) and Pavankumar *et al.* (2014).

Non-significant negative correlation of plant height for number of immature pods per plant was observed by Sirisha (2005). Patil *et al.* (2006), Kumar *et al.* (2012) and Reddy *et al.* (2017) observed non-significant negative correlation of plant height with 100-seed weight, whereas non-significant negative correlation of plant height with harvest index was reported by Reddy *et al.* (2017), Kumar *et al.* (2012) and Sirisha (2005). Non-significant positive association with shelling percentage was in accordance with the report of Sirisha (2005).

4.4.1.1.13 Number of pegs per plant :

Number of pegs per plant exhibited significant and positive correlation with number of mature pods plant ($r_p = 0.776^{**}$, $r_g = 0.845$), number of immature pods plant ($r_p = 0.608^{**}$, $r_g = 0.770$), and harvest index ($r_p = 0.286^{**}$, $r_g = 0.342$). It exhibited significant negative relationship with shelling percentage ($r_p = -0.188^*$, $r_g = -0.216$) and 100-seed weight ($r_p = -0.440^{**}$, $r_g = -0.544$). Reddy *et al.* (2017) reported significant positive relationship of number of pegs per plant with number of mature pods plant.

4.4.1.1.14 Number of mature pods per plant :

Significant positive relationship of number of mature pods per plant was observed with number of immature pods per plant ($r_p = 0.450^{**}$, $r_g = 0.542$) and harvest index ($r_p = 0.404^*$, $r_g = 0.439$). Whereas it exhibited non-significant negative relationship with shelling percentage ($r_p = -0.149$, $r_g = -0.169$) and 100-seed weight ($r_p = -0.523$, $r_g = -0.586$).

Non- significant negative relationship of number of mature pods per plant with shelling percentage and 100-seed weight was reported by Kumar *et al.* (2012) and Hampannavar *et al.* (2018).

4.4.1.1.15 Number of immature pods per plant :

Number of immature pods per plant exhibited significant negative correlation with shelling percentage ($r_p = -0.182^*$, $r_g = -0.242$) and 100-seed weight ($r_p = -0.311^{**}$, $r_g = -0.357$). It also exhibited non-significant negative relationship with harvest index ($r_p = -0.006$, $r_g = -0.026$). Significant and negative relationship of number of immature pods per plant with 100-seed weight was reported by Hampannavar *et al.* (2018).

4.4.1.1.16 Shelling percentage :

Shelling percentage exhibited significant and positive relationship with 100-seed weight ($r_p = 0.205^*$, $r_g = 0.241$) and harvest index ($r_p = 0.268$, $r_g = 0.302$). Nirmala and Jayalakshmi (2015) and Kumar *et al.* (2012) reported significant and positive relationship of shelling percentage with harvest index.

4.4.1.1.17 100-seed weight :

Non-significant negative correlation of 100-seed weight was observed with harvest index ($r_p = -0.120$, $r_g = -0.148$). Giri *et al.* (2009) reported non-significant negative correlation of 100-seed weight was observed with harvest index.

4.4.2 Correlation between Pod Yield and its Component Traits in *Rabi*

The correlation coefficients between pod yield per plant with SPAD chlorophyll meter reading at 60 DAS, Specific leaf area at 60 DAS, Relative Water Content at 80 DAS, shelling out-turn, 100-seed weight, and among themselves are presented in Table 4.26. Pod yield per plant showed significant and positive correlation with shelling percentage ($r_p = 0.249^*$, $r_g = 0.548$) and highly significant negative correlation with RWC ($r_p = -0.414^{**}$, $r_g = -0.491$).

Results of significant positive association of pod yield per plant with shelling percentage was in accordance with the report of Gupta *et al.* (2015) and highly significant negative correlation with RWC was in contrary to the report of John and Reddy (2016). Pod yield per plant exhibited non-significant negative correlation with SLA at 60 DAS ($r_p = -0.220$, $r_g = -0.284$) and SCMR at 60 DAS ($r_p = -0.229$, $r_g = -0.294$). 100-seed weight shows non-significant positive association ($r_p = 0.009$, $r_g = 0.025$) with pod yield per plant.

Non-significant negative correlation of pod yield per plant with SLA at 60 DAS was in accordance with the reports of Kyaw *et al.* (2017). Nirmala and Jayalakshmi (2015) reported non-significant negative correlation of pod yield per plant with SCMR at 60 DAS. Nirmala and Jayalakshmi (2015) reported non-significant positive correlation of pod yield per plant with 100-seed weight.

4.4.2.1 Inter-correlation among Traits

4.4.2.1.1 SCMR at 60 DAS :

SCMR at 60 DAS showed non-significant positive correlation with SLA at 60 DAS ($r_p = 0.150$, $r_g = 0.200$), RWC ($r_p = 0.100$, $r_g = 0.136$) and shelling percentage ($r_p = 0.103$, $r_g = 0.204$). It exhibited significant positive correlation with 100-seed weight ($r_p = 0.251^*$, $r_g = 0.285$).

Table 4.26. Genotypic and phenotypic correlation coefficient analysis for pod yield per plant and its components in groundnut (*Rabi*, 2017-18)

Character	SLA at 60 DAS	RWC at 80 DAS	Shelling %	100 Seed Weight	Pod yield per plant
SCMR at 60 DAS					
r_p	0.150	0.100	0.103	0.251*	-0.229
r_g	0.200	0.136	0.204	0.285*	-0.294*
SLA at 60 DAS					
r_p	1	0.295*	-0.122	0.183	-0.220
r_g	1	0.300*	-0.167	0.187	-0.284*
RWC at 80 DAS					
r_p		1	-0.301*	-0.142	-0.414**
r_g		1	-0.442**	-0.148	-0.491**
Shelling %					
r_p			1	0.216	0.249*
r_g			1	0.266*	0.548**
100 Seed Weight					
r_p				1	0.009
r_g				1	0.025
Pod yield per plant					
r_p					1
r_g					1

** - Significant at 1% level, * - Significant at 5% level

Pavankumar *et al.* (2014) reported non-significant positive correlation of SCMR with SLA at 60 DAS. Non-significant positive correlation of SCMR with shelling percentage was in accordance with the reports of Pavankumar *et al.* (2014) and Nirmala and Jayalakshmi (2015). Significant positive correlation of SCMR with 100-seed weight was observed by Kyaw *et al.* (2017).

4.4.2.1.2 SLA at 60 DAS :

SLA at 60 DAS exhibited significant positive association with RWC ($r_p = 0.295^*$, $r_g = 0.300$) . Non-significant positive association of SLA at 60 DAS was observed for 100-seed weight ($r_p = 0.183$, $r_g = 0.187$). Shelling percentage recorded non-significant negative correlation ($r_p = -0.122$, $r_g = -0.167$) with SLA at 60 DAS which was in correspondence with the report of Kyaw *et al.* (2017).

4.4.2.1.3 RWC:

Significant negative correlation of RWC was observed for shelling percentage ($r_p = -0.301^*$, $r_g = -0.442$). RWC also exhibited non-significant negative correlation with 100-seed weight ($r_p = -0.142$, $r_g = -0.148$).

4.4.2.1.4 Shelling percentage :

Shelling percentage exhibited non-significant positive relationship with 100-seed weight ($r_p = 0.216$, $r_g = 0.266$). Pavankumar *et al.* (2014) and Mandal *et al.* (2017) reported non-significant and positive relationship of shelling percentage with 100-seed weight.

From the discussion, we could infer that the characters *viz.*, number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant and harvest index recorded significant positive correlation with pod yield per plant in *kharif* and shelling percentage recorded significant positive

correlation with pod yield per plant in *rabi* indicating that increase in these traits would result in increase in the pod yield.

Relative water content in *rabi* showed significant negative relation with pod yield per plant. Hence judicious selection programme might be formulated by repeated intermating to break the negative correlation of RWC with pod yield per plant. Identification of important yield contributing characters and information about the correlation with yield and also with each other are necessary in developing efficient breeding strategy in order to produce improved genotypes in any crop species.

Thus, emphasis should be given for these characters during selection process to bring about improvement in the yield potential of groundnut genotypes. Among these, selection for easily observable traits would finally increase the mean performance of all concerned interdependent characters and hence would be helpful in order to get improved pod yield.

4.5 PATH COEFFICIENT ANALYSIS

Path coefficient analysis separates the correlation coefficients into components of direct and indirect effects and helps in assessment of the relative importance of each causal factor affecting pod yield.

Path coefficient analysis of different physiological and yield parameters on pod yield based on correlations in 32 genotypes of groundnut in *kharif* and *rabi* seasons are furnished in Table 4.27 and 4.28 respectively and illustrated phenotypic and genotypic path diagrams in Fig 4.21, Fig 4.22 and Fig 4.23, Fig 4.24 respectively. Path coefficients were worked only for those characters which have significant correlation with pod yield.

4.5.1 Direct Effects and Indirect Effects in *kharif* :

The results of path co-efficient analysis revealed that direct contribution to pod yield per plant was from harvest index ($P = 0.4707$; $G = 0.6541$), number of pegs per plant ($P = 0.3466$; $G = 0.5109$), number of

Table 4.27. Genotypic and phenotypic path coefficient analysis for pod yield per plant and its components in groundnut (*Kharif*, 2017)

Character	PB	SB	PP	MP	IP	HI	Correlation with PYP
PB	P	0.16592	0.12401	0.0085	0.01662	-0.074	0.295**
	G	0.25525	0.20597	-0.00992	0.07454	-0.11726	0.389**
SB	P	0.03828	0.23453	0.00797	0.01651	-0.1117	0.288**
	G	-0.01482	0.33028	-0.01059	0.07377	-0.16535	0.389**
PP	P	0.01936	0.06963	0.34662	0.07303	0.1346	0.663**
	G	-0.00773	0.11372	0.51094	-0.09646	0.22391	0.840**
MP	P	0.00489	0.01987	0.26913	0.09405	0.18996	0.593**
	G	-0.00167	0.03063	0.43179	-0.11414	0.28725	0.701**
IP	P	0.02758	0.11878	0.21061	0.04233	-0.0026	0.429**
	G	-0.01149	0.19574	0.39353	-0.06185	0.01727	0.658**
HI	P	-0.0085	-0.0557	0.09913	0.03796	0.47066	0.543**
	G	0.00344	-0.08348	0.17489	-0.05012	0.65414	0.702**

Residual Effect (Phenotypic): 0.36107

Residual Effect (Genotypic): -0.01153

Bold: Direct effects; Normal: Indirect effects

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

PB- Number of primary branches per plant; SB- Number of secondary branches per plant; PP- Number of pegs per plant; MP- Number of mature pods per plant; IP- Number of immature pods per plant; HI- Harvest index (%); PYP- Pod yield per plant (g)

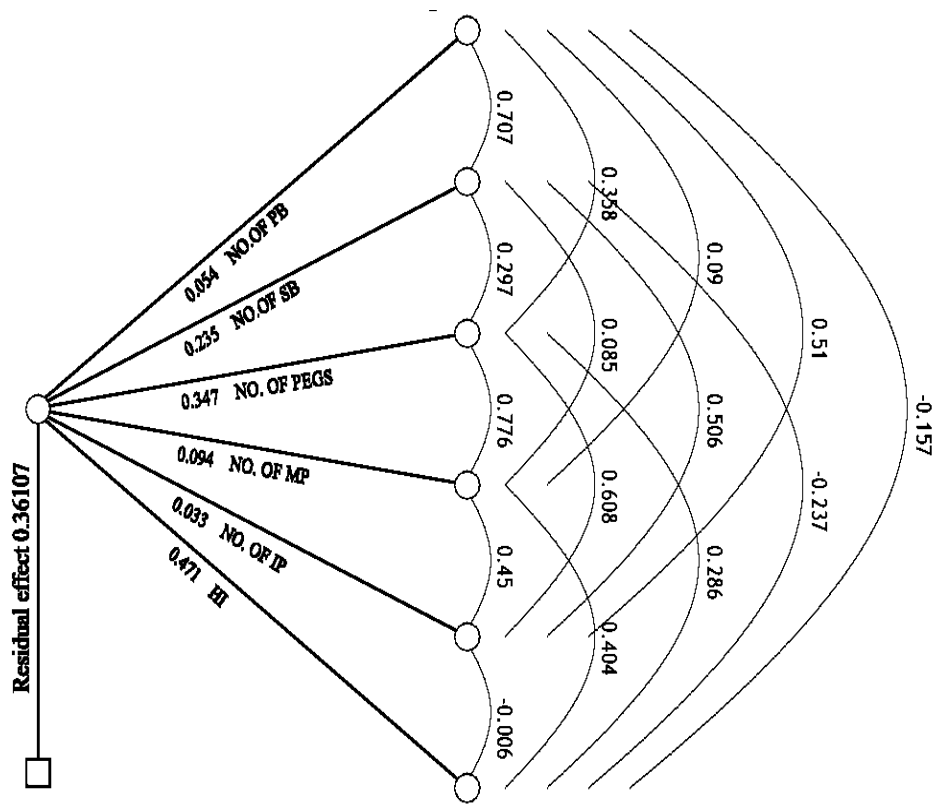


Fig 4.21. Phenotypic path diagram of pod yield per plant and different morphological characters in 32 groundnut genotypes (Kharif, 2017)

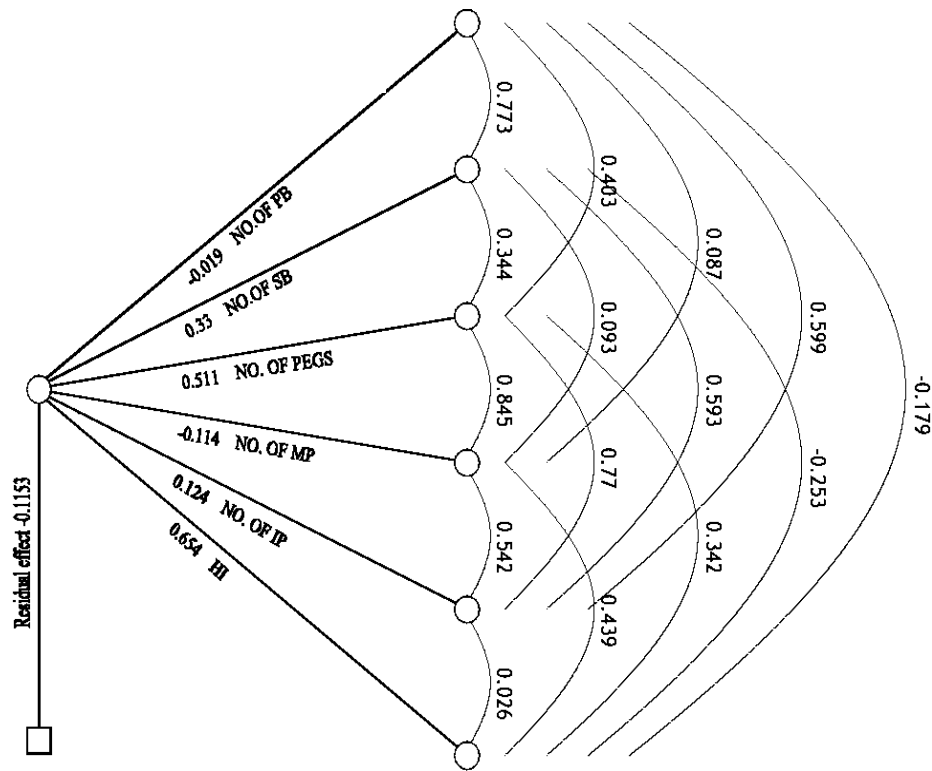


Fig 4.22. Genotypic path diagram of pod yield per plant and different morphological characters in 32 groundnut genotypes(Kharif, 2017)

Table 4.28. Genotypic and phenotypic path coefficient analysis for pod yield per plant and its components in groundnut (*Rabi*, 2017-18)

Character		RWC at 80 DAS	Shelling percentage	Correlation with Pod yield per plant
RWC at 80 DAS	P	-0.37267	-0.04132	-0.414**
	G	-0.30913	-0.18158	-0.491**
Shelling percentage	P	0.11221	0.13724	0.249*
	G	0.13654	0.41111	0.548**

Residual Effect (Phenotypic): 0.81148

Residual Effect (Genotypic): 0.62315

Bold: Direct effects; Normal: Indirect effects

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

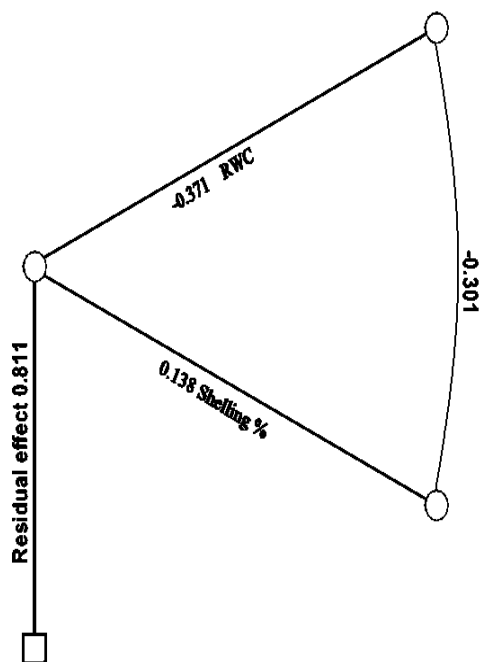


Fig 4.23. Phenotypic path diagram of pod yield per plant and different physiological characters in 32 groundnut genotypes (*Rabi*, 2017- 18)

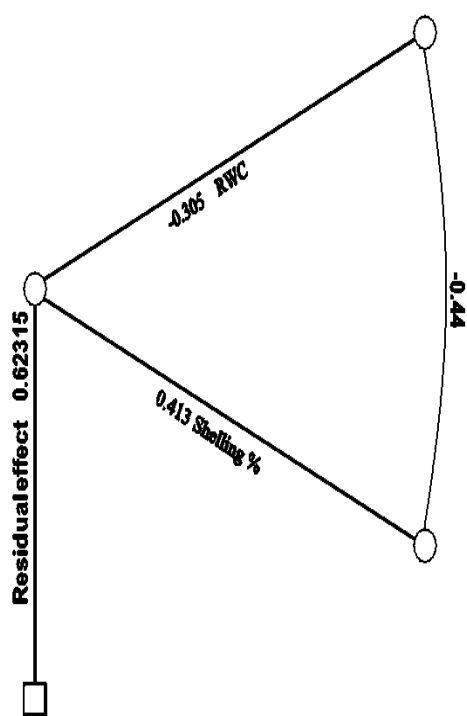


Fig 4.24. Genotypic path diagram of pod yield per plant and different physiological characters in 32 groundnut genotypes(*Rabi*, 2017-18)

secondary branches per plant ($P = 0.2345$; $G = 0.3303$), number of mature pods per plant ($P = 0.0941$; $G = -0.1141$), number of primary branches per plant ($P = 0.0541$; $G = -0.0192$) and number of immature pods per plant ($P = 0.0326$; $G = 0.1245$).

4.5.1.1 Number of primary branches per plant :

Significant positive correlation was observed between number of primary branches per plant and pod yield per plant (0.295^{**}). This correlation was also due to its positive direct effect (0.0541) followed by low positive indirect effect via total number of secondary branches per plant (0.1659), number of pegs per plant (0.1240), number of mature pods per plant (0.0085) and number of immature pods per plant (0.0166). The indirect effect via harvest index (-0.074) was low and negative. The results corroborate with reports of Kumar *et al.* (2012) and Nirmala and Jayalakshmi (2015)

4.5.1.2 Number of secondary branches per plant :

The direct effect of number of secondary branches per plant (0.2345) was moderate and positive on pod yield per plant. It showed significant positive association (0.288^{**}) with pod yield per plant. This association was through low positive indirect effect through number of primary branches per plant (0.0383), number of mature pods per plant (0.0080) and number of immature pods per plant (0.0165) followed by low negative indirect effect via harvest index (-0.1117). It exhibited low positive indirect effect via number of pegs per plant (0.1029). Moderate positive direct effect of number of secondary branches per plant was reported by Alam (2014).

4.5.1.3 Number of pegs per plant :

Number of pegs per plant showed high positive direct effect (0.3466) on pod yield per plant. Significant and positive correlation (0.663^{**}) was through its positive indirect effects via number of primary branches per plant (0.0194), number of secondary branches per plant (0.0696), number of mature

Pods per plant (0.0730) and number of immature pods per plant (0.0198) followed by low positive indirect effect via harvest index (0.1346).

4.5.1.4 Number of mature pods per plant :

This trait exhibited significant and positive relation (0.593^{**}) with pod yield per plant through its low positive direct effect (0.0941) and positive indirect effect via number of primary branches per plant (0.0049), number of secondary branches per plant (0.0199) and number of immature pods per plant (0.0147) followed by low positive indirect effect through harvest index (0.1900). This trait also exhibited moderate positive indirect effect through number of pegs per plant (0.2691).

The results of present study are in accordance with the reports of Kumar *et al.* (2012), Reddy *et al.* (2017) and Hampannavar *et al.* (2018).

4.5.1.5 Number of immature pods per plant :

Number of immature pods per plant showed low positive direct effect (0.0326) on pod yield per plant and registered significant and positive association (0.429^{**}) with pod yield per plant. It showed low positive indirect effects via number of primary branches per plant (0.0276) and number of mature pods per plant (0.0423), whereas it exhibited low negative indirect effect via harvest index (-0.0026) on pod yield per plant. It registered low positive indirect effect via number of secondary branches per plant (0.1188) and moderate positive effect via number of pegs per plant (0.2106). The results of present study are in corroboration with the reports of Nirmala and Jayalakshmi (2015).

4.5.1.6 Harvest index :

There was a significant positive correlation (0.543^{**}) between harvest index and pod yield per plant. The direct effect (0.4707) on pod yield per plant was high and positive. The significant positive relation was also due to its low positive indirect effect via number of mature pods per plant (0.0380) and

number of pegs per plant (0.0991) followed by low negative indirect effect through number of primary branches per plant (-0.0085), number of secondary branches per plant (-0.0557) and number of immature pods per plant (-0.0002). Similar results were reported by Korat *et al.* (2010).

4.5.2 Direct Effects and Indirect Effects in *Rabi* :

The results of path co-efficient analysis revealed that direct contribution to pod yield per plant was from shelling percentage ($P = 0.1372$; $G = 0.4111$) and RWC ($P = -0.3727$; $G = -0.3091$).

Significant positive correlation was observed between shelling percentage and pod yield per plant (0.249**). This correlation was through its low positive direct effect (0.1372) followed by low positive indirect effect via RWC (0.1122).

Significant negative correlation was observed between RWC and pod yield per plant (-0.414**). This correlation was through its high negative direct effect (-0.3727) followed by low negative indirect effect via shelling percentage (-0.0413).

In *rabi*, the phenotypic residual effect is 0.8115 indicating all the contributing characters were not included in the study. While in *kharif* residual effect is 0.3611 which indicates that most of the contributing characters were included in the study.

From the above discussion, it is evident that number of mature pods per plant, number of primary branches per plant, number of secondary branches per plant, number of immature pods per plant, number of pegs per plant and harvest index and shelling percentage are the major yield contributing characters in groundnut. Therefore, due emphasis should be given to these characters in formulating selection criteria to evolve high yielding genotypes of groundnut.

Chapter ~ V

Summary & Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation “Genetic diversity analysis for drought resistance and water use efficiency traits in groundnut (*Arachis hypogaea* L.)” was taken up in 32 genotypes of groundnut to study genetic diversity based on physiological, yield, yield attributes and SSR data, to estimate variability and heritability, to study character association and work out path co-efficients among yield, yield attributes and physiological traits. The experiment was laid out in a randomized block design with four replications in *kharif*, 2017 and two replications in *rabi*, 2017-18 at Regional Agricultural Research Station, Tirupati. The data were recorded on five randomly selected plants for the yield and yield attributes viz., number of primary branches per plant, plant height, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, 100-seed weight, shelling percentage, harvest index and pod yield per plant. The data for physiological characters viz., leaf area duration (LAD) and leaf area index (LAI) were recorded through destructive sampling of three plants at 60 and 80 DAS. SCMR, SLA and RWC were recorded based on five randomly selected plants. Root length and root dry mass were recorded based on five randomly selected plants after harvest. Five plants were selected randomly and angle between main axis and first two primary branches was recorded using a protractor in field itself.

Analysis of variance revealed significant differences for all characters indicating the presence of considerable amount of variability among the genotypes. In *kharif*, SG-99 showed high mean performance for pod yield per plant, number of primary branches per plant, number of secondary branches per plant and number of pegs per plant. TCGS-1653 showed high mean for number of mature pods per plant. The genotypes, Dharani and TCGS-1097 recorded the highest shelling percentage, GG-16 showed high mean

performance for 100-seed weight while TCGS-1694 recorded the highest harvest index. The genotype, TCGS-1653 recorded high mean LAD and LAI. The genotypes, Dharani and ICGS 76 showed wider angle between main axis and first two primary branches. R-2001-2 and GPBD-4 recorded the high mean root length and root dry weight respectively. While K 9 exhibited maximum mean SCMR and low SLA which is desirable as it confers high water use efficiency. In *rabi*, TCGS-1694 showed highest pod yield per plant and shelling percentage whereas TCGS-1622 recorded highest 100-seed weight. K 1789, Narayani and K 9 recorded maximum RWC, low SLA and high SCMR respectively.

A perusal of genetic parameters revealed that GCV, PCV, heritability (broad sense) and genetic advance as per cent of mean were high for most of the traits included in the present study except shelling percentage in *kharif* indicating that the traits are amenable for phenotypic selection while in *rabi* pod yield per plant, SLA at 60 DAS and 100 seed weight recorded moderate to high GCV, PCV, moderate to high heritability and high GAM indicating that these characters are governed by additive gene action and simple phenotypic selection could be followed for their improvement. Low GCV, PCV, high to moderate heritability and low GAM was observed for SCMR at 60 DAS, RWC and shelling percentage, indicating that these characters were under the control of non additive gene action and phenotypic selection would not be that effective to improve these characters.

Genetic divergence studies were carried out based on data of physiological, yield and yield attributes using Mahalanobis's D^2 statistic and genetic diversity at molecular level was estimated using SSR markers. Through D^2 analysis, 32 genotypes were grouped into seven clusters in *kharif* and eight clusters in *rabi*.

In *kharif*, the characters, angle between main axis and primary branches at 60 DAS contributed maximum to the diversity followed by plant height, LAI at 80 DAS and angle between main axis and primary branches at 80

DAS. Based on genetic diversity studies in *kharif*, cross combinations proposed are SG 99(cluster VII) × Dharani (cluster III); SG 99(cluster VII) × R 2001-2-1 (cluster III) in order to get transgressive segregants for physiological, yield and yield parameters since these genotypes showed maximum diversity among themselves with desirable yield parameters. Similarly, the cross between genotypes, SG 99 (cluster VII) × K 9 (cluster I) could be suggested for the exploitation of transgressive segregants for high yield coupled with drought tolerance. Canonical analysis also confirmed the clustering pattern obtained by D² analysis. In *rabi*, the characters, SLA at 60 DAS, 100 seed weight and RWC at 80 DAS were found to be contributing more to divergence and cross combinations proposed are GPBD-4 (cluster II) × GG-16 (cluster VIII); GG-16 (cluster VIII) × TCGS-1694 (cluster V) in order to get transgressive segregants for yield and yield parameters. Similarly, the crosses between genotypes, GG-16 (cluster VIII) × K 9 (cluster III); GG-16 (cluster VIII) × Narayani (cluster II) could be suggested for the exploitation of transgressive segregants for high yield coupled with drought tolerance.

Assessment of molecular diversity using SSR markers revealed that there was a high level of genetic variation among 10 groundnut genotypes selected. Eleven primers out of 27 primers screened were polymorphic. The markers, PM 45 and SEQ5D05 are highly informative. The similarity coefficient values ranged from 0.34 to 0.703 indicating the presence of wide range of genetic diversity at molecular level among the 10 genotypes. The dendrogram of ten genotypes consisted of five clusters, two genotypes each in cluster I (TCGS-1694 and K 1725), cluster III (TCGS-1157 and TCGS-1616) and cluster IV (K 9 and Narayani) whereas three genotypes in cluster II (Dharani, TCGS-1622 and TCGS-1073) and one genotype in cluster V (GG-20). Ten genotypes showed different banding pattern with eleven polymorphic primers. IPAHM 123 primer amplified an unique allele of 140 bp size in TCGS-1622. In K 1725 a specific allele of 340 bp with IPAHM 689 was amplified. PM 3 amplified unique allele of 170 bp in Narayani. In K 9,

specific alleles of 135 bp and 328 bp were amplified with PM 418 and IPAHM 105 respectively. PM 45 amplified an unique allele of 125 bp in TCGS-1157. In GG-20 and TCGS-1616 unique alleles of 290 and 265bp were amplified respectively with SEQ2G4. In Narayani, three fragments of 295, 250 and 230 bp were amplified with SEQ5D05. Thus, genotype specific banding patterns observed with specific primers would help in the identification of the genotypes.

The clustering pattern was different in different methods used. Genotypes with dissimilar pedigrees were grouped into the same cluster while genotypes with same pedigrees are farther apart. Likewise certain genotypes were grouped together in either of the ways i.e. grouping through *kharif*/SSR data or *rabi*/SSR data or *kharif/rabi* data. TCGS-1694 and K 1725 were grouped in one cluster when grouping of genotypes was done in both ways i.e. based on *kharif* data and SSR based analysis. While GG-20, K. Anantha, K 6 and J 89 were grouped in one cluster when grouping of genotypes was done in both ways i.e. based on *kharif* data and *rabi* data. Similarly R 2001-2-1 and Dharani appeared together in one cluster, while R-2001-3, TCGS-1630 and R-2001-3-1 were grouped in one cluster; K 1805, ICG 86325 and TCGS-1616 formed a cluster; TCGS-1157 and K 1725 were grouped in one cluster; TCGS-1694, TCGS-1073 and TCGS-1696 appeared together in one cluster when grouping was carried out based on physiological, yield and yield attributes data in *kharif* and *rabi*.

Character association studies indicated that number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant and harvest index recorded significant positive correlation with pod yield per plant in *kharif* and shelling percentage recorded significant positive correlation with pod yield per plant in *rabi*. Hence, these characters could be considered in formulating selection criteria in breeding programme aimed at improvement of yield in groundnut.

The results of path co-efficient analysis revealed that direct contribution to pod yield per plant was from harvest index, number of pegs per plant, number of secondary branches per plant, number of mature pods per plant, number of primary branches per plant and number of immature pods per plant in *kharif* and shelling percentage in *rabi*. Thus, in a selection programme aimed at improvement of pod yield, due emphasis should be given for these traits.

Future line of work

From divergence studies, it has become very clear that a lot of variation exists among genotypes studied. Specific alleles for some genotypes were identified in this study, if these alleles were confirmed as unique over a broader range of groundnut genotypes, then these genotype specific unique alleles can be used for identification of these genotypes directly. In the present global context, it is essential to develop DNA finger prints for each groundnut genotype.

With the available variation, it is possible to produce high yielding ideal ideotypes suitable for drought prone situations through hybridization involving genotypes from divergent clusters.

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Appendices

APPENDICES

APPENDIX A: Weather Data

Center	Month	Rainfall (mm)	No. of rainy days	Temperature		Relative humidity		Sunshine (hrs per day)
				Max.	Min.	Morning	Evening	
RARS, Tirupati	May, 17	17.4	3	39.6	27.7	77.0	37.0	7.1
	June, 17	112.0	8	36.4	26.7	68.2	40.5	4.7
	July, 17	93.6	7	36.0	26.8	67.0	41.1	4.6
	Aug, 17	285.0	11	33.0	24.7	82.5	57.3	4.1
	Sep, 17	262.2	13	32.4	24.1	87.1	63.2	4.4
	Oct, 17	214.6	14	31.8	23.3	87.6	63.4	4.5
	Nov, 17	157.2	9	29.4	21.8	87.9	65.8	4.0
	Dec, 17	13.2	1	29.4	18.7	88.8	53.3	6.8
	Jan, 18	0.0	0	29.8	16.1	87.9	48.4	7.8
	Feb, 18	28.4	1	32.1	16.6	87.1	36.0	8.9
	Mar, 18	12.8	1	35.6	20.5	81.4	34.5	7.8
Total rainfall and rainy days / Mean Max. and Min. temp	June -Oct Nov - Mar	1196.6 967.4 211.6	68	33.2	22.4	82.0	49.1	8.6
Average of last decade		1028	52.9	33.99	22.38	77.43	46.38	5.92

APPENDIX B: Buffers and stock solutions

1. DNA ISOLATION BUFFERS

CTAB extraction buffer (100 ml)

1 M Tris (pH 8.0)	-	10 ml
5M NaCl	-	28 ml
0.5 M EDTA	-	4 ml
2% CTAB	-	2 g
1% PVP	-	1 g
0.1% Mercaptoethanol	-	100 µl

Chloroform : Isoamyl alcohol mixture (24:1)

Chloroform	-	24 ml
Isoamyl alcohol	-	1 ml
Stored at 4 ⁰ C		

Absolute ethanol - Stored at 4⁰ C

70% Ethanol

Absolute ethanol	-	70 ml
Distilled water	-	30 ml

90 % ethanol

Absolute ethanol	-	90 ml
Distilled water	-	10 ml

2. AGAROSE GEL ELECTROPHORESIS:

10X TBE buffer, pH 8.3 (Stock solution)

Tris base	-108 g
Boric acid	- 55 g
EDTA	- 9.3 g
Distilled water	- 1000 ml

Composition of loading dye

Glycerol	- 2 ml
10X TBE	- 600 µl
Bromophenol blue (saturated)	- 2 ml
Water	- 300 µl
10 % SDS	- 600 µl
0.5 M EDTA	- 500 µl

Ethidium bromide

Ethidium bromide	- 10 mg
Sterile distilled water	- 1 ml

APPENDIX C

Components of Master Mix Used in Polymerase Chain Reaction

Components	Stock concentration	Working concentration per reaction
Sterile distilled water	-	3.25 µl
PCR buffer	10X	1X (1 µl)
MgCl ₂	25 mM	0.1 Mm (0.4 µl)
dNTPs	10mM	0.25 µl
Taq polymerase	5 U/µl	0.05U (0.1 µl)
SSR primers (Forward)	10 picomoles	1 µl
SSR primers (Reverse)	10 picomoles	1 µl
DNA	50 ng/µl	3 µl
Total		10 ml

**GENETIC DIVERSITY ANALYSIS FOR DROUGHT
RESISTANCE AND WATER USE EFFICIENCY
TRAITS IN GROUNDNUT (*Arachis hypogaea* L.)**

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ABSTRACT

A study was undertaken to determine the genetic divergence, variability, character association and path co-efficients in 32 genotypes of groundnut for 19 traits in *kharif* and 6 traits in *rabi*. Analysis of variance indicated existence of significant genotypic differences for all the characters studied. From the study of genetic parameters, out of 19 traits studied except shelling percentage, all other traits recorded moderate to high GCV, heritability and GAM in *kharif*. In *rabi* out of six characters studied three traits, SCMR, RWC and shelling percentage recorded low GCV, high to moderate heritability and low GAM.

Genetic divergence studies by Mahalanobis's D^2 analysis revealed considerable diversity among 32 genotypes of groundnut and were grouped into seven and eight clusters in *kharif* and *rabi* respectively. Based on these studies, cross combinations between genotypes in cluster VII and cluster III in *kharif* and cluster VIII and cluster II, cluster VIII and cluster V in *rabi* are proposed to get transgressive segregants for yield and yield parameters. SSR marker studies detected a high level of genetic variation among the ten groundnut genotypes selected. A high degree of polymorphism was obtained with the markers, PM 45(0.95) and SEQ5D05 (0.75).

Character association studies revealed significant positive correlation of number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant and harvest index with pod yield per plant. Path co-efficient analysis also indicated that these characters were important attributes directly influencing the pod yield in groundnut.