GENETIC ANALYSIS OF YIELD, YIELD ATTRIBUTES AND WATER USE EFFICIENCY RELATED TRAITS IN GROUNDNUT (*Arachis hypogaea* L.)

By

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B.Sc. (Hons.) Ag.

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DECLARATION

I, **Ms. SOMISETTY DIVYA SREE ,** hereby declare that the thesis entitled **"GENETIC ANALYSIS OF YIELD, YIELD ATTRIBUTES AND WATER USE EFFICIENCY RELATED 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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CERTIFICATE

Ms. SOMISETTY DIVYA SREE has satisfactorily prosecuted the course of research and that thesis entitled **"GENETIC ANALYSIS OF YIELD, YIELD ATTRIBUTES AND WATER USE EFFICIENCY RELATED 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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This is to certify that the thesis entitled **"GENETIC ANALYSIS OF YIELD, YIELD ATTRIBUTES AND WATER USE EFFICIENCY RELATED TRAITS IN GROUNDNUT (*Arachis hypogaea* L.)"** submitted in partial fulfilment 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. SOMISETTY DIVYA SREE** under our guidance and supervision.

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

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Divya Sree....✍

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LIST OF SYMBOLS AND ABBREVIATIONS

@	:	At the rate
%	:	Per cent
ºC	:	Degree Celsius
$\overline{X}$	:	Grand mean
μ	:	General mean
σ^2_g	:	Genotypic variance
σ^2_p	:	Phenotypic variance
AICRP	:	All India Coordinated Research Project
ANOVA	:	Analysis of variance
cm	:	Centimetre
$cm^2\ g^{-1}$	:	Centimetre square per gram
CD	:	Critical difference
Cont.	:	Continued
Cov_g	:	Genotypic covariance
Cov_p	:	Phenotypic covariance
CV	:	Co-efficient of variation
D	:	Intra cluster distances
D^2	:	Inter cluster distances
DAS	:	Days after sowing
df	:	Degrees of freedom
DFF	:	Days to 50% flowering
DM	:	Days to maturity
et al.,	:	And others
Fig.	:	Figure
FYM	:	Farm yard manure
G	:	Gram
G × E	:	Genotype × Environment interaction

GA	:	Genetic advance
GAM	:	Genetic advance as per cent of mean
GCV	:	Genotypic co-efficient of variation
h^2 (bs)	:	Heritability in broad sense
ha	:	Hectare
HI	:	Harvest index
HKW	:	Hundred kernel weight
i.e.,	:	That is
Kg	:	Kilogram
KYP	:	Kernel yield plant^{-1}
M	:	Meters
Max.	:	Maximum
Min.	:	Minimum
Mt	:	Million tonnes
No.	:	Number
NPB	:	Number of primary branches plant^{-1}
NSB	:	Number of secondary branches plant^{-1}
PCV	:	Phenotypic co-efficient of variation
Per se	:	As such with mean
PH	:	Plant height
P_{RY}	:	Residual effect
PYP	:	Pod yield plant^{-1}
r_g	:	Genotypic correlation coefficient
r_p	:	Phenotypic correlation coefficient
RARS	:	Regional Agricultural Research Station
RBD	:	Randomised Block Design
S. No.	:	Serial Number
SCMR	:	SPAD chlorophyll meter reading

SE(d)	:	Standard error difference
SE(m)	:	Standard error of mean
SLA	:	Specific leaf area
SMK	:	Sound mature kernel
SP	:	Shelling per cent
SPAD	:	Soil Plant Analytical Development
RWC	:	Relative water content
t ha^{-1}	:	Tonnes per hectare
via	:	Through
viz.,	:	Namely
WUE	:	Water use efficiency

ABSTRACT

Name of the Author	:	**SOMISETTY DIVYA SREE**
Title of thesis	:	**"GENETIC ANALYSIS OF YIELD, YIELD ATTRIBUTES AND WATER USE EFFICIENCY RELATED TRAITS IN GROUNDNUT (*Arachis hypogaea* L.)"**
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At the dry land farm of S. V. Agricultural College, Tirupati, during *rabi* in 2021-2022, a randomised block design with three replications was used to conduct the present study which was titled "Genetic analysis of yield, yield attributes and water use efficiency related traits in groundnut (*Arachis hypogaea* L.)." It included 36 genotypes comprised of 26 advanced breeding lines and ten released varieties. Data was obtained on five randomly chosen plants in order to identify the most promising genotypes to estimate genetic parameters, evaluate genetic diversity among genotypes and examine correlations and path co-efficient analysis for characteristics linked to the yield, yield attributes and water use efficiency.

Analysis of variance (ANOVA) indicated extremely significant differences for all the characters among all the genotypes for each character under study demonstrating that genotypes differ considerably. The traits include days to 50% flowering, days to maturity, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, kernel yield plant^{-1} (g), hundred kernel weight (g), shelling per cent, sound mature kernel per cent, harvest index (%), SPAD chlorophyll meter reading at 60 DAS, specific leaf area at 60 DAS (cm^2 gm^{-1}), relative water content (%) and pod yield plant^{-1} (g).

A thorough examination of *per se* performance showed that the genotypes TCGS-2223, TCGS-2040, TCGS-2039, TCGS-2230 and TCGS-2053 were superior for the majority of traits related to yield, yield attributes and water use efficiency.

Number of secondary branches plant^{-1} and number of primary branches plant^{-1} showed higher estimations of GCV and PCV. Number of primary

branches plant^{-1}, number of secondary branches plant^{-1}, pod yield plant^{-1}, kernel yield plant^{-1}, plant height and specific leaf area at 60 DAS showed high heritability coupled with high genetic advance as per cent of mean which suggests that predominance of additive gene action in the expression of these characters and that selection would be effective in enhancing these traits.

Thirty six groundnut genotypes were grouped into nine clusters using D^2 analysis. The clusters VI–IX, VI–VIII, I–IX, V–IX and VII–VIII were discovered to be increasingly divergent in decreasing order of their magnitude based on the inter cluster distances. Hence the genotypes of these clusters could be used as parents in the hybridization programme and crossing between them would produce transgressive segregants. The cross combinations K-6 × TCGS-2053 and TCGS-2235 × TCGS-2053 could be recommended to improve water use efficiency related traits. Greeshma × TCGS-2053 and TCGS-2223 × TCGS-2230 could be suggested to obtain transgressive segregants for yield and yield attributes in groundnut by comparing the genetic divergence between clusters and *per se* performance of genotypes.

The most significant contribution to diversity was made by shelling per cent followed by pod yield plant^{-1}, SPAD chlorophyll meter reading at 60 DAS, kernel yield plant^{-1}, number of secondary branches plant^{-1} and specific leaf area at 60 DAS. This proved that these traits could be valued when segregating populations are selected during hybridization.

Character association analysis revealed a highly significant positive correlation between kernel yield plant^{-1}, number of primary branches plant^{-1}, SPAD chlorophyll meter reading at 60 DAS, harvest index and the sound mature kernel per cent with the pod yield plant^{-1} as well as between these traits at both the phenotypic and genotypic levels. In order to develop these characteristics and boost the pod yield plant^{-1}; proper emphasis should be placed on these attributes.

The path analysis revealed that the direct impact of the kernel yield plant^{-1} on the pod yield plant^{-1} was highly positive and it was followed by the, SPAD chlorophyll meter reading at 60 DAS, harvest index and plant height.

Overall analysis of the present study showed that the genotypes TCGS-2053, K-6, TCGS-2235, Greeshma, TCGS-2223 and TCGS-2230 were determined to be promising for yield, yield attributes and water use efficiency related traits. Hence these genotypes can be included in the crossing programme for the development of high yielding varieties with high water use efficiency.

Chapter - I

Introduction

Chapter I

INTRODUCTION

The cultivated groundnut (*Arachis hypogaea* L.) is a self –pollinated crop and allotetraploid with 2n=4x=40. It belongs to the sub-family Papilionaceae of the family Leguminosae. Groundnut is also known as peanut, goober nut, monkey nut, manilanut, earthnut and occupies pre-eminent position in national edible oil economy and is known as “King of oilseeds” and “Poor man’s Cashewnut”. It is a native of South America where it was first domesticated in Paraguay valleys.

Groundnut is widely accepted as the most important source of nutrition to both human and animals due to its high oil (45-50%) and protein (25%) content. Besides oil and protein, groundnut also contains carbohydrates (8-14%), minerals, vitamins A, B and some members of B_2 group especially thiamin and niacin. Groundnut also provides nutrients to the soil and its cultivation improves soil fertility by nitrogen fixation that makes it an important component for crop rotation. It is grown as a sole crop, intercrop or mixed crop (Rao *et al*., 1990; Ghosh, 2004). These multiple uses of groundnut makes it an excellent cash crop for both national and international trade in several emerging and also developed countries.

Globally, it is cultivated in an area of 29.92 Mha with annual production of 55.30 Mt and productivity of 1851 kg ha^{-1} (FAOSTAT, 2020-2021). In India, groundnut covers an area of 6.09 Mha with a production of 10.21 Mt and productivity of 1676 kg ha^{-1}. In Andhra Pradesh, it is cultivated in an area of 0.87 Mha with a production of 0.78 Mt and productivity of 894 kg ha^{-1} (Directorate of Economics and Statistics, 2021).

Mainly groundnut is cultivated as a rainfed crop but is also grown as irrigated crop. During *rabi* season, due to the depletion of ground water resources water shortage is usual during the crop period. Hence, there is urge to find out water use efficiency (WUE) genotypes in groundnut. WUE is an

important trait which contributes to productivity when there are limited water resources. The productivity of the crop can be enhanced by identifying the genotypes that use the limited resources of water more efficiently (Arunkumar *et al*., 2017). The natural capacity of groundnut to moderately tolerate drought renders it suitable to be grown largely under rain dependent conditions especially by the resource-poor farmers.

The development of genotypes with high water use efficiency (WUE) under limited water availability is necessary since frequent droughts are one of the limiting factors that negatively affect groundnut yield especially in rainfed areas. In groundnut, WUE is associated with the SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA) and relative water content (RWC). SCMR, SLA and RWC can be utilised as surrogate traits to choose genotypes with high WUE. When these physiological traits are used as selection criteria in breeding programmes or in the selection of productive genotypes, we will be greatly assisted in bringing genetic improvements for improving WUE in groundnut genotypes ultimately leading to the evolution of better genotypes adapted to drought conditions.

Because of the practical difficulties involved in direct measurement of WUE; indirect methods of WUE like SPAD chlorophyll meter readings (SCMR), specific leaf area (SLA) and relative water content (RWC) are calculated (Babitha *et al*., 2006). SCMR measures the green colour intensity and this is associated with chlorophyll density in groundnut. Under water stress conditions, maintaining the high chlorophyll density is associated with high WUE in groundnut. SLA is inversely associated with WUE. SLA is the measure of leaf thickness and low SLA genotypes produces high dry matter during drought conditions (Janila *et al*., 2015).

Lack of genetic variability even between the botanical groups of groundnut as evidenced by molecular analysis limits the improvement of the crop. Hence, the groundnut genotypes were evaluated to assess the nature and magnitude of genetic variability among the genotypes for further utilization in

the breeding programmes. Genotypic coefficient of variability estimate gives good implication for genetic potential in crop improvement through selection. The variability in the population is largely due to genetic cause with least environment effect; the possibility of selecting superior genotype is a prerequisite for obtaining higher yield which is the ultimate expression of various yield contributing characters.

Genetic variability is essential for crop improvement as it provides large scope for selection. The effectiveness of selection depends on the nature, extent and magnitude of genetic variability present in the population. Hence, PCV and GCV estimates are calculated to know the role of the environment in the expression of characters (Gupta *et al*., 2015a).

It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimate of heritability in order to plan an efficient breeding programme. Heritability is the ratio of phenotypic variance to the genotypic variance. Heritability estimates helps in the effective selection for desired traits and there by maximum genetic gain can be achieved. Genetic advance is the genetic improvement of progeny selection over the original population. High Heritability coupled with high genetic advance is more reliable for the selection of traits (Kakeeto *et al*., 2019).

Yield is a complex character that is polygenic and highly influenced by the environment. Thereby, selection based on yield alone restricts the improvement. But, selection based on the highly heritable yield attributes is most effective. The correlation between characters may exists due to various reasons such as pleiotropy and genetic linkage. An understanding of the direction and extent of association of the component characters with economic yield is an essential prerequisite for formulating best selection strategy in groundnut breeding programmes. Correlation studies helps to know the nature and extent of association of yield with different yield components. Hence, for better improvement of yield; it is essential to incorporate the correlation studies in breeding programme (Prabhu *et al*., 2015). Genotypic correlation

revealed the existence of real association whereas the phenotypic correlations may occur by chance (Bhargavi *et al*., 2017b).

The correlation coefficient may be confounded with indirect effect due to common association inherent in trait interrelationships. Therefore, information derived from the correlation coefficients can be augmented by partitioning correlation coefficients into direct and indirect effects by path coefficient analysis and gives more realistic relationship of the characters and help in effective selection (Korat *et al*., 2010).

The diversity study is a pre-requisite for any hybridization programme. Most of the times selecting the parents for hybridization based only on the phenotypic characters does not give effective results. But, selection of parents based on intra cluster and inter cluster distances and cluster means helps in the production of transgressive segregrants or better recombinants (Hampannavar and Khan, 2018a).

Realizing the impact of drought on yield attributes, there is a need to study on genetic potential of groundnut genotypes with high WUE and yield. Hence, the present investigation was framed with the following objectives:

Objectives:

1. To identify the promising genotypes for yield, yield attributes and water use efficiency (WUE) related traits.
2. To study genetic variability, heritability and genetic advance for yield, yield attributes and WUE related traits.
3. To study correlations among the yield, yield attributes and WUE related traits.
4. To study the genetic diversity among the genotypes using D^2 statistics for the yield, yield attributes and WUE related traits.

Chapter - II

Review of Literature

Chapter – II

REVIEW OF LITERATURE

The genetic improvement of economically important traits in groundnut requires adequate knowledge of their inheritance pattern, genetic variability and relative contribution of genetic and non-genetic components in their expression and inter-relationships.

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

2.1 Genetic parameters (variability, heritability and genetic advance)

2.2 Genetic divergence

2.3 Character association

2.4 Path co-efficient analysis

2.1 GENETIC PARAMETERS

Genetic variability is the basic requirement for crop improvement as it provides wider scope for selection. Thus the effectiveness of selection depends on the nature, extent and magnitude of genetic variability present in the population and to the extent to which it is heritable. The PCV and GCV estimates are calculated to know the role of environment in the expression of the characters. Genotypic coefficient of variability estimates gives good implication for genetic potential in crop improvement through selection.

The study of genetic advance with variability estimates further clarify the nature of the character that can be improved through selection. Heritability is an important parameter as it determines the response to selection. Heritability and genetic advance are very useful biometrical tools for breeders in determining the direction and magnitude of selection. The degree of success depends on the magnitude of heritability as it measures the relative

amount of the heritable portion of variability. High heritability alone is not enough to make efficient selection in the advanced generations unless accompanied by substantial amount of genetic advance. The study of genetic advance with heritability estimates further clarify the nature of gene action controlling character which decides the breeding methodology for the genetic improvement of the character. Hence, the estimates of genetic variability, heritability and genetic advance had an immense value in identifying superior genotypes.

A brief review of work done on variability, heritability and genetic advance in groundnut is presented below.

John *et al.* (2005) studied variability among yield and yield components and stem necrosis disease that helps in selection of high yielding varieties with stem necrosis resistance. High PCV than GCV was recorded for all the characters. High PCV and GCV was recorded for pod yield plant^{-1} followed by plant stand at harvest which indicates that sufficient variation is present for these characters. High heritability and high GAM was observed for plant stand at harvest.

Genetic variability studies conducted by Korat *et al*. (2009) on 80 diverse groundnut genotypes revealed high PCV and GCV for number of secondary branches plant^{-1}. They have also observed high heritability along with high genetic advance as per cent of mean for number of secondary branches plant^{-1} and number of aerial pegs plant^{-1} which indicated that these characters were governed by additive gene action.

Shoba *et al.* (2009) carried out crosses to develop disease resistant parents using TMV-2 as female parent and determined various genetic parameters like variability, heritability and genetic advance as per cent of mean for nine characters and observed that all the characters exhibited high PCV than GCV for all the characters.

Dolma *et al*. (2010b) reported the highest genotypic and phenotypic coefficient of variation for kernel yield plant^{-1}, plant height, pod yield plant^{-1} and 100 kernel weight in groundnut. Similarly, high heritability coupled with high genetic advance was observed for these traits indicating the scope for their improvement through selection.

Meta and Monpara (2010) evaluated 50 groundnut genotypes and examined that high GCV and PCV for pods plant^{-1}, pod yield plant^{-1} and kernel yield plant^{-1}. High heritability and high genetic advance as per cent of mean for plant height and hundred pod weight indicating additive gene expression on these characters.

Raut *et al.* (2010) observed high values of GCV, PCV and genetic advance for number of primary branches plant^{-1}, plant height, number of mature pods plant^{-1}, number of immature pods plant^{-1}, kernel yield plant^{-1} and pod yield plant^{-1} in most of the crosses of groundnut.

John *et al.* (2011) studied that JL-220 of groundnut recorded higher performance for protein per cent, number of mature pods, hundred kernel weight and harvest index and ICGV 99029 recorded higher performance for stomatal conductance, number of secondary branches plant^{-1}, kernel yield plant^{-1} and pod yield plant^{-1}. High heritability and high genetic advance per mean was recorded for number of secondary branches plant^{-1} which indicates additive gene action and thereby less influence of the environment on these characters and hence selection is effective. Moderate heritability and high GAM was observed for number of pods plant^{-1}, SLA and dry haulms plant^{-1} which indicates both additive and non-additive gene action.

Nandini *et al.* (2011) reported that pod yield plant^{-1} in groundnut recorded maximum GCV followed by kernel yield plant^{-1}, number of pods plant^{-1}, sound mature kernel per cent, SLA, number of branches plant^{-1}, shelling per cent, plant height and SCMR while low heritability and moderate genetic advance as per cent of mean was observed for SCMR.

Vekariya *et al.* (2011b) studied 50 genotypes of groundnut and recorded highest GCV and PCV for number of mature pods plant^{-1}, protein content, kernel yield plant^{-1}, harvest index, biological yield plant^{-1} and hundred kernel weight. They have also observed high heritability coupled with high genetic advance as per cent of mean for number of mature pods plant^{-1}, kernel yield plant^{-1} and pod yield plant^{-1} indicating that these traits were governed by additive gene action.

Narasimhulu *et al.* (2012) conducted genetic variability studies in 18 genotypes for nine characters and recorded high heritability along with high genetic advance as per cent of mean for pod yield plant^{-1}, kernel yield plant^{-1} and shelling per cent which indicates additive gene action for these characters and improvement can be made by selection of these characters.

John *et al.* (2013) evaluated 37 advanced breeding lines and found phenotypic coefficient of variation was slightly higher than genotypic coefficient of variation for all the traits indicating presence of environmental effect for the traits. The highest genotypic coefficient of variation was observed for days to 50 % flowering (45.58%) followed by pod yield plant^{-1} (46.67%), stem rot incidence (36.51%), number of immature pods plant^{-1} (35.80%) and number of secondary branches plant^{-1} (35.75%).

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

Dewangan *et al.* (2015) investigated on 50 groundnut genotypes and significant variability was recorded for days to 50% flowering, plant height, number of branches plant^{-1}, days to maturity, number of pods plant^{-1}, number of kernels per pod, seed index (hundred seed weight), pod yield plant^{-1}, sound matured kernel (%) and shelling (%). High heritability was observed for plant

height (99%), seed index (94%) and pod yield plant^{-1} (83%). High value of genetic advance was observed for plant height (21.92).

Gupta *et al*. (2015c) and co-workers studied 60 genotypes of Virginia groundnut and evaluated during *kharif* 2013 for variability parameters. For characters like plant height, number of branches plant^{-1}, number of mature pods plant^{-1}, hundred pod weight, hundred kernel weight, kernel yield plant^{-1} and harvest index; the PCV and GCV were high. High heritability and genetic advance as per cent of mean was observed for hundred pod weight, hundred kernel weight, kernel yield plant^{-1} which indicates that these traits are mainly governed by additive gene action and there by responsive for selection for further improvement of these traits.

PCV was greater than GCV for all the characters studied by Jibrin *et al*. (2016) which indicates the influence of environment on the characters. Heritability was moderate to high except for kernel size which indicates that selection of such traits would enhance the oil content and other agronomic traits in groundnut.

Three F_2 populations derived from crosses *viz*., KCG-6 × ICGV-91114, KCG-6 ×v TG-69 and TMV-2 × ICGV-00350 were assessed by Shashikumara *et al.* (2016) and found high PCV and GCV for pod yield, kernel yield, total pods, matured pods and oil yield plant^{-1} in all the crosses indicating wide range of variability. High heritability coupled with high genetic advance of mean (GAM) was noticed for matured pods, kernel yield, oil yield, pod yield plant^{-1}, harvest index and shelling per cent in all the three crosses which indicated the involvement of additive gene action in controlling these traits.

Srivalli and Nadaf (2016) studied the genetic variability of 299 RILS for the physiological traits of groundnut under water stress. The observations revealed that RWC at 30 days after stress has moderate to high heritability coupled with high genetic advance per mean which indicates that selection is effective at later stages of stress. SLA and SCMR has low to moderate

heritability and genetic advance per mean which indicates that these characters are influenced by the environment and hence limits the selection.

Bhakal and Lal (2017) conducted variability studies for yield and its contributing traits in groundnut and reported that highest genotypic coefficient of variation was observed for plant height at 20 DAS and high heritability coupled with high genegtic advance as per cent of mean for plant height at 60 DAS which indicates predominant additive gene action.

Bhargavi *et al.* (2017a) evaluated 20 Spanish bunch groundnut genotypes for variability, heritability and genetic advance as per cent of mean for 19 characters. The results indicated that the high PCV and GCV were observed for number of mature pods plant^{-1}, high heritability coupled with high genetic advance as per cent of mean were recorded for number of mature pods plant^{-1}, biological yield plant^{-1}, pod yield plant^{-1}, pod yield per hectare, kernel yield plant^{-1}, kernel yield per hectare, hundred kernel weight and oil yield per hectare indicating the preponderance of additive gene action which might be exploited through simple selection procedures.

Chavadhari *et al*. (2017b) evaluated 70 groundnut genotypes for quantitative and yield parameters and observed high GCV for kernel yield plant^{-1} followed by the number of branches plant^{-1}, harvest index and biological yield plant^{-1}. High estimates of heritability coupled with high genetic advance as per cent of mean was observed for kernel yield plant^{-1}, hundred kernel weight, plant height, hundred pod weight, biological yield plant^{-1}, harvest index and number of branches plant^{-1} indicating the preponderance of additive gene action.

Kamdi *et al*. (2017) evaluated 18 local collections of groundnut and reported higher phenotypic coefficients of variation than genotypic coefficient of variation. They also observed small differences between genotypic and phenotypic variability for number of mature pods plant^{-1}, weight of dry haulms plant^{-1} and weight of dry pods suggesting that these characters were less influenced by the environment.

Mandal *et al.* (2017) evaluate the genetic variability for 13 characters in 19 genotypes and observed high GCV, high heritability coupled with high genetic advance as per cent of mean in case of kernel yield plant^{-1}, number of pods plant^{-1}, number of kernels plant^{-1} and hundred kernel weight indicating the role of additive gene in expressing these traits and effectiveness of selection.

Yusuf *et al.* (2017a) evaluated 16 groundnut genotypes for 12 quantitative characters and observed high to moderate estimates of GCV and PCV for all the characters except for shelling per cent and number of secondary branches which indicates that these characters can be selected for yield improvement**.**

Nayak (2018) studied genetic variability, heritability and genetic advance among 20 groundnut genotypes during *rabi* 2016-2017 and observed high GCV, heritability and genetic advance per mean for characters like hundred kernel weight, hundred pod weight, dry pod yield and these are governed by additive gene action. Traits like shelling per cent, sound mature kernel and final plant stand shows moderate heritability and high genetic advance which shows predominant additive gene action.

Hampannavar *et al.* (2018b) studied genetic parameters like variability, heritability and genetic advance as per cent of mean for 13 different characters among 144 groundnut genotypes during *Kharif* 2015. The traits plant height, number of primary branches plant^{-1}, number of mature and immature pods plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, haulm yield plant^{-1} and dry pod yield plant^{-1} had high GCV, PCV, heritability and genetic advance as the per cent of mean which indicates additive gene action and thereby improvement can be effectively done by phenotypic selection for these characters.

Sab *et al.* (2018) studied genetic variation and association for nine characters for 34 advanced breeding lines of groundnut genotypes for WUE and yield traits. High PCV and GCV were observed for pod yield plant^{-1},

kernel yield plant^{-1} and number of pods plant^{-1} which indicates that variability is present between these characters. High heritability and high genetic advance per mean was recorded for SLA and yield related traits. High heritability and low genetic advance per mean was recorded for SCMR, days to first flowering and primary branches plant^{-1} which indicates additive and non-additive gene action. The observations revealed that SCMR and yield related traits are strongly correlated with pod yield plant^{-1} while SLA has negative correlation with pod yield plant^{-1}.

Nagaveni and Khan (2019a) assessed 49 terminal drought groundnut genotypes and recorded high PCV and GCV for immature pods plant^{-1}, dry pod yield and haulms yield under normal and controlled conditions. They have also observed high heritability coupled with high genetic advance as per cent of mean for plant height, primary branches plant^{-1}, mature pods plant^{-1}, haulms yield, dry pod yield, hundred kernel weight, SLA, SPAD chlorophyll meter reading and harvest index indicating that these traits are mainly governed by additive gene action.

Shinde *et al.* (2019) studied variability and diversity studies among F_5 progenies of eight crosses of groundnut and reported that PCV was higher than GCV for all the characters and higher GCV and PCV was observed for number of branches plant^{-1} followed by number of immature pods plant^{-1}, number of mature pods plant^{-1} and dry pod yield plant^{-1}.

Veer (2021) investigated on 14 groundnut genotypes and evaluated for 12 quantitative characters. Maximum GCV and PCV was recorded for kernel yield (18.45 q/ha). Maximum heritability was recorded for plant height (31.97 cm) and high genetic advance as per cent of mean for field emergence (235.5%). Hence these characters can be selected for further improvement in the future.

Mitra *et al.* (2021) investigated on 31 groundnut genotypes and observed high GCV and high PCV for number of pods plant^{-1}, secondary branches, kernel width, and pod yield. Pod length, pod yield and number of

pods plant^{-1} showed high heritability and high genetic advance which indicates additive gene action for these traits.

2.2 GENETIC DIVERGENCE

Success of plant breeding programme depends largely on the choice of appropriate parents. It is expected that the utilization of divergent parents in hybridization results in promising recombinants. Genetic improvement mainly depends upon the amount of genetic variability present in the population. Selection of parents based on Mahalanobis D^2 statistics (1936) is more reliable method as the requisite knowledge in respect of a mass of characters is available prior to the crossing programme.

A brief resume of work done on genetic diversity in groundnut is presented here under:

Dolma *et al.* (2010a) evaluated 33 genotypes of groundnut from different geographical regions and grouped them into six clusters. The inter cluster distance was maximum between cluster IV and V followed by cluster III and V. Based on inter cluster distance and *per se* performance the genotypes from these clusters are suggested for inclusion in the hybridization programme to evolve high yielding and late leaf spot resistant genotypes.

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

Nikam and Thaware (2010) studied genetic divergence among 38 genotypes of groundnut by using Mahalanobis D^2 statistics. The genotypes were grouped into nine clusters. The maximum inter-cluster distance was

observed between cluster VI and VII, followed by cluster II and IX indicated that these groups of genotypes were highly divergent from each other. The genotype in above clusters revealed substantial differences in the means for important yield contributing characters and were found to be potential parents based on cluster mean and genetic diversity.

Venkateswarlu *et al*. (2011) studied 74 groundnut genotypes and grouped them into 12 clusters based on D^2 analysis and suggested that there is no relationship between geographical distribution and genetic diversity. They also reported that the characters *viz.,* hundred kernel weight, shelling per cent and harvest index contributed maximum towards genetic divergence.

Suneetha *et al.* (2013) carried out diversity analysis for 29 released and pre-released groundnut genotypes during *kharif* and classified into nine clusters. Intra- cluster D^2 values and distances (D) were high within the group V *i.e.,* 26.83 and 5.18 respectively. Inter-cluster average D^2 values ranged from 11.02 (between group IV and VIII) to 57.76 (between group V and IX). Hence the genotypes from these clusters can be selected for obtaining better transgressive segregants.

Yadav *et al.* (2014) evaluated 60 genotypes of groundnut for the genetic variability and genetic diversity by considering D^2 analysis and grouped them into 12 clusters. They found that the maximum inter-cluster distance between clusters III and X carrying one and two genotypes from each cluster and minimum inter cluster distance was observed between clusters VII and XI.

Gupta *et al.* (2015b) evaluated 60 groundnut genotypes and grouped them into thirteen clusters. They observed that maximum inter-cluster distance (D=36.51) was observed between clusters III and V followed by clusters IV and V (D=32.67) and II and IV (D=24.21) indicating that the genotypes from these clusters can be considered for obtaining better segregants in the future breeding programmes.

Vivekananda *et al.* (2015) classified 31 genotypes into seven clusters in which cluster I contains largest number of genotypes. Maximum intercluster distance is between cluster I and cluster VI. Based on the cluster distances and cluster means the genotypes from cluster I, III, V and VI could be selected for hybridization programme.

Bhakal and Lal (2015) studied genetic divergence using D^2 statistics of 40 genotypes of groundnut of different geographic origin for 11 characters. The cluster VI was the largest consisting of 12 genotypes followed by cluster V which comprises of seven genotypes, cluster I and cluster VII have six genotypes each, cluster III, II, and IV comprises of four, three and two genotypes respectively. The diversity among the genotypes is measured by intra-cluster and inter-cluster distance and the genotypes that present in diverse clusters can be used as promising parents for hybridization programme.

Vasanthi *et al*. (2015) evaluated 29 groundnut genotypes and grouped into eight clusters based on ten physiological characters *viz.*, leaf area duration, leaf area index, crop growth rate, net assimilation rate, specific leaf area, SCMR, harvest index and pod yield plant^{-1} through D^2 statistics. The highest inter-cluster distance was recorded between cluster VI (Tirupati-4 and K^{-1}34) and VII (TCGS-647). Based on intra and inter- cluster distances and cluster means, parents were identified for further breeding programmes for isolation of useful transgressive segregants.

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

By conducting genetic diversity studies Raghuwanshi *et al.* (2016) grouped 50 groundnut genotypes into 27 clusters using D^2 analysis. The

maximum inter-cluster distance was found between cluster XXVII and XVIII followed by cluster XXVI and XVIII, XXVII and XXIII indicating that genotypes from these clusters could be used as ideal parents for improvement in groundnut.

Chavadhari *et al.* (2017c) grouped 70 groundnut genotypes into eleven clusters based on Mahalanobis D^2 statistics where the maximum inter-cluster distance was observed between clusters IV and XI (D=239.0) followed by clusters VIII and IX (D=235.65) and clusters II and VIII (D=228.02) indicating that the genotypes of these groups are more divergent from each other and the genotypes from these clusters can be used as ideal parents for further improvement.

Fifty groundnut 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 D^2 statistics. SCMR at 60 DAS, protein content, harvest index and hundred kernel weight accounted for 80.98 per cent of the total genetic divergence indicating their importance in the choice of parents for hybridization programme.

Reddy *et al.* (2017) investigated on 30 drought tolerant groundnut genotypes and classified them into six clusters based on Mahalanobis D^2 statistics and observed that maximum diversity between genotypes of cluster I and VI and maximum intra-cluster distance for cluster IV which indicates high variability within this cluster and the genotypes from these clusters could be selected for hybridization programme.

Waghmode *et al.* (2017) estimated the D^2 values and observed the presence of considerable amount of genetic diversity among the 121 groundnut genotypes. Among the clusters, maximum intra cluster distance was recorded within Cluster VII followed by cluster VI and cluster I. The maximum inter cluster distance was observed between cluster VI and VII

followed by cluster II and VII, cluster III and VII indicating wide divergence between these clusters. Variance of cluster means revealed that dry pod yield plant^{-1}, number of kernels per pod, shelling per cent, hundred kernel weight and number of pods plant^{-1} were the main characteristics contributing to divergence. Based on intra and inter cluster distances, cluster means and *per se* performance of genotypes *viz.*, Pratap Mungphali- 2, TGLPS-3, M-III, TG-37 A, TKG-Bold, M-548, R2001^{-1} and TMV (GN)$^{-1}$3 were recommended for future breeding programme.

Genetic diversity studies by Ganvit *et al.* (2018) using Mahalanobis D^2 analysis revealed that maximum contribution to total divergence was by hundred pod weight followed by shelling per cent, kernel yield plant^{-1}, hundred kernel weight, plant height and days to 50% flowering. Based on maximum genetic distance, they advised that crossing of genotypes from cluster X and IX, IX with II and cluster VIII with II which may lead to broad spectrum of favourable genetic variability for yield improvement in groundnut.

Hampannavar and Khan (2018a) measured genetic diversity by D^2 statistics among 144 genotypes for 13 characters. These genotypes were grouped into 16 clusters. The maximum inter-cluster distance was observed between the cluster-XI and XVI followed by cluster IV and XVI. Thereby crossing between these two clusters helps in the production of better recombinants or transgressive segregants.

Nagaveni and Khan (2019b) conducted genetic diversity experiments by using D^2 statistics of 49 drought tolerant groundnut genotypes and classified them into seven clusters. Cluster III consists of maximum number of genotypes followed by Cluster I and Cluster II. The genotypes from the most diverse clusters could be used for the exploitation of heterosis in further crop improvement programmes.

Mitra *et al.* (2021) conducted an experiment with thirty one groundnut accessions and grouped them into thirteen clusters based on D^2 statistics. The

intercluster distance is maximum between the clusters X (two accessions) and XII (one accession) which indicates that the crossing between these clusters helps in the production of transgressive segregants or better recombinants.

2.3 CHARACTER ASSOCIATION

Yield is a complex quantitative character governed by a large number of genes and is greatly affected by environment. Hence, the selection of superior genotypes based on yield alone will not give a fruitful result. Association of yield components and yield thus assumed special importance as the basis for selecting desired strains. Genetic correlation between different characters often arises due to its tight linkage or pleiotropy. Correlation coefficient reveals the type, nature and magnitude of correlation between any pair of characters. Phenotypic correlation is the association between two characters which can be directly observed and 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 gene action.

A brief review of literature on the association of characters in groundnut is presented here under.

Abraham (1990) studied 42 bunch varieties of groundnut and observed that kernel yield had significant positive correlation with pods plant^{-1}, kernels plant^{-1}, hundred kernel weight and shelling per cent.

Jayalakshmi and Reddy (2003) estimated that harvest index, mature pod number plant^{-1} and specific leaf area were associated with each other and also kernel yield which indicated that selection for these traits would be helpful in improving the yield of groundnut.

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

Meta and Monpara (2010) studied correlation for 50 elite genotypes and reported that pod yield plant^{-1} has strong positive association with kernel yield plant^{-1}, number of pods plant^{-1}, shelling out turn and oil content that indicates that these characters significantly increase the yield.

Hiremath *et al.* (2011) conducted correlation studies and observed that number of primary branches, pod weight plant^{-1}, hundred kernel weight, sound mature kernel per cent and oil yield showed significant positive association with pod plant^{-1}.

Vekariya *et al.* (2011a) revealed that the magnitudes of genotypic correlation coefficients were higher as compared to the corresponding phenotypic correlation coefficients. The pod yield plant^{-1} had highly significant and positive correlations at phenotypic levels with number of mature pods plant^{-1}, hundred pod weight, hundred kernel weight, kernel yield plant^{-1}, biological yield plant^{-1} and harvest index.

Zaman *et al.* (2011) observed high significant positive association of seed yield with nut size, number of nuts plant^{-1}, kernel size and days to 50 % flowering.

Babariya and Dobariya (2012) conducted correlation studies by using hundred genotypes and revealed that the traits like days to maturity, plant height, number of pods plant^{-1}, kernel yield plant^{-1}, number of mature pods plant^{-1}, hundred kernel weight, biological yield plant^{-1} and harvest index have strong positive correlation with pod yield.

Narasimhulu *et al.* (2012) recorded that pod yield plant^{-1} had significant positive association with kernel yield plant^{-1}, shelling per cent and sound mature kernel per cent at both genotypic and phenotypic levels.

Makinde and Ariyo (2013) studied correlation analysis in 22 genotypes for ten characters under two environments. They found that number of pods plant^{-1} showed significant positive correlation with yield plant^{-1} in both environments and also had the largest direct positive effect on yield plant^{-1}

(0.66 and 0.70). They observed significant genotype and genotype × environment interactions on yield plant^{-1}.

Alam (2014) conducted correlation studies in 45 groundnut genotypes for pod yield and its yield components and observed that genotypic correlation coefficients are higher than phenotypic correlation coefficients which indicates that there is strong inherent association between these traits. Secondary branches plant^{-1}, harvest index, hundred pod weight, hundred kernel weight, pod size, disease incidence and canopy temperature have strong positive association with pod yield.

Rao *et al.* (2014) studied inter-relationships among 50 groundnut genotypes and revealed significant positive correlation of dry pod yield with kernel yield, number of pods plant^{-1}, hundred kernel weight and dry haulms yield.

Gupta *et al.* (2015c) carried out correlation studies in 60 genotypes and revealed that pod yield plant^{-1} had high significant and positive correlation with number of mature pods plant^{-1}, hundred pod weight, shelling out turn, kernel yield plant^{-1}, biological yield plant^{-1} and harvest index.

Manjubhargavi *et al.* (2015) carried out correlation analysis and revealed that kernel yield plant^{-1} was significantly and positively correlated with days to 50% flowering, primary branches plant^{-1}, total number of pods plant^{-1}, number of mature pods plant^{-1}, pod yield plant^{-1}, harvest index, hundred seed weight and protein content.

Prabhu *et al*. (2015) studied that genetic association plays a significant role to study the interrelationship and relative contribution of different characters towards crop improvement. Correlation analysis with yield and other yield components were carried out to identify the selection indices in BC_2F_1 generation of two crosses *viz.*, CO-7 X GPBD-4 and CO-7 X COG-0437. From this study of correlation analysis, selection can be done based on number of pods plant^{-1}, hundred pod weight, hundred kernel weight and shell weight for improving pod yield and kernel yield plant^{-1} in groundnut.

Character association studies was done by Kumara *et al.* (2015) among fourteen characters in F_2 segregating generations of three groundnut crosses and revealed that SLA had significant negative correlation with SCMR, total pods plant^{-1}, matured pods plant^{-1}, kernel yield and pod yield. They have also observed significant positive correlation of traits SCMR, matured pods plant^{-1}, harvest index, kernel yield, oil yield and SMK per cent with pod yield.

Six F_2 crosses of groundnut genotypes were evaluated for character association among yield attributing and physiological traits by Vinutha *et al.* (2015) and revealed high association of pod and kernel yield with number of pods plant^{-1} and sound mature kernel at phenotypic level. The physiological traits SLA and SCMR showed significant negative correlation with each other in all the crosses except in cross GKVK-5 × GPBD-4.

Aparna *et al*. (2017) carried out correlation for pod yield and its contributing characters and reported that pod yield plant^{-1} was significantly positively correlated with harvest index, hundred kernel weight, kernel yield plant^{-1}, number of mature pods plant^{-1}, total number of pods plant^{-1}, shelling per cent and number of pegs plant^{-1}.

Correlation and path coefficient analysis for yield and its contributing traits in groundnut germplasm was studied by Bhakal and Lal (2017). The phenotypic and genotypic correlation analysis revealed that plant height at 40 DAS and hundred kernel weight was significantly and positively correlated with pod yield plant^{-1}. They also observed that the highest positive direct effect on pod yield plant^{-1} was exerted by kernel yield and kernel uniformity.

Bhargavi *et al.* (2017b) carried out correlation studies for pod yield and its component characters in 10 genotypes of Virginia bunch groundnut and the results obtained revealed that hundred kernel weight and kernel yield plant^{-1} were found to have significant influence on pod yield. Hence, simultaneous selection based on hundred kernel weight and kernel yield plant^{-1} seems to be more promising in improving the pod yield in Virginia bunch groundnut. On contrary, negative significant association of pod yield with SCMR at 60 DAS,

SCMR at 70 DAS and SCMR at maturity was observed by them at genotypic level.

Hugar and Savithramma (2017) studied 230 RILs of cross NRCG 12568 × NRCG^{-1}2326 along with two checks TMV-2 and KCG-2 recorded that pod yield plant^{-1} was significantly and positively associated with primary branches plant^{-1}, SCMR, pods plant^{-1} and kernel yield plant^{-1} whereas it was negatively associated with SLA and SMK per cent.

Mandal *et al.* (2017) conducted correlation studies and found that genotypic correlation was found more significant than phenotypic correlation indicating that there was prevalence of environmental interaction and strong association between characters genetically and there was some scope for selection of better yielding types. Plant height, number of pods plant^{-1}, number of kernels plant^{-1}, shelling per cent, SMK, harvest index reflected significantly positive correlation with the number of pods plant^{-1} and number of kernels plant^{-1} both at genotypic and phenotypic levels. So these characters might be considered for selection of better yielding genotypes.

Studies on character association for kernel yield and its component characters in six parents and their fifteen F_1 crosses in groundnut by Reddy *et al.* (2017) revealed higher genotypic correlations than the phenotypic correlations indicating strong inherent association between the two corresponding characters and selection for these characters might be rewarding. They also observed that the characters pod yield plant^{-1}, mature pods plant^{-1}, hundred kernel weight, pods plant^{-1}, pegs plant^{-1}, harvest index and shelling per cent had highly significant and positive association with kernel yield plant^{-1} and also exhibited significant positive inter-correlations among themselves.

Character association studies by Yusuf *et al.* (2017b) in sixteen groundnut genotypes for twelve characters and revealed that the kernel yield per hectare showed positive and significant genetic correlation with pod weight plant^{-1}, seed weight plant^{-1} and hundred kernel weight. They also

reported that kernel yield was negatively correlated with number of kernels per pod at genotypic, environmental and phenotypic levels.

Nayak (2018) conducted correlation studies for fifteen groundnut genotypes and revealed that hundred pod weight, sound mature kernel and hundred kernel weight had significant positive association with pod yield plant^{-1} and will significantly contribute to the pod yield plant^{-1}.

Hampannavar *et al.* (2018b) conducted correlation studies on 144 groundnut genotypes and observed that kernel yield plant^{-1}, mature pods plant^{-1}, sound mature kernel and haulms yield plant^{-1} had significant positive correlation with dry pod yield at both phenotypic and genotypic level but hundred kernel weight showed the significant positive correlation with pod yield only at genotypic level. They also observed that the traits like days to 50% flowering, days to maturity, number of immature pods plant^{-1} and shelling per cent had negative correlation with dry pod yield plant^{-1} at both phenotypic and genotypic level, whereas shelling per cent had significant positive correlation at phenotypic level.

Rathod and Toprope (2018) conducted correlation studies in 18 groundnut genotypes and inferred that pod yield plant^{-1} exhibited positive significant association with number of pods plant^{-1}, total sugar, kernel yield, non-reducing sugar, 100 kernel weight, SCMR, harvest index, oil content and shelling per cent.

Sab *et al.* (2018) studied 34 advanced breeding lines of groundnut genotypes for WUE and yield traits. The observations revealed that SCMR and yield related traits are strongly correlated with pod yield plant^{-1} while SLA has negative correlation with pod yield plant^{-1}.

Correlation analysis by Kumar *et al.* (2019) for pod yield and quality traits in 20 genotypes of groundnut revealed that pod yield had significant and highly positive correlations with plant height, primary branches plant^{-1}, pods

plant^{-1}, hundred pod weight, hundred sound mature kernel, kernel yield and harvest index, while negative and significant for days to 50% flowering.

Kumari and Sashidaran (2020) conducted correlation studies in 50 groundnut genotypes and revealed that the kernel yield has strong positive correlation with number of mature pods plant^{-1}, pod yield plant^{-1} and hundred pods mass which indicates that these traits can be selected for improvement of crop yield.

2.4 PATH COEFFICIENT ANALYSIS

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

A brief review of literature on the path coefficient analysis in groundnut is presented here under.

Korat *et al*. (2010) tested 80 bunch groundnut genotypes and reported highest positive direct effect of biological yield plant^{-1} and harvest index on pod yield as well as positive indirect effect of hundred kernel weight contributed *via* biological yield plant^{-1} and harvest index on pod yield.

Zaman *et al*. (2011) revealed high positive direct effect of number of mature nuts plant^{-1} followed by kernel size, shelling per cent, days to 50% flowering and days to maturity on seed yield per hectare. It was also found that branches plant^{-1}, plant height, nuts plant^{-1}, nut size, kernel size, days to

50% flowering, shelling per cent and days to maturity were identified as important characters which could be used in selection for yield.

Kumar *et al*. (2012) evaluated 50 genotypes of groundnut and revealed that high direct effects of kernel yield plant^{-1} and harvest index on pod yield were identified as important characters which could be used in selection for rapid improvement in pod yield of groundnut.

Path analysis studies conducted by Shoba *et al.* (2012) in F_3 generation for three crosses (TMV-2 × COG-0437, TMV-2 × COG-0438 and TMV-2 × ICGV-97150) of groundnut indicated that pod yield plant^{-1} exerted maximum positive direct effect on kernel yield plant^{-1} followed by shelling per cent and hundred kernel weight in all the three crosses. The traits *viz.*, plant height (for the cross TMV-2 × ICGV- 97150), number of branches plant^{-1} (all the three crosses) and number of pods plant^{-1} (for the cross TMV- 2 × ICGV-97150) indicated negative direct effect on kernel yield plant^{-1}.

Alam (2014) carried out path analysis for pod yield and its yield component characters in 45 genotypes of groundnut and indicated that harvest index had highest positive direct effect on pod yield followed by secondary branches plant^{-1} and primary branches plant^{-1}, while SPAD meter reading exerted the maximum negative direct effect on pod yield followed by pod index. They also noticed that high indirect contribution was observed *via* pod index on pod yield.

Rao *et al.* (2014) tested 50 genotypes of groundnut and reported that number of pods plant^{-1} and hundred kernel weight contributed high positive direct effect on pod yield.

John and Reddy (2015) reported that pod yield plant^{-1} had high positive direct effect with kernel yield plant^{-1} followed by days to 50% flowering and hundred kernel weight. They also found that the direct effects of dry haulms yield plant^{-1}, protein per cent, days to maturity, number of well-filled mature pods plant^{-1}, number of primary branches plant^{-1} and oil per cent were found

to be positive with kernel yield plant^{-1} which had maximum positive direct effect on pod yield plant^{-1} indicating the importance of kernel yield in determining the pod yield.

Patil *et al*. (2015) evaluated 49 groundnut genotypes and observed that the number of mature pods plant^{-1} had high positive direct effect on pod yield plant^{-1}. Hence, they opined that branches plant^{-1}, height of main axis, pods plant^{-1}, kernel weight plant^{-1}, days to 50% flowering, shelling per cent and days to maturity were identified as important characters which could be used in selection for yield.

Rasheed *et al*. (2015) evaluated 13 diverse origin groundnut genotypes for path analysis and revealed that there is a maximum positive direct contribution towards pod yield by pod length, hundred kernel weight and sound mature kernel per cent. Hence, selection for these characters would help in rapid improvement in pod yield plant^{-1}.

Jain *et al*. (2016) carried out path analysis of yield and its components in a study involving 24 genotypes of groundnut and reported high direct effects of kernel yield plant^{-1}, plant height and matured pods plant^{-1} on pod yield plant^{-1}. Hence, selection for these characters would help in rapid improvement in pod yield plant^{-1}.

Path coefficient analysis by Pranesh *et al.* (2017) in 64 M_3 mutants of groundnut genotypes revealed that pod yield plant^{-1}, hundred seed weight, plant spread and plant dry weight had high direct positive effect on seed yield and pod yield had highest indirect effect on seed yield.

Reddy *et al.* (2017) carried out path analysis for kernel yield and its component characters in six parents and their fifteen F_1 crosses in groundnut and inferred that pod yield exerted the highest positive direct effect on kernel yield followed by shelling per cent and pegs plant^{-1}. They also observed the positive indirect effects of pod yield on kernel yield through days to maturity,

plant height, pegs plant^{-1}, pods plant^{-1}, mature pods plant^{-1}, harvest index and hundred kernel weight.

Hampannavar *et al.* (2018b) evaluated 144 groundnut genotypes for path analysis and revealed that kernel yield plant^{-1} had highest direct effect on dry pod yield. The traits like number of mature pods plant^{-1}, sound mature kernel and haulms yield had the high and positive indirect effect on dry pod yield *via* kernel yield.

Path analysis of 30 groundnut genotypes by Kadam *et al.* (2018) revealed that characters like dry biomass, fresh fodder yield plant^{-1} exhibited high direct effect as well as strong association with dry pod yield plant^{-1} indicating true and perfect relationship between them.

Rathod and Toprope (2018) studied path analysis of 18 Spanish bunch groundnut genotypes and revealed that total sugar, kernel yield, 100 kernel weight, SCMR, days to maturity and oil content exerted the positive direct effect on pod yield whereas, shelling per cent and harvest index had maximum indirect effects on pod yield plant^{-1}.

John *et al.* (2019) reported that pod yield plant^{-1} had high positive direct effect with number of primary branches plant^{-1} followed by sound mature kernel per cent, hundred kernel weight and number of well filled and mature pods plant^{-1}. Hence direct selection for these traits would be effective.

Path analysis of 20 groundnut genotypes by Kumar *et al.* (2019) revealed that hundred sound mature kernel and pods plant^{-1} had high positive direct effect and also highly significant positive correlation with pod yield. Therefore, they suggested that selection for these traits might be helpful in identifying genotypes with high pod yield in groundnut.

Mahmoud *et al.* (2020) evaluated 16 groundnut genotypes for path analysis and observed that the maximum positive indirect effects were obtained by pods weight plant^{-1}, followed by number of pods plant^{-1} indicating that the indirect selection for pod yields through these traits would

be effective for groundnut improvement. The second order path analysis showed that seeds weight plant^{-1} had the considerable positive direct and indirect effect towards number of pods plant^{-1} and pods weight plant^{-1}.

Mohapatra and Khan (2020) studied four F_3 crosses of groundnut genotypes and observed that high positive direct effect by kernel yield plant^{-1} in two crosses *viz.,* Kadri-9 × GPBD-4 and ICGV-00351 × Sunoleic-95R. Indirect effects of kernel yield plant^{-1} on pod yield through number of mature pods plant^{-1}, haulm yield plant^{-1} and hundred kernel weight in cross Kadri-9 × GPBD-4 and ICGV-00351 × Sunoleic-95R and indirect effects of protein content on pod yield through plant height, number of mature pods plant^{-1}, kernel yield plant^{-1} and shelling per cent in cross ICGV-00351 × GPBD-4 and Kadri-9 × Sunoleic-95R were important contributing traits.

Chapter - III

Material and Methods

Chapter III

MATERIAL AND METHODS

The experimental material used and methods followed pertaining to the present investigation entitled “Genetic analysis of yield, yield attributes and water use efficiency related traits in groundnut (*Arachis hypogaea* L.)” are briefly described here under.

3.1 LOCATION OF THE EXPERIMENTAL SITE

The field experiment was conducted at dry land farm of S. V. Agricultural College, Tirupati during *rabi* 2021-2022, located at an altitude of 182.9 m above mean sea level, 13°N latitude and 79°E longitude and situated in Southern agro-climatic zone of Andhra Pradesh.

3.2 MATERIAL

The materials used in the present study consisted of 36 genotypes (26 advanced breeding lines + 10 released varieties) of groundnut. The materials were made available for the study by the Principal Scientist (Groundnut breeding), Regional Agricultural Research Station (RARS), Tirupati, Andhra Pradesh. The list of 36 genotypes of groundnut and their pedigree are furnished in Table 3.1.

3.3 METHOD

3.3.1 Field Layout

Thirty six genotypes of groundnut were sown during *rabi* 2021-2022 in a Randomized Block Design (RBD) with three replications (plate 1). All the entries were sown on 10th December, 2021. In each replication, every genotype was sown in three rows of 3m length with a spacing of 22.5 cm between the rows and 10 cm between the plants within the row.

Table 3.1. List of 36 genotypes of groundnut (26 advanced breeding lines + 10 released varieties) and their pedigree

S. No.	Entry	Pedigree
1	TCGS-1694	K-6 x ICG(FDRS)79
2	TCGS-1798	ICGV-06188 x TCGS-1043
3	TCGS-2004	TCGS-1157 x TCGS-1043
4	TCGS-2038	TCGS-1157 x TCGS-1043
5	TCGS-2039	TCGS-1157 x TCGS-1073
6	TCGS-2040	TCGS-1157 x TCGS-1073
7	TCGS-2041	TCGS-1157 x TCGS-1043
8	TCGS-2044	TCGS-1157 x TCGS-1073
9	TCGS-2049	TCGS-1157 x TCGS-1073
10	TCGS-2051	TCGS-1157 x TCGS-1073
11	TCGS-2052	TCGS-1157 x TCGS-1043
12	TCGS-2053	TCGS-1157 x TCGS-1073
13	TCGS-2055	TCGS-1157 x TCGS-1073
14	TCGS-2057	TCGS-1157 x TCGS-1043
15	TCGS-2060	TCGS-1157 x TCGS-1043
16	TCGS-2068	TCGS-1157 x TCGS-1043
17	TCGS-2217	Dharani x Narayani
18	TCGS-2219	Dharani x ICGV-06100
19	TCGS-2223	Dharani x ICGV-06188
20	TCGS-2227	K-6 x ICG (FDRS) 79
21	TCGS-2229	K-6 x ICGV-06100
22	TCGS-2230	K-6 x ICGV-06100
23	TCGS-2233	Dharani x ICGV-06188
24	TCGS-2235	Dharani x ICGV-06045
25	TCGS-2278	K-6 x ICG (FDRS) 79
26	TCGS-2317	TAG-24 x Dharani
27	Dharani	VRI-2 x TCGP-6
28	Dheeraj	Narayani x JAL 30
29	Greeshma	TIR 46 x JUG 37
30	K-6	JL-24 x Ah 316/S
31	K-9	Kadiri 4 x Vemana
32	Narayani	JL-24 x Ah 316/S
33	Rohini	Tirupati-4 x TIR-45
34	TAG-24	TGS-2 x TGE-1
35	Tirupati-1	E.C-106983/3
36	Tirupati-4	JL-24 x Ah 316/S

Plate 3.1. Field view of the experimental plot

3.3.2 Crop Husbandry

The field was ploughed and harrowed until a fine tilth of soil was obtained. FYM @ 10 t ha^{-1} was applied at the time of field preparation. Seed treatment was done with Bavistin @ 3g kg^{-1}. The crop was raised under irrigated conditions and recommended dose of chemical fertilizers at the rate of 30 kg N, 40 kg P_2O_5 and 50 kg K_2O ha^{-1} in the form of urea, single super phosphate, muriate of potash and 500 kg of gypsum ha^{-1} was applied at peak flowering stage. Cultural practices like weeding were followed to maintain good crop growth apart from need based plant protection measures adopted during the crop season for controlling diseases and pests.

3.3.3 Data Recording

Observations were recorded for all the genotypes separately on randomly chosen five competitive plants in each genotype in each replication for all the characters except days to 50% flowering and days to maturity which were recorded on plot basis. The details of the data recorded were as follows.

3.3.3.1 Morphological, yield and yield attributing traits

3.3.3.1.1 Days to 50% flowering

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

3.3.3.1.2 Days to maturity

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

3.3.3.1.3 Plant height (cm)

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

3.3.3.1.4 Number of primary branches plant^{-1}

Total number of primary branches originating from the main axis were counted at the time of harvest and recorded.

3.3.3.1.5 Number of secondary branches plant^{-1}

Total number of secondary branches originating from the primary branches were counted at the time of harvest and recorded.

3.3.3.1.6 Kernel yield plant^{-1} (g)

The kernels obtained from each individual plant were weighed in grams using electronic top pan balance (precision of 0.001 g).

3.3.3.1.7 Hundred kernel weight (g)

The weight of randomly selected hundred kernels from each genotype for each replication was recorded as hundred kernel weight using electronic top pan balance (precision of 0.001 g).

3.3.3.1.8 Shelling per cent (%)

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

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

3.3.3.1.9 Sound mature kernel per cent (SMK) (%)

The per cent of good, sound mature kernels separated from hulls for each genotype in each replication were recorded.

Sound mature kernel per cent was calculated using the following formula

$$\text{SMK}(\%) = \frac{\text{Weight of sound mature kernels } (\text{g})}{\text{Weight of total kernels } (\text{g})} \times 100$$

3.3.3.1.10 Harvest index (%)

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

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

3.3.3.1.11 Pod yield plant^{-1} (g)

The weight of all those pods obtained from each individual plant was recorded in grams with the help of electronic top pan balance (precision of 0.001 g).

3.3.3.2 Water use efficiency (WUE) related traits

Data for the following characters were recorded on the sampled plants.

3.3.3.2.1 SPAD chlorophyll meter reading (SCMR) at 60 DAS

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

3.3.3.2.2 Specific leaf area (SLA) (cm^2 g^{-1}) at 60 DAS

The leaves were collected from five randomly selected plants from each genotype in each replication at 60 DAS and leaf area was estimated using Leaf area meter (LICOR model-3hundred). Dry weight was recorded by keeping the samples in hot air oven at 80^{0}C for atleast 48 hours and used for estimation of specific leaf area using the following formula

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

3.3.3.2.3 Relative water content (%)

Relative water content was measured according to the method described by Barrs and Weatherley (1962). Relative water content is a reliable drought avoidance parameter adopted by plants. Leaflets were collected from the third leaf from the top of the main axis of each genotype and were soaked in water for 6 hours and were allowed to gain turgidity. Turgid weights were recorded and dried in hot air oven at 80^0C for atleast 48 hours to record dry weight. RWC was estimated and expressed in per cent using the formula

$$\text{RWC}=\frac{(\text{fresh weight - dry weight})}{(\text{turgid weight - dry weight})}\times 100$$

3.4 STATISTICAL ANALYSIS

The treatment means for each character over three replications were subjected to the following statistical analysis. The statistical package used was INDOSTAT.

3.4.1 Analysis of Variance

The data collected on individual characters were subjected to method of analysis of variance commonly applicable to randomized block design as per mathematical model proposed by Panse and Sukhatme (1961).

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

Where,

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

μ = General mean

g_i = Effect of ith genotype

γ_j = Effect of jth replication

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

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

Source of variation	Degrees of freedom	Sum of squares	Mean sum of squares	Expected Mean sum of squares	F ratio
Replications	(r-1)	RSS	Mr	-	Mr/Me
Genotypes	(g-1)	GSS	Mg	$\sigma_e^2 + r\sigma_g^2$	Mg/Me
Error	(r-1) (g-1)	ESS	Me	σ_e^2	-
Total	(rg-1)	TSS			

Where,

r = Number of replications

g = Number of genotypes

Mr = Mean sum of squares due to replications

Mg = Mean sum of squares due to genotypes

Me = Mean sum of squares due to error.

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

3.4.2 Estimation of Genetic parameters

3.4.2.1 Variance

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

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

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

σ_g^2 = Genotypic variance

σ_e^2 = Error variance

3.4.2.2 Genotypic and phenotypic coefficient of variation

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

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

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

Where, σ_g, 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

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

$$h^2_{(bs)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

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

σ_g^2 = Genotypic variance

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

σ_e^2 = Environmental variance

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

Less than 30 % - Low

30 – 60 % - Moderate

More than 60% - High

3.4.2.4 Genetic advance

Genetic advance refers to the expected genetic gain or improvement in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates, the genetic advance was estimated by the following formula given by Johnson *et al.* (1955a).

$$GA = K \sigma_p h^2_{(bs)}$$

Where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

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

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

3.4.2.5 Genetic advance as per cent of mean (GAM)

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

$$GAM = \frac{GA}{\overline{X}} x\ 100$$

Where,

GA = Genetic advance

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

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

Less than 10% - Low

10 – 20 % - Moderate

More than 20% - High

3.4.3 Genetic Divergence Analysis:

3.4.3.1 Mahalanobis D^2 analysis

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

3.4.3.1.1 Test of significance

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

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

$$\text{`}\Lambda\text{'} = \frac{(E)}{(E+V)}$$

Where,

Λ = Wilk's criterion

(E) = Determinant of error matrix and

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

The significance of ' Λ ' was tested by

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

Where,

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

n = Degrees of freedom of error + varieties

p = Number of characters

q = Number of genotypes – 1

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

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

3.4.3.1.2 Transformation of correlated variables

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

3.4.3.1.3 Computation of D^2 values

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

$$D^2_{ij} = p\sum_{t=1}\left(\bar{Y}_{it} - \bar{Y}_{jt}\right)^2$$

Where,

$\bar{Y}_{it}$ *is* uncorrelated mean value of *i*th genotype for character 't'

$\bar{Y}_{jt}$ is uncorrelated mean value of *j*th genotype for character 't'

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

3.4.3.1.4 Testing the significance of D^2 values

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

3.4.3.1.5 Grouping of genotypes into various clusters

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

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

3.4.3.1.6 Average intra cluster distance

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

$$\frac{\sum D_i^2}{n}$$

Where,

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

3.4.3.1.7 Average inter cluster distance

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

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

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

3.4.3.1.8 Cluster diagram

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

3.4.3.1.9 Contribution of individual characters towards divergence

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

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

Where,

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

M = All possible combinations of number of genotypic pairs

3.4.4. Character association analysis

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

3.4.4.1 Genotypic correlation coefficient (r_g)

$$r_g\,(x_i x_j) = \frac{Cov_g\left(x_i x_j\right)}{\sqrt{V_g\left(x_i\right).V_g\left(x_j\right)}}$$

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 coefficient (r_p)

$$r_p\,(x_i x_j) = \frac{Cov_p\left(x_i x_j\right)}{\sqrt{V_p\left(x_i\right).V_p\left(x_j\right)}}$$

Where,

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

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

$Cov_p\,(x_i x_j)$= Phenotypic covariance between 'ith' and 'jth' characters.

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

3.4.5 Path coefficient analysis

Path coefficient analysis was carried out by the procedure originally proposed by Wright (1921) which was subsequently elaborated by Dewey and

Lu (1959) to estimate the direct and indirect effects of the individual characters on yield.

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

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

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

. . . . . .

. . . . . .

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

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:

$$A \qquad\qquad C \qquad\qquad B$$

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

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

Where,

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

Then, direct effects were calculated as follows:

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

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

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

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

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

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

The variability, genetic parameters, genetic divergence, character association and path analysis for fourteen characters were examined in 36 groundnut genotypes. The information gathered on these characters was subjected to statistical analysis; the findings of which were provided here.

4.1 ANALYSIS OF VARIANCE

The results of the analysis of variance on the data collected using fourteen characters were shown in Table 4.1. For all the characters *i.e.*, days to 50% flowering, days to maturity, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, shelling per cent, sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS, specific leaf area at 60 DAS, relative water content and pod yield plant^{-1} highly significant differences were found among all the genotypes.

4.2 *PER SE* PERFORMANCE

Table 4.2 provides information on the *per se* performance of 36 groundnut genotypes in terms of yield, yield attributes and water use efficiency related traits.

Table 4.1. Analysis of variance for yield, yield attributes and water use efficiency (WUE) related traits in 36 genotypes of groundnut

S. No.	Characters	Mean sum of squares		
		Replications (df:2)	Genotypes (df:35)	Error (df:70)
1	Days to 50% flowering	2.815	14.701**	2.710
2	Days to maturity	1.861	18.198**	1.680
3	Plant height (cm)	1.685	56.210**	4.728
4	Number of primary branches plant^{-1}	0.328	3.831**	0.109
5	Number of secondary branches plant^{-1}	0.180	1.659**	0.069
6	Kernel yield plant^{-1} (g)	0.108	9.454**	0.476
7	Hundred kernel weight (g)	39.433	73.824**	24.466
8	Shelling per cent (%)	1.757	157.744**	17.271
9	Sound mature kernel (%)	112.236	270.267**	84.253
10	Harvest index (%)	64.824	367.870**	67.886
11	SPAD chlorophyll meter reading at 60 DAS	1.629	11.539**	4.670
12	Specific leaf area at 60 DAS (cm^2 gm^{-1})	259.032	3595.106**	407.379
13	Relative water content (%)	32.903	54.532**	23.053
14	Pod yield plant^{-1} (g)	0.285	19.792**	0.923

** Significant at 1% level

Table 4.2. *Per se* performance for yield, yield attributes and water use efficiency (WUE) related traits in 36 genotypes of groundnut

GENOTYPES	DFF	DM	PH	NPB	NSB	KYP	HKW	SP	SMK	HI	SCMR	SLA	RWC	PYP
TCGS-1694	23.67	105.33	38.87	6.63	2.20	8.29	56.13	58.01	52.60	57.26	44.47	225.78	82.06	14.28
TCGS-1798	29.00	107.33	35.93	5.73	0.53	8.18	66.40	69.37	38.97	32.00	47.27	119.22	80.08	11.78
TCGS-2004	26.00	105.00	34.40	4.43	2.53	11.54	42.93	77.84	54.17	55.55	46.77	236.47	87.67	14.82
TCGS-2038	30.00	111.00	29.70	4.50	2.13	9.17	52.47	74.34	49.30	55.08	45.60	256.67	81.54	12.33
TCGS-2039	26.33	107.00	34.60	5.80	2.40	11.99	53.93	71.04	60.03	45.63	48.47	218.43	85.56	16.88
TCGS-2040	26.33	105.33	33.10	6.87	2.40	14.31	49.47	73.19	60.93	62.88	48.63	176.30	83.48	19.55
TCGS-2041	27.33	107.33	30.53	6.45	1.40	11.07	56.87	67.41	55.73	58.01	49.27	194.93	84.40	16.41
TCGS-2044	31.33	111.00	41.40	5.00	1.20	9.62	56.13	79.29	56.53	24.95	49.67	203.86	81.64	12.13
TCGS-2049	30.00	111.67	38.83	5.03	0.27	8.09	43.47	58.56	37.67	60.71	45.77	229.07	89.23	13.81
TCGS-2051	28.33	107.67	25.67	7.57	1.27	12.05	49.00	75.13	42.43	58.32	46.43	233.62	79.55	16.04
TCGS-2052	30.33	112.00	45.97	7.08	0.80	10.43	44.87	63.46	41.40	62.84	50.33	241.22	78.29	16.43
TCGS-2053	27.33	104.67	34.11	8.82	0.80	15.36	50.13	63.60	63.80	71.45	49.50	217.65	84.25	24.14
TCGS-2055	27.00	107.33	33.33	4.52	1.47	12.31	48.53	70.17	57.33	51.73	48.63	165.61	88.60	17.54
TCGS-2057	28.00	105.67	36.17	4.57	1.27	10.27	57.80	76.20	60.37	33.12	49.80	227.47	82.04	13.48
TCGS-2060	28.67	108.67	37.07	4.67	1.20	12.25	50.53	78.36	55.03	46.29	48.73	210.58	69.24	15.63
TCGS-2068	25.33	105.33	30.87	4.30	0.20	8.94	40.67	69.67	41.13	57.60	45.27	265.35	85.53	12.83
TCGS-2217	25.00	104.67	33.20	5.33	2.20	9.94	50.33	64.46	39.47	57.06	50.40	242.60	92.53	15.41
TCGS-2219	24.33	105.00	33.27	4.33	1.53	10.02	52.60	78.37	43.97	43.09	45.97	141.47	86.45	12.79
TCGS-2223	24.33	105.67	36.20	6.62	2.07	14.54	52.60	78.48	56.93	66.04	50.77	167.12	86.58	18.52
TCGS-2227	26.67	106.33	36.50	4.15	1.53	9.84	53.80	73.07	44.37	42.94	49.60	198.94	84.61	13.46
TCGS-2229	25.67	107.33	36.40	4.23	2.73	8.77	51.80	77.75	38.47	51.74	43.83	202.06	90.54	11.28
TCGS-2230	24.33	103.67	26.13	3.87	2.47	10.00	50.80	57.26	49.20	69.79	48.53	226.22	85.23	17.46
TCGS-2233	22.00	101.67	36.47	4.07	1.80	11.51	48.93	67.22	50.77	51.17	46.80	217.82	86.29	17.11
TCGS-2235	27.33	106.67	38.00	5.97	2.07	12.15	54.07	79.87	60.70	34.26	48.30	227.81	86.87	14.21
TCGS-2278	23.67	103.00	32.80	5.65	0.33	11.57	50.00	62.38	47.37	46.78	47.43	178.87	83.63	18.54
TCGS-2317	28.00	106.00	38.93	5.13	1.60	12.17	53.13	69.58	68.43	47.86	46.83	136.33	84.85	17.48
Dharani	24.00	105.33	33.71	4.78	2.47	11.36	49.07	71.69	52.93	47.09	47.97	192.16	86.30	15.85
Dheeraj	26.00	104.00	35.07	4.25	0.40	11.07	54.47	72.26	50.47	48.32	46.17	201.85	88.67	15.31
Greeshma	23.67	103.00	40.80	4.22	0.80	7.74	45.07	63.73	40.83	60.77	47.97	204.48	86.16	12.15

Cont.

Table 4.2 (cont.).

GENOTYPES	DFF	DM	PH	NPB	NSB	KYP	HKW	SP	SMK	HI	SCMR	SLA	RWC	PYP
K-6	26.00	103.33	39.33	4.65	1.60	11.42	47.40	74.69	60.53	46.28	43.30	164.54	80.46	15.28
K-9	27.67	107.67	42.13	5.42	1.20	10.77	48.27	65.98	42.47	65.02	50.33	204.49	89.89	16.32
Narayani	24.67	104.00	32.78	5.27	0.20	11.56	44.53	75.39	45.67	49.98	47.30	233.02	84.24	15.33
Rohini	25.67	105.67	32.13	4.73	1.53	10.06	45.33	74.38	72.17	34.22	48.03	193.95	83.09	13.52
TAG-24	30.00	109.00	30.70	4.85	2.33	11.31	47.40	77.19	62.41	51.35	44.47	263.66	81.22	14.65
Tirupati-1	27.33	105.67	40.27	4.23	1.87	12.77	47.53	77.50	47.53	38.22	47.23	241.98	79.19	15.36
Tirupati-4	26.33	105.00	39.27	5.48	1.27	11.14	47.87	78.25	34.03	56.54	45.87	210.27	80.79	13.22
MEAN	**26.60**	**106.25**	**35.41**	**5.26**	**1.50**	**10.93**	**50.40**	**71.73**	**51.00**	**51.17**	**47.55**	**207.55**	**84.19**	**15.32**
MAX	**31.33**	**112.00**	**45.97**	**8.82**	**2.73**	**15.36**	**66.40**	**79.87**	**72.17**	**71.45**	**50.77**	**265.35**	**92.53**	**24.14**
MIN	**22.00**	**101.67**	**25.67**	**3.87**	**0.20**	**7.74**	**40.67**	**57.26**	**34.03**	**24.95**	**43.30**	**119.22**	**69.24**	**11.28**
C.V	**6.19**	**1.22**	**6.14**	**6.29**	**17.55**	**6.31**	**9.81**	**5.79**	**18.00**	**16.10**	**4.55**	**9.72**	**5.70**	**6.27**
SE(m)	**0.94**	**0.74**	**1.24**	**0.19**	**0.15**	**0.39**	**2.82**	**2.37**	**5.23**	**4.69**	**1.23**	**11.49**	**2.73**	**0.55**
SE(d)	**1.34**	**1.06**	**1.78**	**0.27**	**0.21**	**0.56**	**4.04**	**3.40**	**7.49**	**6.73**	**1.76**	**16.47**	**3.92**	**0.78**
C.D	**2.68**	**2.11**	**3.54**	**0.54**	**0.45**	**1.12**	**8.05**	**6.77**	**14.95**	**13.42**	**3.52**	**32.87**	**7.82**	**1.56**

DFF : Days to 50% flowering

DM : Days to maturity

PH : Plant height (cm)

NPB : Number of primary branches plant^{-1}

NSB : Number of secondary branches plant^{-1}

KYP : Kernel yield plant^{-1} (g)

HKW : Hundred kernel weight (g)

SP : Shelling per cent (%)

SMK : Sound mature kernel (%)

HI : Harvest index (%)

SCMR : SPAD chlorophyll meter reading at 60 DAS

SLA : Specific leaf area at 60 DAS (cm^2 gm^{-1})

RWC : Relative water content (%)

PYP : Pod yield plant^{-1} (g)

4.2.1 Days to 50 % flowering

The mean number of days to 50% flowering ranged from 22.00 days (TCGS-2044) to 31.33 days (TCGS-2233). When compared to the average, nineteen genotypes reached blooming early (26.60 days). As a result, these genotypes can be used as donor parents in the hybridization programme to develop short duration genotypes.

4.2.2 Days to maturity

The mean number of days to maturity ranged from 101.67 (TCGS-2233) to 112.00 days (TCGS-2052). Twenty one genotypes reached maturity sooner than the average of 106.25 days. In order to develop short duration genotypes, these genotypes can be used in the hybridization programme as donor parents.

4.2.3 Plant height (cm)

With a general mean of 35.41 cm, the mean values for plant height ranged from 25.67 cm (TCGS-2051) to 45.97 cm (TCGS-2052). Eighteen genotypes showed better *per se* performance than the average (35.41 cm).

4.2.4 Number of primary branches plant^{-1}

Number of primary branches plant^{-1} count ranged from 3.87 (TCGS-2230) to 8.82 (TCGS-2053). Fifteen genotypes recorded more number of primary branches plant^{-1} than the average of 5.26.

4.2.5 Number of secondary branches plant^{-1}

Number of secondary branches plant^{-1} were between 0.20 (TCGS-2068 and Narayani) and 2.73 (TCGS-2229). Nineteen genotypes recorded more secondary branches plant^{-1} than the average of 1.50.

4.2.6 Kernel yield plant^{-1} (g)

Kernel yield plant^{-1} mean varied from 7.74 g (Greeshma) to 15.36 g. (TCGS-2053) and twenty genotypes showed higher yields than general mean of 10.93 g.

4.2.7 Hundred kernel weight (g)

The mean values for hundred kernel weight ranged from 40.67 g (TCGS-2068) to 66.40 g. (TCGS-1798). Sixteen genotypes recorded hundred kernel weights greater than the average of 50.40 g.

4.2.8 Shelling per cent

Nineteen genotypes had higher shelling per cent than the overall mean of 71.73%, with mean values for shelling per cent ranging from 57.26% (TCGS-2230) to 79.87% (TCGS-2235).

4.2.9 Sound mature kernel (%)

With an overall mean value of 51.00%, the mean values for this character ranged from 34.03% (Tirupati-4) to 72.17% (Rohini). Seventeen genotypes registered sound mature kernel percentages that were higher than the average of 51.00%.

4.2.10 Harvest index (%)

Nineteen genotypes recorded higher harvest indices than the average of 51.17%. The genotype means varied from 24.95% (TCGS-2044) to 71.45% (TCGS-2053).

4.2.11 SPAD chlorophyll meter reading (SCMR) at 60 DAS

With a general mean of 47.55, the mean values for the SPAD chlorophyll meter reading (SCMR) at 60 DAS ranged from 43.30 (K-6) to 50.77 (TCGS-2223). Eighteen genotypes obtained higher SPAD chlorophyll readings than the average of 47.55.

4.2.12 Specific leaf area at 60 DAS (SLA) (cm^2 g^{-1})

The mean values of specific leaf area at 60 DAS from 119.22 cm^2 g^{-1} (TCGS-1798) to 265.35 cm^2 g^{-1} (TCGS-2068) and seventeen genotypes showed lower specific leaf area than their overall mean of 207.55 cm^2 g^{-1}.

4.2.13 Relative water content (%)

The mean percentages of relative water content ranged from 69.24% (TCGS-2060) to 92.53% (TCGS-2217). Twenty one genotypes revealed higher relative water content than their average (84.19%).

4.2.14 Pod yield plant^{-1} (g)

Genotypes for pod yield plant^{-1} ranged from 11.28 g (TCGS-2229) to 24.14 g (TCGS-2053) and eighteen genotypes showed higher pod yield plant^{-1} than the general mean of 15.32 g.

The top five genotypes for each character was determined based on *per se* performance, and they were listed in Table 4.3. Table 4.4 provides a list of the promising genotypes that were identified for several traits. These genotypes are deserving of use in the improvement of characters.

For pod yield plant^{-1}; the genotypes TCGS-2223, TCGS-2040, TCGS-2039, TCGS-2230, TCGS-2053, TCGS-2055, TCGS-2317, TCGS-2278, TCGS-2233 and TCGS-2052 shown improved performance. The performance of TCGS-2223 was also better in terms of days to 50% flowering, days to maturity, primary branches plant^{-1}, number of secondary branches plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, shelling per cent, sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS, specific leaf area at 60 DAS and relative water content. Additionally, the genotype TCGS-2040 outperformed other traits such as harvest index, SPAD chlorophyll meter reading at 60 DAS, specific leaf area at 60 DAS, days to 50% flowering, days to maturity, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, shelling per cent and sound mature kernel per cent. The genotype TCGS-2039 performed better in terms of plant height, number of primary and secondary branches plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, sound mature kernel per cent, SPAD chlorophyll meter reading at 60 DAS, relative water content and days to 50% flowering. In terms of days to 50% flowering, days to maturity, plant height,

number of secondary branches plant^{-1}, hundred kernel weight, harvest index, SPAD chlorophyll meter reading at 60 DAS, relative water content and pod yield plant^{-1} the genotype TCGS-2230 performed better. Plant height, number of primary branches plant^{-1}, kernel yield plant^{-1}, sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS, relative water content and pod yield plant^{-1} performed better with the genotype TCGS-2053. The genotype TCGS-2055 outperformed other genotypes in terms of plant height, sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS, specific leaf area at 60 DAS and relative water content. In terms of days to maturity, number of secondary branches plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, sound mature kernel per cent, specific leaf area at 60 DAS and relative water content, the genotype TCGS-2317 recorded higher values.

The genotype TCGS-2278 showed better performance for plant height, number of primary branches plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, shelling per cent, sound mature kernel per cent and specific leaf area at 60 DAS. It also came to flowering and maturity earlier. The genotype TCGS-2233 reached flowering and maturity earlier and shown superior performance in terms of number of secondary branches plant^{-1}, the kernel yield plant^{-1} and the relative water content.

For the parameters number of primary branches plant^{-1}, harvest index, SPAD chlorophyll meter reading at 60 DAS and pod yield plant^{-1}; TCGS-2052 showed improved performance. In light of this, the genotypes TCGS-2223, TCGS-2040, TCGS-2039, TCGS-2230, TCGS-2053, TCGS-2055, TCGS-2317, TCGS-2278, TCGS-2233 and TCGS-2052 were promising and may be used as parents in a breeding programme to improve yield and the contributing characteristics.

K-6 exhibited light rose lustrous testa, low SLA and matured earlier than TCGS-1694. However, TCGS-1694 was short statured exhibiting foliar disease resistance, high SCMR and high RWC than K-6.

TCGS-2053

TCGS-2040

TCGS-2278

Plate 4.1. Promising genotypes of groundnut based on *per se* performance for pod yield plant^{-1}

TCGS-2223

TCGS-2055

Plate 4.2. Promising genotypes of groundnut based on *per se* performance for pod yield plant^{-1}

Table 4.3. List of top five genotypes based on *per se* performance in groundnut

S. No	Characters	Genotypes
1	Days to 50% flowering	TCGS-2233, Greeshma, TCGS-2278, TCGS-1694 and Dharani
2	Days to maturity	TCGS-2233, Greeshma, TCGS-2278, TCGS-2230 and K-6
3	Plant height (cm)	TCGS-2051, TCGS-2230, TCGS-2038, TCGS-2041 and TAG-24
4	Number of primary branches plant^{-1}	TCGS-2053, TCGS-2051, TCGS-2052, TCGS-1694 and TCGS-2223
5	Number of secondary branches plant^{-1}	TCGS-2229, TCGS-2004, TCGS-2230, Dharani and TCGS-2039
6	Kernel yield plant^{-1} (g)	TCGS-2053, TCGS-2223, TCGS-2040, Tirupati-1 and TCGS-2055
7	Hundred kernel weight (g)	TCGS-1798, TCGS-2057, TCGS-2041, TCGS-2044 and TCGS-1694
8	Shelling per cent (%)	TCGS-2235, Tirupati-4, Tirupati-1, TCGS-2044 and TCGS-2223
9	Sound mature kernel (%)	Rohini, TCGS-2317, TCGS-2053, TAG-24 and TCGS-2040
10	Harvest index (%)	TCGS-2053, TCGS-2230, TCGS-2223, TCGS-2040 and TCGS-2052
11	SPAD chlorophyll meter reading at 60 DAS	TCGS-2223, TCGS-2217, TCGS-2052, K-9 and TCGS-2057
12	Specific leaf area at 60 DAS (cm^2 gm^{-1})	TCGS-1798, TCGS-2317, TCGS-2219, K-6 and TCGS-2055
13	Relative water content (%)	TCGS-2217, TCGS-2229, K-9, TCGS-2049 and TCGS-2055
14	Pod yield plant $^{-1}$ (g)	TCGS-2053, TCGS-2040, TCGS-2278, TCGS-2223 and TCGS-2055

Table 4.4. Identification of promising genotypes for yield, yield attributes and water use efficiency (WUE) related traits in groundnut

S. No.	Genotypes	Characters
1	TCGS-2223	DFF, DM, NPB, NSB, KYP, HKW, SP, SMK, HI, SCMR, SLA, RWC and PYP.
2	TCGS-2040	DFF, DM, PH, NPB, NSB, KYP, SP, SMK, HI, SCMR, SLA and PYP.
3	TCGS-2039	DFF, PH, NPB, NSB, KYP, HKW, SMK, SCMR, RWC and PYP.
4	TCGS-2230	DFF, DM, PH, NSB, HKW, HI, SCMR, RWC and PYP.
5	TCGS-2053	PH, NPB, KYP, SMK, HI, SCMR, RWC and PYP.
6	TCGS-2055	PH, KYP, SMK, HI, SCMR, SLA, RWC and PYP.
7	TCGS-2317	DM, NSB, KYP, HKW, SMK, SLA, RWC and PYP.
8	TCGS-2278	DFF, DM, PH, NPB, KYP, SLA and PYP.
9	TCGS-2233	DFF, DM, NSB, KYP, RWC and PYP.
10	TCGS-2052	NPB, HI, SCMR and PYP.

DFF : Days to 50% flowering
DM : Days to maturity
PH : Plant height (cm)
NPB : Number of primary branches plant^{-1}
NSB : Number of secondary branches plant^{-1}
KYP : Kernel yield plant^{-1} (g)
HKW : Hundred kernel weight (g)
SP : Shelling per cent (%)
SMK : Sound mature kernel (%)
HI : Harvest index (%)
SCMR : SPAD chlorophyll meter reading at 60 DAS
SLA : Specific leaf area at 60 DAS (cm^2 gm^{-1})
RWC : Relative water content (%)
PYP : Pod yield plant^{-1} (g)

4.3 VARIABILITY AND GENETIC PARAMETERS

Genetic diversity is necessary for crop improvement since it gives more options for selection. Depending on the nature, extent and magnitude of genetic variability present in the population; selection may or may not be effective. Therefore the estimates of PCV and GCV are generated to determine the level of variability. Estimates of heritability and genetic advance further defines the nature of character that can be enhanced by selection.

4.3.1 Estimation of Variability and Genetic Parameters

In Table 4.5, the genetic advance and genetic advance as per cent of mean for fourteen traits involving 36 genotypes of groundnut were shown together with the phenotypic and genotypic coefficients of variation.

4.3.1.1 Variability Studies

It was discovered that the phenotypic coefficient of variation for every character under study was higher than the genotypic coefficient of variation, showing that the environment had an impact on these qualities. The findings of John *et al.* (2005), Shoba *et al.* (2009), Narasimhulu *et al.* (2012), Jibrin *et al.* (2016), Kamdi *et al.* (2017), Hampannavar *et al.* (2018b), Nagaveni and Khan (2019a) and others reported similar results.

Number of secondary branches plant^{-1} (GCV: 48.48%; PCV: 51.55%) and number of primary branches plant^{-1} (GCV: 21.20%; PCV: 22.11%) showed high GCV and PCV indicating sufficient amount of variation among genotypes and the need for further improvement of these characters and the selection would be effective.

The findings of Korat *et al.* (2009) and John *et al.* (2012) support the current study of significant GCV and PCV for number of secondary branches plant^{-1}. According to Raut *et al.* (2010), Gupta *et al.* (2015a) and Hampannavar *et al.* (2018b); higher estimations of GCV and PCV were found for number of primary branches plant^{-1}.

Harvest index (GCV: 19.54%; PCV: 25.32%) and sound mature kernels (GCV: 15.44%; PCV: 23.71%) exhibited moderate GCV and high PCV.

The reports of John *et al.* (2012) and Gupta *et al.* (2015a) were in agreement with the harvest index's moderate GCV and high PCV. Moderate GCV and high PCV for sound mature kernel per cent is similar to the findings of the results of Meta and Monpara (2010).

Pod yield plant^{-1} (GCV: 16.38%; PCV: 17.54%), kernel yield plant^{-1} (GCV: 15.83%; PCV: 17.04%), specific leaf area at 60 DAS (GCV: 15.71%; PCV: 18.47%) and plant height (GCV: 11.70%; PCV: 13.21%) exhibited moderate GCV and PCV.

The results of Nandini *et al.* (2011) was in agreement with the moderate estimations of GCV and PCV for pod yield plant^{-1}. In terms of plant height, kernel yield plant^{-1} and pod yield plant^{-1}; Bhakal and Lal (2017)'s findings were consistent with the current report of modest GCV and PCV. Moderate estimations of GCV and PCV for specific leaf area were consistent with Nagaveni and Khan's findings (2019a). GCV and PCV estimates for plant height were moderate, in line with studies of Yusuf *et al.* (2017a) and Chavadhari *et al.* (2017a).

Hundred kernel weight (GCV: 8.05%; PCV: 12.69%) and shelling per cent (GCV: 9.54%; PCV: 11.16%) showed low GCV and moderate PCV.

Lower estimations of GCV and moderate PCV for hundred kernel weight agreed with John *et al.* (2005) findings. The results of Dewangan *et al.* (2015) and Gupta *et al.* (2015a) were consistent with lower estimates of GCV and moderate PCV for shelling per cent.

Low values for GCV and PCV were recorded for the characters days to 50% flowering (GCV: 7.52%; PCV: 9.74%), relative water content (GCV: 3.85%; PCV: 6.88%), SPAD chlorophyll meter reading at 60 DAS (GCV: 3.18%; PCV: 5.55%) and days to maturity (GCV: 2.21%; PCV: 2.52%).

Lower estimates of GCV and PCV for days to 50% flowering were consistent with the findings of Chavadhari *et al.* (2017b), Nayak (2018), Hampannavar *et al.* (2018b) and Nagaveni and Khan (2019a). Whereas, low variability for relative water content was consistent with Nagaveni and Khan's findings (2019a). The SPAD chlorophyll meter reading at 60 DAS in the current investigation revealed low values of GCV and PCV. These findings were consistent with those of John *et al.* (2008) and Bhargavi *et al.* (2017a). The low variability estimates for days to maturity obtained were in consistent with the results of Chavadhari *et al.* (2017b) and Rathod and Toprope (2018).

4.3.1.2 Heritability

High heritability was found for the number of primary branches plant^{-1} (91.90%), number of secondary branches plant^{-1} (88.40%), pod yield plant^{-1} (87.20%), kernel yield plant^{-1} (86.30%), plant height (78.40%), days to maturity (76.60%), shelling per cent (73.10%) and specific leaf area at 60 DAS (72.30%) indicating that the environment has the least influence on the expression of these characteristics.

Characters with moderate heritability included days to 50% flowering (59.60%), harvest index (59.60%), sound mature kernel per cent (42.40%) and hundred kernel weight (40.20 %), the SPAD chlorophyll meter reading at 60 DAS (32.90%) and relative water content (31.30%).

4.3.1.3 Genetic advance

Specific leaf area at 60 DAS (57.09%) showed high genetic advance but harvest index (15.90%), shelling per cent (12.05%) and sound mature kernel per cent (10.56%) recorded moderate genetic advancement. Other traits including plant height (7.56%), hundred kernel weight (5.30%), pod yield plant^{-1} (4.83%), days to maturity (4.23%), relative water content (3.73%), kernel yield plant^{-1} (3.31%), days to 50% flowering (3.18%), number of primary branches plant^{-1} (2.20%), SPAD chlorophyll meter reading at 60 DAS

(1.79%) and number of secondary branches plant^{-1} (1.41%) recorded low genetic advance.

4.3.1.4 Genetic advance as per cent of mean

Higher genetic advance as per cent of the mean was found for the number of secondary branches plant^{-1} (93.90%), number of primary branches plant^{-1} (41.86%), pod yield plant^{-1} (31.50%), harvest index (31.07%), kernel yield plant^{-1} (30.28%), specific leaf area at 60 DAS (27.51%), plant height (21.34%) and sound mature kernel per cent (20.71%) indicating that these characters were controlled by the additive gene effect and selection for these characters is effective.

Characters such as shelling per cent (16.80%), days to 50% flowering (11.95%) and hundred kernel weight (10.51%) showed moderate genetic advance as per cent of the mean. Relative water content (4.43%), days to maturity (3.98%) and SPAD chlorophyll meter reading at 60 DAS (3.76%) were the features that showed the lowest genetic advance as per cent of the mean.

Heritability in broad sense includes additive, dominance and epistatic gene effects, it will be reliable only if accompanied by high genetic advance. High heritability coupled with high genetic advance as per cent of mean were recorded for characters *viz.,* number of primary branches plant^{-1} (h^2_{bs}= 91.90 %, GAM = 41.86 %), number of secondary branches plant^{-1} (h^2_{bs}= 88.40 %, GAM = 93.90 %), pod yield plant^{-1} (h^2_{bs}= 87.20 %, GAM = 31.50 %), kernel yield plant^{-1} (h^2_{bs}= 86.30 %, GAM = 30.28 %), plant height (h^2_{bs}= 78.40 %, GAM = 21.34 %) and specific leaf area at 60 DAS (h^2_{bs}= 72.30 %, GAM = 27.51 %) which indicates preponderance of additive gene action in expression of these characters and the selection would be effective for these characters.

John *et al.* (2012) and Mitra *et al.* (2021) revealed strong heritability together with high genetic advance as per cent of mean for number of secondary branches plant^{-1}. Similar types of findings for kernel yield plant^{-1}

and pod yield plant^{-1} were published by Dolma *et al.* (2010b), Vekariya *et al.* (2011b) and Narasimhulu *et al.* (2012). Dolma *et al.* (2010b), Chavadhari *et al.* (2017b) and Raza *et al.* (2018) reported strong heritability together with high genetic advance as per cent of mean for plant height.

Sab *et al.* (2018) and Nagaveni and Khan's findings (2019a) on high heritability and high genetic advance as per cent of mean for specific leaf area at 60 DAS are similar to these findings.

Shelling per cent (h^2_{bs}= 73.10%, GAM= 16.80%) showed high heritability and moderate genetic advance as per cent of mean. The findings of Dewangan *et al.* (2015), Gupta *et al.* (2015a), Mandal *et al.* (2017) and Veer (2021) were comparable in that they had high heritability along with moderate genetic advance as per cent of the mean for shelling per cent.

Days to maturity (h^2_{bs}= 76.60%, GAM= 3.98%) showed high heritability and low genetic advance as per cent of mean which suggested the presence of non-additive gene action. Selection for such features may not be profitable since high heritability results from the positive influence of environment rather than genotype.

Ashusthosh *et al.* (2017), Nayak (2018) and Veer (2021) demonstrated high heritability and little genetic advance as per cent of mean for days to maturity.

For the characters harvest index (h^2_{bs}= 59.60%, GAM = 31.07%) and sound mature kernel per cent (h^2_{bs}= 42.40%, GAM = 20.71%); moderate heritability and substantial genetic advance as per cent of mean were recorded.

John *et al.* (2012) and Gupta *et al.* (2015a) revealed moderate heritability along with high genetic advance as per cent of mean for harvest index.

For the characters, days to 50% flowering (h^2_{bs}= 59.60%, GAM = 11.95%) and hundred kernel weight (h^2_{bs}= 40.20%, GAM = 10.51%);

moderate heritability and moderate genetic advance as per cent of mean were recorded.

Patidar *et al.* (2014) and Shashikumara *et al.* (2016) reported modest genetic advance as per cent of mean and moderate heritability for days to 50% flowering. Patil *et al.* (2014) and Shinde *et al.* (2019) both reported results for moderate heritability along with moderate genetic advance as per cent of mean for hundred kernel weight.

For the SPAD chlorophyll meter reading at 60 DAS (h^2_{bs}= 32.90%, GAM = 3.76%) and relative water content (h^2_{bs}= 31.30%, GAM = 4.43%); moderate heritability and low genetic advance as per cent of mean was observed had moderate heritability and low genetic advance as per cent of mean, indicating that these traits were heavily influenced by environmental factors and that selection would be unsuccessful.

However low heritability and low genetic advance as per cent of mean were identical to the findings of John *et al.* (2012) for the SPAD chlorophyll meter reading at 60 DAS.

4.4. GENETIC DIVERGENCE

The choice of the appropriate parents plays a key role in the success of plant breeding programme. The best recombinants are produced by crossing most genetically diverse parents. The level of population heterogeneity has a major impact on genetic progress. By using Mahalanobis D^2 statistics (1936) analysis, 36 genotypes of groundnut were quantitatively evaluated in the current study. Table 4.6 provides an analysis of the dispersion of 36 groundnut genotypes.

Table 4.5. Mean, range, co-efficient of variation, heritability (broad sense) and genetic advance as per cent of mean for yield, yield attributes and water use efficiency (WUE) related traits in 36 genotypes of groundnut

S. No.	Character	Mean	Range		Variance		Co-efficient of variation		Heritability (Broad sense) (%)	Genetic Advance (GA)	Genetic advance as percent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic (%)	Phenotypic (%)			
1	Days to 50% flowering	26.60	22.00	31.33	4.00	6.71	7.52	9.74	59.60	3.18	11.95
2	Days to maturity	106.25	101.67	112.00	5.51	7.19	2.21	2.52	76.60	4.23	3.98
3	Plant height (cm)	35.41	25.67	45.97	17.16	21.89	11.70	13.21	78.40	7.56	21.34
4	Number of primary branches plant^{-1}	5.25	3.87	8.82	1.24	1.35	21.20	22.11	91.90	2.20	41.86
5	Number of secondary branches plant^{-1}	1.50	0.20	2.73	0.53	0.60	48.48	51.55	88.40	1.41	93.90
6	Kernel yield plant^{-1} (g)	10.93	7.74	15.36	2.99	3.47	15.83	17.04	86.30	3.31	30.28
7	Hundred kernel weight (g)	50.40	40.67	66.40	16.45	40.92	8.05	12.69	40.20	5.30	10.51
8	Shelling per cent (%)	71.73	57.26	85.50	46.82	64.10	9.54	11.16	73.10	12.05	16.80
9	Sound mature kernel (%)	51.00	34.03	72.17	62.01	146.26	15.44	23.71	42.40	10.56	20.71
10	Harvest index (%)	51.17	24.95	71.45	100.00	167.88	19.54	25.32	59.60	15.90	31.07
11	SPAD chlorophyll meter reading at 60 DAS	47.55	43.30	50.77	2.29	6.96	3.18	5.55	32.90	1.79	3.76
12	Specific leaf area at 60 DAS (cm2 gm^{-1})	207.55	11.22	265.35	1062.58	1469.96	15.71	18.47	72.30	57.09	27.51
13	Relative water content (%)	84.19	69.24	92.53	10.49	33.55	3.85	6.88	31.30	3.73	4.43
14	Pod yield plant $^{-1}$ (g)	15.32	11.28	24.14	6.29	7.21	16.38	17.54	87.20	4.83	31.50

Table 4.6. Analysis of variance for dispersion of 36 genotypes of groundnut

Source of variation	Degree of freedom	Mean sum of squares
Genotype	35	-5.0833E+07**
Error	69	2.5785E+07
Total	104	0.0000E+00

4.4.1 Genetic divergence

Using Tocher's approach (Rao, 1952); 36 groundnut genotypes were divided into nine clusters. Table 4.7 and Fig 4.1. shows the distribution of genotypes into several clusters. The largest cluster *i.e.*, Cluster I contains fifteen genotypes. Cluster IV includes seven genotypes, Cluster VI has five, Cluster V has three, Cluster VII contains two and Cluster V contains three genotypes respectively.

The remaining clusters (II, III, VIII, and IX) are monogenotypic.

4.4.2 Inter and intra cluster distances

Average inter and intra cluster D^2 and D values are provided in Table 4.8 and a cluster diagram is shown in Fig 4.2. Cluster VI and IX had the greatest distance between them (2611.50) followed by cluster VI and VIII (2438.09), cluster I and IX (2080.02), V and IX (1846.08) and cluster VII and VIII (1684.13). The genotypes of these clusters were genetically near and had the most gene complexes as evidenced by the smallest inter-cluster distance of 24.99 between clusters II and III, cluster III and IV (199.08) and cluster II and IV (201.24).

Cluster VI (304.88) had the largest intra-cluster distance followed by Cluster IV (235.43), Cluster I (199.27) and Cluster VII (136.87). Since they are monogenotypic clusters, the intra-cluster distance for the remaining clusters namely II, III, VIII and IX is zero.

The presence of greater genetic diversity between the clusters than within them is indicated by the fact that inter-cluster distances were greater than intra-cluster distances. The clusters VI–IX, VI–VIII, I–IX, V–IX and VII–VIII were discovered to be increasingly divergent in decreasing order of their magnitude based on inter cluster distances. Therefore, it is possible to use the genotypes from these clusters as potential parents and it is advised to cross them in order to produce a wide range of diversity for the efficient selection of different traits.

4.4.2.1 Cluster means

Cluster means for yield, yield attributes and Water use efficiency related traits in 36 genotypes were presented in Table 4.9.

Days to 50% flowering cluster averages ranged from 24.33 days (cluster VIII) to 27.33 days (cluster IX) with a mean of 26.24 days overall. The cluster means for clusters VIII, VII and V were lower than the average.

Days to maturity cluster averages ranged from 103.67 days (for cluster VIII) to 107.33 days (for cluster III), with a mean overall of 105.91 days. Lower cluster means than the overall mean were found in clusters VIII, IX, VII and VI.

Cluster means for plant height varied from 26.13 (VIII) to 39.50 (V) with a general mean of 34.65. Lower values than the general cluster mean were recorded for clusters VIII, III, I, IX and II.

For the number of primary branches plant^{-1}; Clusters IX, VII and II showed greater values of cluster means than the overall Cluster mean (5.60). The range of the cluster means was 3.87 (VIII) to 8.82 (IX).

For the number of secondary branches plant^{-1}; Clusters VIII, II, VII and VI showed cluster means that were greater than the overall cluster mean of 1.67. The range of the cluster means was 0.80 (IX) to 2.47 (VIII).

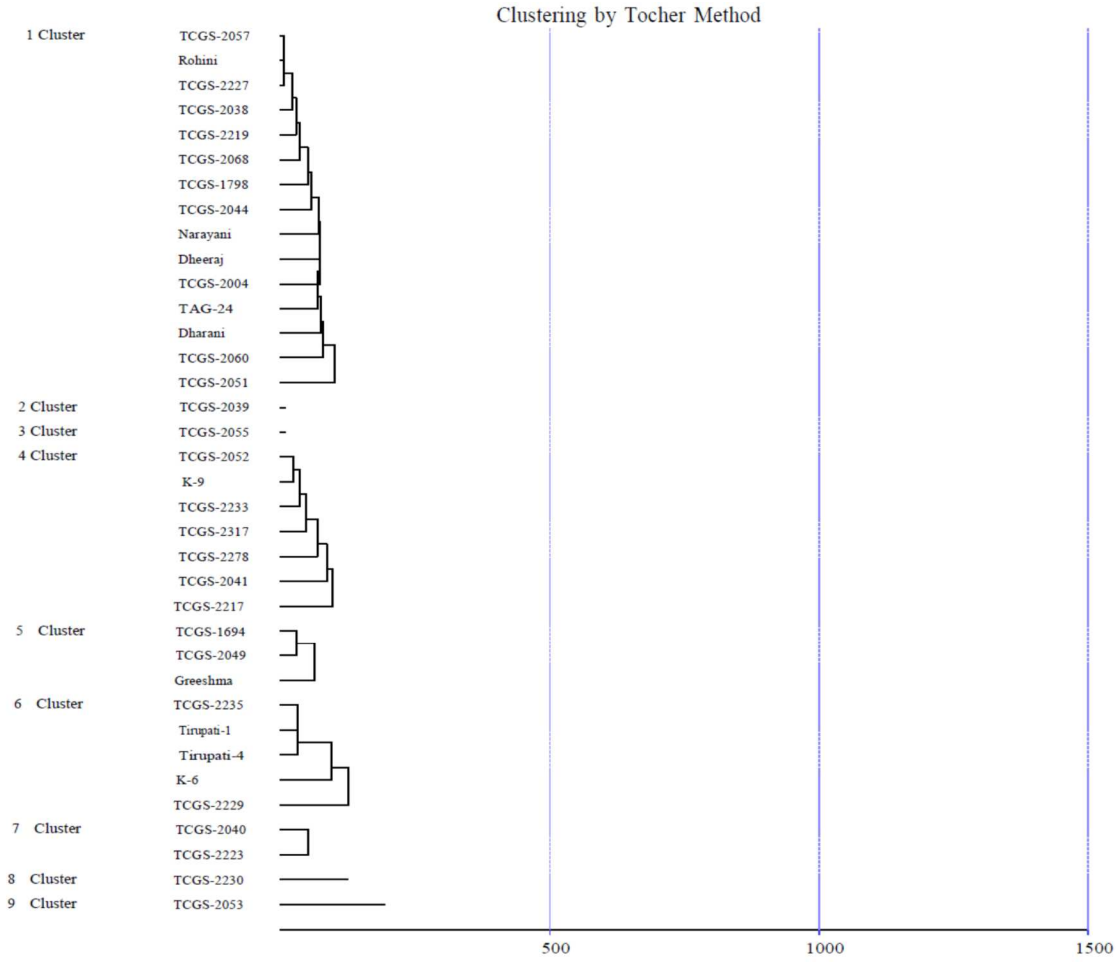

Fig. 4.1. Grouping of 36 genotypes of groundnut into nine clusters using Tocher's method

Tocher Method

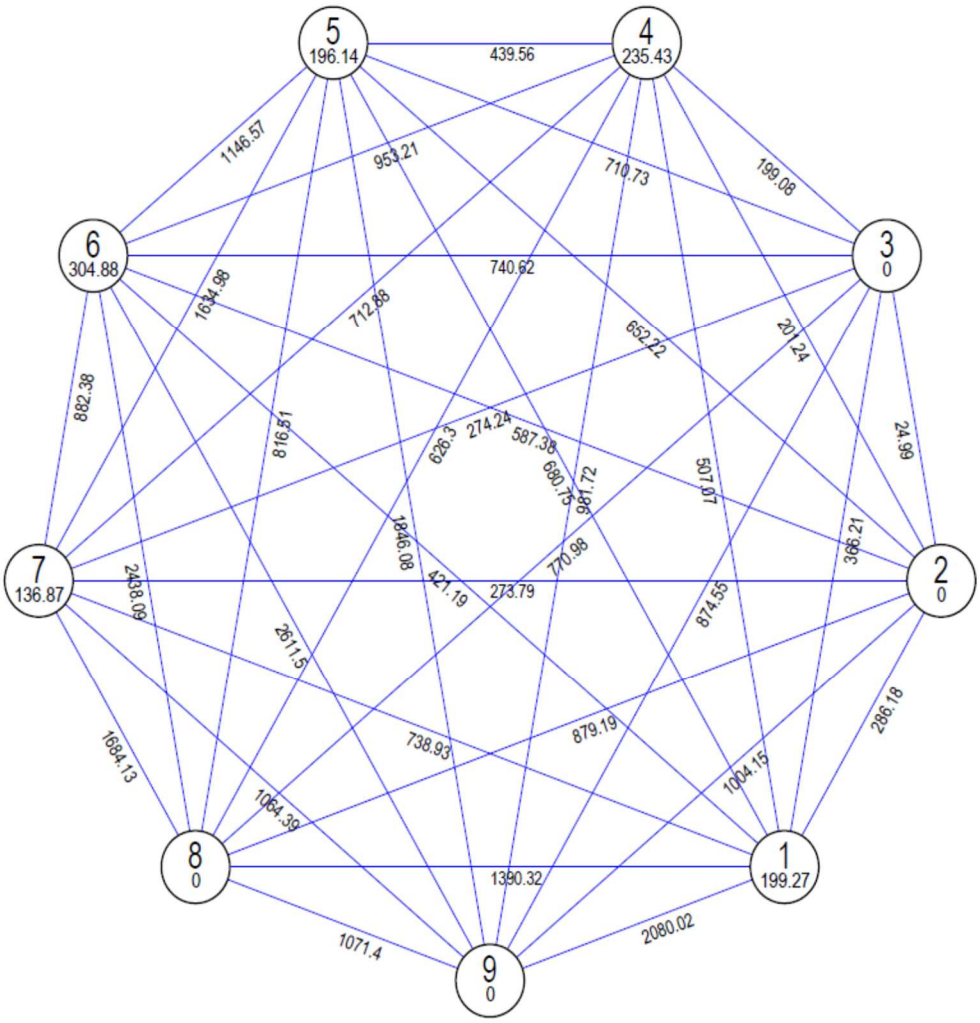

Fig. 4.2. Average inter and intra-cluster (D^2) distances among nine clusters of groundnut

Kernel yield plant^{-1} displayed an overall cluster mean of 11.66. The range was 8.04 (V) to 15.36. (IX). The cluster means in clusters IX, VII, III, and II were greater than the average (11.66).

With a general mean of 50.40 g, the hundred kernel weight recorded the greatest cluster mean in cluster II (53.93 g) and the lowest cluster mean in cluster V (48.22 g). Clusters II, VII, I and VIII all had higher values than the overall mean.

Shelling per cent ranged from 57.26% (VIII) to 81.06% (VI) with a general cluster mean of 68.86%. Clusters VI, VII, I, II and III displayed higher percentages of shelling than the average for all clusters (68.86%).

With a general mean of 53.55%, cluster means for sound mature kernel per cent ranged from 43.70% (V) to 63.80% (IX). Cluster means for Clusters IX, II, VII and III were greater than the average cluster mean (53.55%).

The cluster means for the harvest index ranged from 45.33% (I) to 71.45% (IX). The cluster means for clusters IX, VIII, VII and V were greater than the average cluster mean (56.55%).

With a general mean of 48.07, the cluster means for the SPAD chlorophyll meter reading at 60 DAS ranged from 45.71 (VI) to 49.70 (VII). Clusters VII, IX, IV, III, VIII and II had higher SCMR values than the overall cluster mean.

The range of the cluster means for specific leaf area at 60 DAS was 165.61 cm^2 gm^{-1} (III) to 226.22 cm^2 gm^{-1} (VIII). Clusters III and VII showed lower SLA than the average for the cluster (204.77 cm^2 gm^{-1}).

With a general mean of 85.17%, cluster values for relative water content ranged from 82.79% (I) to 88.60% (III). The clusters III, V, IV, II and VIII were found to have higher relative water content than the average cluster mean.

Table 4.7. Clustering of genotypes based on Tocher's method in groundnut

S. NO.	CLUSTER NUMBER	NUMBER OF GENOTYPES	GENOTYPES
1	I	15	TCGS-2057, Rohini, TCGS-2227, TCGS-2038, TCGS-2219, TCGS-2068, TCGS-1798, TCGS-2044, Narayani, Dheeraj, TCGS-2004, TAG-24, Dharani, TCGS-2060 and TCGS-2051
2	II	1	TCGS-2039
3	III	1	TCGS-2055
4	IV	7	TCGS-2052, K-9, TCGS-2233, TCGS-2317, TCGS-2278, TCGS-2041 and TCGS-2217
5	V	3	TCGS-1694, TCGS-2049 and Greeshma
6	VI	5	TCGS-2235, Tirupati-1, Tirupati-4, K-6 and TCGS-2229
7	VII	2	TCGS-2040 and TCGS-2223
8	VIII	1	TCGS-2230
9	IX	1	TCGS-2053

Table 4.8. Average inter (above diagonal) and intra cluster (diagonal) D^2 and D values (in parenthesis) for nine clusters in 36 genotypes of groundnut

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	199.27 (14.12)	286.18 (16.92)	366.21 (19.14)	507.07 (22.52)	680.75 (26.09)	421.19 (20.52)	738.93 (27.18)	1390.32 (37.29)	2080.02 (45.61)
II		0.00 (0.00)	24.99 (5.00)	201.24 (14.19)	652.22 (25.54)	587.38 (24.24)	273.79 (16.55)	879.19 (29.65)	104.15 (31.69)
III			0.00 (0.00)	199.08 (14.11)	710.73 (26.66)	740.62 (27.21)	274.24 (16.56)	770.98 (27.77)	874.55 (29.57)
IV				235.43 (15.34)	439.56 (20.97)	953.21 (30.87)	712.88 (26.70)	626.30 (25.03)	981.72 (31.33)
V					196.14 (14.00)	1146.57 (33.86)	1634.98 (40.43)	816.51 (28.57)	1846.08 (42.97)
VI						304.88 (17.46)	882.38 (29.70)	2438.09 (49.38)	2611.50 (51.10)
VII							136.87 (11.70)	1684.13 (41.04)	1064.39 (32.62)
VIII								0.00 (0.00)	1071.40 (32.73)
IX									0.00 (0.00)

Table 4.9. Cluster means for yield, yield attributes and water use efficiency (WUE) related traits in 36 genotypes of groundnut

	Characters														Productivity Traits	
Clusters	**DFF**	**DM**	**PH**	**NPB**	**NSB**	**KYP**	**HKW**	**SP**	**SMK**	**HI**	**SCMR**	**SLA**	**RWC**	**PYP**	**Total Score**	**Final Rank**
I	27.20(9)	106.73(7)	33.69(3)	4.88(7)	1.36(6)	10.48(7)	50.88(3)	74.84(3)	51.33(5)	45.33(9)	47.27(7)	211.89(5)	82.79(9)	14.00(7)	87	8
II	26.33(5)	107.00(8)	34.60(5)	5.80(3)	2.40(2)	11.99(4)	**53.93(1)**	71.05(4)	60.03(2)	45.63(7)	48.47(6)	218.43(7)	85.56(4)	16.88(6)	61	3
III	27.00(7)	107.33(9)	33.33(2)	4.52(8)	1.47(5)	12.31(3)	48.53(8)	70.17(5)	57.33(4)	51.73(6)	48.63(4)	**165.61(1)**	**88.60(1)**	17.54(3)	66	4
IV	26.29(4)	106.05(5)	37.15(7)	5.59(4)	1.33(7)	11.06(6)	50.34(5)	65.79(6)	49.38(6)	55.5(5)	48.77(3)	202.32(3)	85.70(3)	16.82(5)	69	6
V	25.78(3)	106.67(6)	39.50(9)	5.29(5)	1.0(8)	8.04(9)	48.22(9)	60.10(8)	43.70(9)	59.58(4)	46.07(8)	219.78(8)	85.82(2)	13.41(9)	97	9
VI	26.53(6)	105.60(4)	38.65(8)	4.91(6)	1.91(4)	11.25(5)	49.73(7)	**81.06(1)**	48.25(8)	45.41(8)	45.71(9)	209.33(4)	83.57(8)	13.87(8)	86	7
VII	25.33(2)	105.50(3)	34.65(6)	6.74(2)	2.23(3)	14.43(2)	51.03(2)	75.84(2)	58.93(3)	64.46(3)	**49.70(1)**	171.71(2)	85.03(6)	19.03(2)	39	1
VIII	**24.33(1)**	**103.67(1)**	**26.13(1)**	3.87(9)	**2.47(1)**	10.00(8)	50.80(4)	57.26(9)	49.20(7)	69.79(2)	48.53(5)	226.22(9)	85.23(5)	17.46(4)	66	4
IX	27.33(8)	104.67(2)	34.11(4)	**8.82(1)**	0.80(9)	**15.36(1)**	50.13(6)	63.60(7)	**63.80(1)**	**71.45(1)**	49.50(2)	217.65(6)	84.25(7)	**24.14(1)**	56	2
Mean	**26.24**	**105.91**	**34.65**	**5.60**	**1.67**	**11.66**	**50.40**	**68.86**	**53.55**	**56.55**	**48.07**	**204.77**	**85.17**	**17.02**		

Note: Numbers in the parenthesis indicates the ranks based on cluster mean. Total score is the summation of rank numbers for all characters based on which final rank indicated. Bold numbers indicated highest mean values for each character.

DFF : Days to 50% flowering
DM : Days to maturity
PH : Plant height (cm)
NPB : Number of primary branches plant^{-1}
NSB : Number of secondary branches plant^{-1}
KYP : Kernel yield plant^{-1} (g)
HKW : Hundred kernel weight (g)
SP : Shelling per cent (%)
SMK : Sound mature kernel (%)
HI : Harvest index (%)
SCMR : SPAD chlorophyll meter reading at 60 DAS
SLA : Specific leaf area at 60 DAS (cm^2 gm^{-1})
RWC : Relative water content (%)
PYP : Pod yield plant^{-1} (g)

For pod yield plant^{-1}, cluster values ranged from 13.41 g (V) to 24.14 g (IX) with a cluster mean overall of 17.02 g. Pod yield plant^{-1} was higher in Clusters IX, VII, III, and VIII than the overall cluster mean.

4.4.3 Relative contribution of individual characters towards divergence

Table 4.10 illustrates the contribution of different traits to genetic divergence. The trait shelling per cent was ranked first for 234 times and contributed the most to genetic divergence (37.14%) followed by pod yield plant^{-1} (36.35%), SPAD chlorophyll meter reading at 60 DAS (21.59%), kernel yield plant^{-1} (3.81%), number of secondary branches plant^{-1} (0.79%) and specific leaf area at 60 DAS (0.32%).

The traits plant height, number of primary branches plant^{-1}, sound mature kernel per cent, hundred kernel weight, days to 50% flowering, days to maturity, harvest index and relative water content did not contribute to genetic divergence.

This leads to the conclusion that it would be advantageous to hybridise across divergent clusters with high mean values for the specific qualities that need to be enhanced in order to produce superior varieties.

Comparing genetic divergence between clusters and *per se* performance of genotypes, the cross combinations K-6 × TCGS-2053 and TCGS-2235 × TCGS-2053 could be recommended to increase water use efficiency related traits in groundnut. Whereas, the cross combinations Greeshma × TCGS-2053 and TCGS-2223 × TCGS-2230 could be recommended to obtain transgressive segregants for yield, yield attributes.

TCGS-2053 (Cluster IX) registered highest pod yield plant^{-1} than all the other genotypes. However it is late maturing genotype with lower performance for kernel yield plant^{-1}, hundred kernel weight, shelling per cent, sound mature kernel per cent and specific leaf area at 60 DAS.

K-6 (Cluster VI) matured earlier and also registered lower specific leaf area at 60 DAS whereas less pod yield plant^{-1}. TCGS-2235 has low pod yield

Table 4.10. Relative contribution of various characters towards genetic diversity in groundnut

S. No.	Characters	Number of times ranked first	Contribution (%)
1	Days to 50% flowering	0	0.00%
2	Days to maturity	0	0.00%
3	Plant height (cm)	0	0.00%
4	Number of primary branches plant^{-1}	0	0.00%
5	Number of secondary branches plant^{-1}	5	0.79%
6	Kernel yield plant^{-1} (g)	24	3.81%
7	Hundred kernel weight (g)	0	0.00%
8	Shelling per cent	234	37.14%
9	Sound mature kernel (%)	0	0.00%
10	Harvest index (%)	0	0.00%
11	SPAD chlorophyll meter reading at 60 DAS	136	21.59%
12	Specific leaf area at 60 DAS (cm^2 gm^{-1})	2	0.32%
13	Relative water content (%)	0	0.00%
14	Pod yield plant^{-1} (g)	229	36.35%

plant^{-1} but had good shelling per cent (85.50%). Greeshma (Cluster V) bloomed and matured earlier but has a lesser pod yield plant^{-1}. Hence the crosses K-6 × TCGS-2053, TCGS-2235 × TCGS-2053, Greeshma × TCGS-2053 were recommended for utilization in the breeding programme.

TCGS-2223 (Cluster VII) exhibited lesser specific leaf area at 60 DAS and also registered higher performance for kernel yield plant^{-1} and sound mature kernel per cent which are lacking in the genotype TCGS-2230 (Cluster VIII) whereas it shows greater performance for plant height and number of secondary branches plant^{-1}. Therefore, the cross TCGS-2223 × TCGS-2230 can be suggested to obtain transgressive segregants for yield, yield attributes and water use efficiency related traits in groundnut.

4.4.4 Cluster diagram

D^2 values were used to create a cluster diagram that illustrates the relationship between various populations. Clusters III and VII had the greatest distance between them indicating the greatest divergence while clusters V and VI had the smallest distance indicating the least divergence.

4.5 CHARACTER ASSOCIATION ANALYSIS

Being affected by polygenes and the environment; yield became a complex quantitative characteristic. As a result, choosing superior genotypes only on the basis of yield does not produce worthwhile outcomes. Studying correlations can reveal the strength and direction of the relationship between yield and its constituent parts. As a result, the association of yield components became more significant as the foundation for choosing good genotypes.

Tight linkage or pleiotropic effects frequently produce genetic association. If the correlation is high, pleiotropy is probably more significant; if the correlation is low, the traits are likely to be inherited independently.

In order to determine the sort of association that exists between the traits, phenotypic and genotypic correlations were computed for fourteen characters among 36 genotypes of groundnut.

TCGS-2053

K-6

TCGS-2235

Plate 4.3. Promising genotypes of groundnut based on *per se* performance and divergence analysis

Greeshma

TCGS-2223

TCGS-2230

Plate 4.4. Promising genotypes of groundnut based on *per se* performance and divergence analysis

4.5.1 Correlation of yield, yield attributes and water use efficiency related traits with pod yield plant^{-1}

In order to determine the sort of association that exists between the traits, phenotypic (r_p) and genotypic (r_g) correlations were computed for fourteen characters among 36 groundnut genotypes.

Pod yield plant^{-1} registered highly positive and significant association with kernel yield plant^{-1} (r_p=0.825**; r_g=0.799**), number of primary branches plant^{-1} (r_p=0.538**; r_g=0.598**), SPAD chlorophyll meter reading at 60 DAS (r_p=0.466** ; r_g=0.337**), harvest index (r_p=0.380**; r_g=0.588**) and sound mature kernel per cent (r_p=0.305**; r_g=0.509**).

It was concluded from this that by increasing the kernel yield plant^{-1}, number of primary branches plant^{-1}, SPAD chlorophyll meter reading at 60 DAS, harvest index and sound mature kernel per cent would simultaneously increase the pod yield plant^{-1}.

Jayalakshmi and Reddy (2003), Kumara *et al.* (2015), Reddy *et al.* (2017) and Hampannavar *et al.* (2018b) all provided data with a substantial positive correlation between pod yield plant^{-1} and kernel yield plant^{-1}.

The results of Hiremath *et al.* (2011) and Rathod and Toprope (2018) are comparable and there was a significant correlation between the number of primary branches plant^{-1} and pod yield plant^{-1}.

According to Kumara *et al.* (2015), the SPAD chlorophyll meter value at 60 DAS was significantly positively correlated with pod yield plant^{-1}.

The findings of Alam (2014) and Sab *et al.* (2018) were similar to those of the significant correlation of harvest index with pod yield plant^{-1}.

The results of Meta and Monpara (2010), Narasimhulu *et al.* (2012) and Prabhu *et al.* (2015) were in agreement with the findings of the significant correlation of sound mature kernel per cent with pod yield plant^{1}.

Table 4.11. Phenotypic (r_p) and genotypic (r_g) correlation coefficients for yield, yield attributes and water use efficiency (WUE) related traits in 36 genotypes of groundnut

Characters		DM	PH	NPB	NSB	KYP	HKW	SP	SMK	HI	SCMR	SLA	RWC	Correlation with PYP
DFF	r_p	0.669**	0.149	0.182	-0.127	-0.048	0.062	0.141	0.081	-0.142	0.059	0.149	-0.205*	-0.141
	r_g	1.015**	0.228*	0.200*	-0.195*	-0.047	0.269**	0.243*	0.067	-0.259*	0.159	0.158	-0.612**	-0.173
DM	r_p		0.167	0.159	-0.030	-0.166	0.084	0.086	-0.102	-0.072	0.095	0.166	-0.130	-0.210*
	r_g		0.219*	0.174	-0.047	-0.237*	0.080	0.071	-0.058	-0.086	0.119	0.239*	-0.398**	-0.285**
PH	r_p			0.008	-0.159	0.001	0.008	0.185	-0.083	-0.155	0.344**	-0.074	0.009	-0.035
	r_g			0.003	-0.190	-0.188	-0.014	-0.044	-0.165	-0.177	-0.043	-0.185	-0.192*	-0.225*
NPB	r_p				-0.097	0.434**	0.095	-0.156	0.128	0.283**	0.218*	-0.003	-0.136	0.538**
	r_g				-0.113	0.486**	0.190*	-0.185	0.163	0.428**	0.383**	-0.039	-0.201*	0.598**
NSB	r_p					0.160 *	0.084	0.204*	0.237**	0.042	-0.038	0.039	0.089	0.027
	r_g					0.185*	0.142	0.250**	0.384**	0.047	-0.0755	0.097	0.221*	0.033
KYP	r_p						-0.065	0.388**	0.382**	0.131	0.425**	-0.062	-0.020	0.825**
	r_g						-0.105	0.249**	0.646**	0.236*	0.243*	-0.150	-0.244*	0.799**
HKW	r_p							0.044	0.234 *	-0.351**	0.116	-0.335**	-0.057	-0.084
	r_g							0.070	-0.006	-0.495**	0.255**	-0.585**	-0.187	-0.133
SP	r_p								0.115	-0.433**	0.200*	0.034	-0.063	-0.146
	r_g								0.221*	-0.583**	-0.438**	-0.060	-0.459**	-0.412**
SMK	r_p									-0.256 **	0.088	-0.124	-0.137	0.305**
	r_g									-0.218*	0.198*	-0.204*	-0.164	0.509**
HI	r_p										-0.023	0.145	0.158	0.380**
	r_g										0.154	0.316**	0.338**	0.588**
SCMR	r_p											0.040	0.184	0.466**
	r_g											-0.176	-0.163	0.337**
SLA	r_p												0.045	-0.046
	r_g												-0.148	-0.125
RWC	r_p													0.085
	r_g													-0.030

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

DFF : Days to 50% flowering
DM : Days to maturity
PH : Plant height (cm)
NPB : Number of primary branches plant^{-1}
NSB : Number of secondary branches plant^{-1}
KYP : Kernel yield plant^{-1} (g)
HKW : Hundred kernel weight (g)
SP : Shelling per cent (%)
SMK : Sound mature kernel (%)
HI : Harvest index (%)
SCMR : SPAD chlorophyll meter reading at 60 DAS
SLA : Specific leaf area at 60 DAS (cm^2 gm^{-1})
RWC : Relative water content (%)
PYP : Pod yield plant^{-1} (g)

Pod yield plant^{-1} showed a non-significant positive correlation with relative water content (r_p=0.085; r_g= -0.030) and number of secondary branches (r_p=0.027; r_g=0.033). On the other hand, Korat *et al.* (2010) found a non-significant negative correlation between the number of secondary branches and pod yield plant^{-1}.

Days to maturity (r_p=-0.210*; r_g=-0.285**), shelling per cent (r_p=-0.146; r_g=-0.412**) and plant height (r_p=-0.035; r_g=-0.225*) all showed a significant negative correlation with pod yield plant^{-1}. The findings of Nayak (2018), Hampannavar *et al.* (2018b) and Sab *et al.* (2018) were comparable in that there was a significant negative association between shelling per cent and pod yield plant^{-1}.

A non-significant negative correlation was seen between days to 50% flowering (r_p=-0.141; r_g= -0.173), hundred kernel weight (r_p=-0.084; r_g= -0.133) and specific leaf area at 60 DAS (r_p=-0.046; r_g= -0.125) with pod yield plant^{-1}. Bhargavi *et al.* (2017b) reported similar findings of a non-significant negative corelation between the days to 50% flowering and the pod yield plant^{-1}. On the other hand, Babariya and Dobariya (2012) found a strong negative correlation between the hundred kernel weight and the pod yield plant^{-1}.

4.5.2 *Inter-se* correlation among yield, yield attributes and water use efficiency related traits

Studies on the correlations between yield, yield attributes and water use efficiency related traits have shown both positive and negative relationships between them and with yield. The increase in yield will result from the improvements in the favourable components. The following is a description of the inter-se relationships among these traits that were evaluated in the current study.

4.5.2.1 Days to 50% flowering

Days to 50% flowering revealed a highly significant positive correlation with days to maturity (r_p=0.669**; r_g=1.015**), number of primary branches plant^{-1} (r_p=0.182; r_g=0.200*), plant height (r_p=0.149; r_g=0.228*), shelling per cent (r_p=0.141; r_g= 0.243*) and hundred kernel weight (r_p= 0.062; r_g= 0.269**). It exhibited negative correlation with relative water content (r_p= -0.205*; r_g= -0.612**) and harvest index (r_p= -0.142; r_g= -0.259*).

Days to 50% flowering and days to maturity were found to significantly and favourably correlated according to Rao *et al.* (2014) and Aparna *et al.* (2017). Manjubhargavi *et al.* (2015) showed similar findings of a substantial and positive correlation of days to 50% flowering with number of primary branches plant^{-1}. According to Makinde and Ariyo (2013) and Aparna *et al.* (2017) there was a significant positive correlation between the days to 50% flowering and the weight of the hundred kernels.

Alam (2014) and Gupta *et al.* (2015c) revealed similar findings of a substantial and negative correlation of days to 50% flowering with harvest index.

4.5.2.2 Days to maturity

Significant positive association of days to maturity was recorded with plant height (r_p= 0.167; r_g= 0.219*) and specific leaf area at 60 DAS (r_p= 0.166; r_g= 0.239*), whereas negative significant association was recorded with kernel yield plant^{-1} (r_p= -0.166; r_g= -0.237*) and relative water content (r_p= -0.130; r_g= -0.398*).

Prior to this, Babariya and Dobariya (2012) found a strong and favourable correlation between plant height and days to maturity.

Rao *et al.* (2014) and Bhargavi *et al.* (2017b) showed similar results of significant and negative correlation of days to maturity with kernel yield plant^{-1}.

4.5.2.3 Plant height (cm)

Substantial positive correlation between plant height and the SPAD chlorophyll meter reading at 60 DAS (r_p= 0.344**; r_g= -0.043) was observed. However, significant negative correlation was seen with respect to relative water content (r_p= 0.009; r_g= -0.192*).

Alam (2014) previously reported similar findings of a substantial and positive correlation between plant height and SPAD chlorophyll meter reading at 60 DAS.

4.5.2.4 Number of primary branches plant^{-1}

The number of primary branches plant^{-1} had a positive and statistically significant relationship with the kernel yield plant^{-1} (r_p= 0.434**; r_g= 0.486**), harvest index (r_p= 0.283**; r_g= 0.428**), SPAD chlorophyll meter reading at 60 DAS (r_p= 0.218**; r_g= 0.383**) and hundred kernel weight (r_p= 0.095; r_g= 0.190*). Relative water content (r_p= -0.136; r_g= -0.201*) showed a significant negative correlation.

An earlier study by Manjubhargavi *et al.* (2015) and another by Aparna *et al.* (2017) found a significant and favourable correlation between the number of primary branches plant^{-1} and kernel production. Kumari and Sasidharan (2020) found a substantial and positive correlation between number of primary branches plant^{-1} and hundred kernel weight.

The strong and favourable correlation between the number of primary branches plant^{-1} and kernel yield plant $^{-1}$ highlights the idea that increasing the number of primary branches plant^{-1} will increase kernel yield.

4.5.2.5 Number of secondary branches plant^{-1}

The trait number of secondary branches plant^{-1} was significantly correlated and positively with sound mature kernel per cent (r_p= 0.237**; r_g= 0.384**), shelling per cent (r_p= 0.204*; r_g= 0.250**), kernel yield plant^{-1} (r_p= 0.160*; r_g= 0.185*) and relative water content (r_p= 0.089; r_g= 0.221*).

The number of secondary branches plant^{-1} has a significant and favourable relationship with kernel yield plant^{-1} which demonstrates that by increasing the number of secondary branches plant^{-1}, there will be an increase in the kernel yield plant^{-1}.

4.5.2.6 Kernel yield plant^{-1} (g)

SPAD chlorophyll meter reading at 60 DAS (r_p= 0.425**; r_g= 0.243*), shelling per cent (r_p= 0.388**; r_g= 0.249**), sound mature kernel per cent (r_p= 0.382**; r_g= 0.646**) and harvest index (r_p= 0.131; r_g= 0.236*) were significantly positively correlated with kernel yield plant^{-1}. Relative water content has a strong negative correlation (r_p= -0.020; r_g= -0.244*).

Both Babariya and Dobariya (2012) and Reddy *et al.* (2017) revealed a strong positive association between kernel yield plant^{-1} and the per cent of shelling. Kernel yield plant^{-1} and sound mature kernel per cent were shown to be significantly and favourably correlated according to Pavan *et al.* (2013) and Vinutha *et al.* (2015). Reddy *et al.* (2017) confirmed similar findings of a substantial positive correlation with the harvest index.

4.5.2.7 Hundred kernel weight (g)

The relationship of hundred kernel weight with sound mature kernel per cent (r_p= 0.234*; r_g= -0.006) and SPAD chlorophyll meter reading at 60 DAS (r_p= 0.116; r_g= 0.255**) was significant and favourable. Both the harvest index (r_p= -0.351**; r_g= -0.495**) and the specific leaf area at 60 DAS (r_p= -0.335**; r_g= -0.585**) showed a significant negative correlation with the hundred kernel weight.

According to Reddy *et al.* (2003); hundred kernel weight showed a significant negative association with SLA and a substantial positive correlation with the SPAD chlorophyll meter reading at 60 DAS. According to Hampannavar *et al.* (2018b); sound mature kernel per cent and hundred kernel weight have a substantial and positive correlation. Rao *et al.*

(2014) showed a significant and favourable correlation between hundred kernel weight and the SPAD chlorophyll meter value at 60 DAS.

4.5.2.8 Shelling per cent

Sound mature kernel per cent (r_p= 0.115; r_g= 0.221*) showed positive and significant correlation with shelling per cent. Relative water content (r_p= -0.063; r_g= -0.459**) and harvest index (r_p= -0.433**; r_g= -0.583**) were shown to have a significant negative correlation.

This trait showed significant positive correlation with SPAD chlorophyll meter reading at 60 DAS (r_p= 0.200*; r_g= -0.438**) at phenotypic level whereas significant negative correlation at genotypic level.

Prior to this study, John *et al.* (2005) and Mandal *et al.* (2017) revealed a similar conclusion of a significant and favourable association of shelling per cent with sound mature kernel per cent.

The harvest index and shelling per cent were found to be significantly and negatively correlated by Abraham (1990).

4.5.2.9 Sound mature kernel per cent

Significantly negative correlations were seen with the harvest index (r_p= -0.256**; r_g= -0.218*) specific leaf area at 60 DAS (r_p= -0.124; r_g= -0.204*) but a significant positive association was seen with the sound mature kernel per cent and the SPAD chlorophyll meter reading at 60 DAS (r_p= 0.088; r_g= 0.198*).

4.5.2.10 Harvest index (%)

With regard to SPAD chlorophyll meter reading at 60 DAS (r_p= 0.158; r_g= 0.338**) and specific leaf area (r_p= 0.145; r_g= 0.316**); harvest index showed a positive and statistically significant correlation.

4.5.2.11 SPAD chlorophyll meter reading at 60 DAS

Relative water content (r_p= 0.184; r_g= -0.163) and specific leaf area at 60 DAS (r_p= 0.040; r_g= -0.176) and exhibited positive and non significant correlation with SPAD chlorophyll meter reading at 60 DAS.

4.5.2.12 Specific leaf area at 60 DAS (cm^2 g^{-1})

Relative water content exhibited (r_p= 0.045; r_g= -0.148) showed positive and non significant correlation with specific leaf area at 60 DAS.

From the character association analysis; kernel yield $plant^{-1}$, number of primary branches $plant^{-1}$, SPAD chlorophyll meter reading at 60 DAS, harvest index and sound mature kernel per cent were all highly significant and positive with pod yield $plant^{-1}$ and among themselves at both the phenotypic and genotypic levels.

Therefore, these characteristics can be regarded as the key yield-attributing traits and proper emphasis should be placed on enhancing groundnut pod yield and kernel yield. Hence selection should be focussed on these traits to enhance groundnut yield.

4.6 PATH CO-EFFICIENT ANALYSIS

The yield is complex in inheritance and is impacted by numerous traits, all of which are interconnected. These features may be interdependent directly on the pod yield $plant^{-1}$ or indirectly through other characters. As a result, the path co-efficient analysis aids in selecting the right characters by dividing the direct and indirect impacts and revealing the true relationship between them.

Direct selection for this attribute will be successful if direct effect equals correlation co-efficient as correlation explains genuine relationships. If the correlation coefficient is positive but the direct effect is weak or non-existent, then the correlation appears to be the result of an indirect effect. In this case, all other elements must be taken into account concurrently. If the correlation coefficient is negative but the direct effect is positive and significant, a limited simultaneous model should be used. This means that

limits should be put in place to eliminate any unfavourable indirect effects so that the direct effect can be utilised.

In the current study, path co-efficient analysis was done on 36 genotypes of groundnut to determine yield, yield attributes and water use efficiency related traits in groundnut.

Due to very negligible residual effect in genotypic path co-efficient analysis only phenotypic path co-efficient analysis is discussed.

4.6.1 Phenotypic path co-efficient analysis

Six characters showed a substantial phenotypic association with pod yield plant^{-1} according to correlation analysis. Eight traits that were highly significant either in phenotypic and genotypic levels underwent path coefficient calculations and the findings were shown in Table 4.12 and Fig. 4.3 respectively.

4.6.1.1 Days to maturity

Days to maturity showed significant negative relationship (-0.2104**) with pod yield plant^{-1}. Direct effect was low and had a negative impact on pod yield plant^{-1} (-0.0195). Through SPAD chlorophyll meter reading at 60 DAS (0.0155), plant height (0.0024) and sound mature kernel per cent (0.0011) this trait demonstrated positive and negligible indirect effects whereas shelling per cent (-0.0473), harvest index (-0.0014) and number of primary branches plant^{-1} (-0.0007) demonstrated negative and negligible indirect effects. Kernel yield plant^{-1} registered negative low indirect effect on pod yield plant^{-1} (-0.1605).

On contrary, Korat *et al.* (2010) observed a negligible negative direct effect on pod yield plant^{-1}. Indirect positive impacts on plant height and sound mature kernel per cent and positive impacts on number of primary branches plant^{-1} were barely detectable according to Pavan *et al.* (2013). Similar results for SPAD chlorophyll meter reading at 60 DAS, shelling per cent and harvest index was reported by Bhargavi *et al.* (2017b).

4.6.1.2 Number of primary branches plant^{-1}

Significant positive correlation was observed between the number of primary branches and pod yield plant^{-1} (0.5377**). The direct impact of this feature on pod yield plant^{-1} was detrimental and insignificant (-0.0046). Kernel yield plant^{-1} (0.4205) showed high positive indirect effect *via* number of primary branches plant^{-1} on pod yield plant^{-1}. The traits shelling per cent (0.0853), SPAD chlorophyll meter reading at 60 DAS (0.0357), harvest index (0.0054) and plant height (0.0001) all showed positive and negligible indirect effect on this trait. However, days to maturity (-0.0031) and sound mature kernel per cent (-0.0014) exhibited negative negligible indirect effects *via* this trait on pod yield plant^{-1}.

The results were in line with the findings of Pavan *et al.* (2013) for plant height and days to maturity. On contrary, negative moderate indirect effects of sound mature kernel per cent was earlier registered by Kumari and Sasidharan (2020).

4.6.1.3 Kernel yield plant^{-1} (g)

Kernel yield plant^{-1} had a substantial positive correlation with pod yield plant^{-1} (0.8252**). Direct impact on pod yield plant^{-1} was high and favourable (0.9688). It had negligible positive indirect effect *via* SPAD chlorophyll meter reading at 60 DAS (0.0694), days to maturity (0.0032), harvest index (0.0025) and plant height (0.0000). It had negative and low indirect effect *via* shelling per cent (-0.2124) whereas negative and negligible indirect effects *via* sound mature kernel per cent (-0.0043) and number of primary branches plant^{-1} (-0.0020).

Jain *et al.* (2016) and Bhargavi *et al.* (2017b) observed a strong favourable direct effect of kernel yield plant^{-1} on pod yield plant^{-1}. With contrast to this, Aparna *et al.* (2017) found that days to maturity and harvest index had negative negligible indirect effects on pod yield plant^{-1}.

Table 4.12 Phenotypic path coefficients for yield, yield attributes and water use efficiency (WUE) related traits in 36 genotypes of groundnut

Characters	DM	PH	NPB	KYP	SP	SMK	HI	SCMR	Correlation with PYP
DM	**-0.0195**	0.0024	-0.0007	-0.1605	-0.0473	0.0011	-0.0014	0.0155	-0.2104*
PH	-0.0032	**0.0144**	0.0000	0.0008	-0.1011	0.0009	-0.0029	0.0562	-0.0351
NPB	-0.0031	0.0001	**-0.0046**	0.4205	0.0853	-0.0014	0.0054	0.0357	0.5377**
KYP	0.0032	0.0000	-0.002	**0.9688**	-0.2124	-0.0043	0.0025	0.0694	0.8252**
SP	-0.0017	0.0027	0.0007	0.3760	**-0.5473**	-0.0013	-0.0082	0.0327	-0.1465
SMK	0.0020	-0.0012	-0.0006	0.3697	-0.0628	**-0.0112**	-0.0049	0.0144	0.3055**
HI	0.0014	-0.0022	-0.0013	0.1270	0.2372	0.0029	**0.0190**	-0.0038	0.3801**
SCMR	-0.0018	0.0049	-0.0010	0.4115	-0.1094	-0.0010	-0.0004	**0.1634**	0.4661**

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

DM : Days to maturity
PH : Plant height (cm)
NPB : Number of primary branches plant^{-1}
KYP : Kernel yield plant^{-1} (g)
SP : Shelling per cent (%)
SMK : Sound mature kernel (%)
HI : Harvest index (%)
SCMR : SPAD chlorophyll meter reading at 60 DAS
PYP : Pod yield plant^{-1} (g)

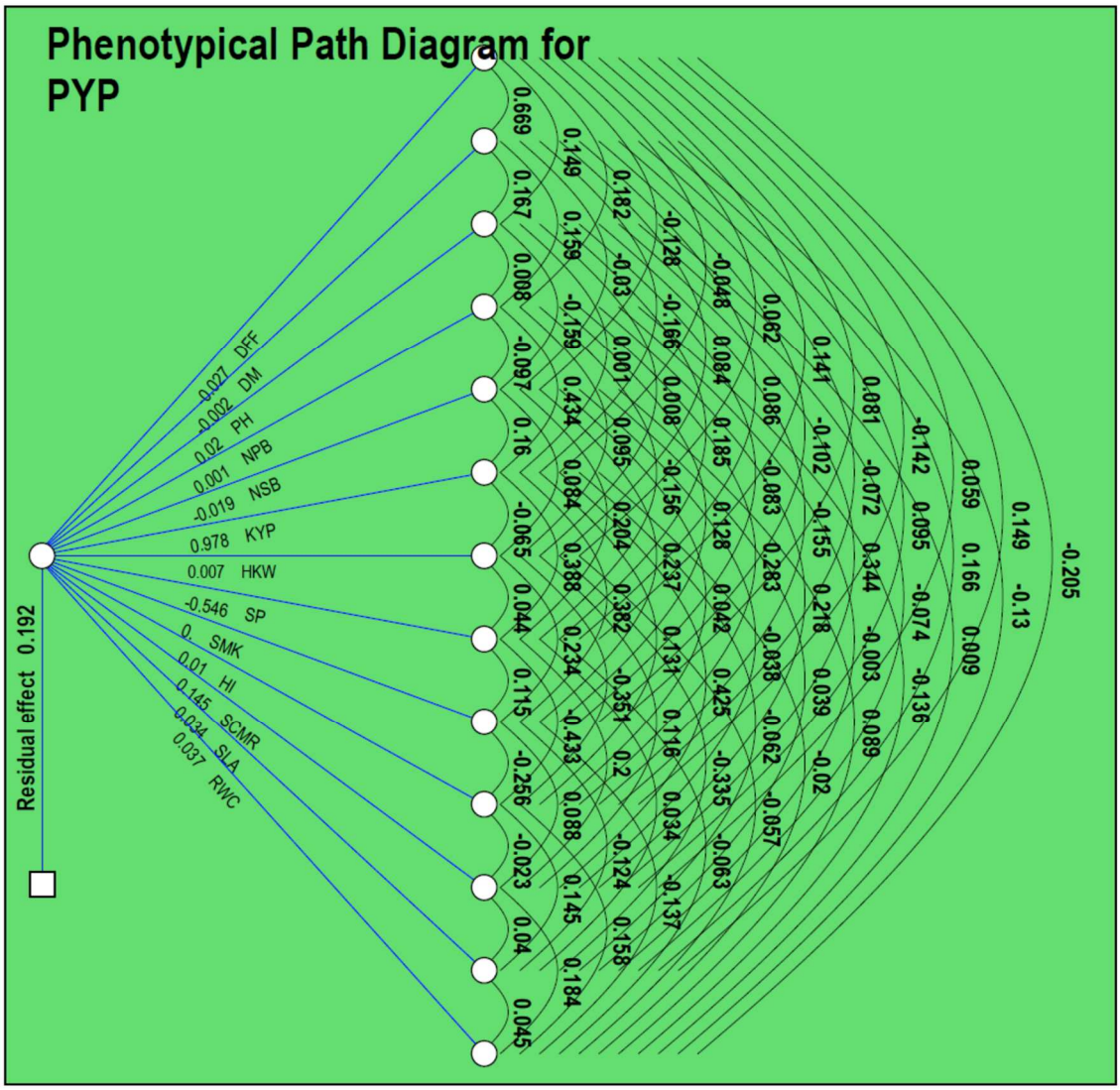

Fig.4.3. Phenotypic path diagram for yield, yield attributes and water use efficiency related traits in groundnut

4.6.1.4 Sound mature kernel per cent

Sound mature kernel per cent (0.3055**) showed a significant positive correlation with pod yield plant^{-1}. Direct impact on pod yield plant^{-1} was detrimental and negligible (-0.0112). Kernel yield plant^{-1} (0.3697) exhibited high positive indirect effects. SPAD chlorophyll meter reading at 60 DAS (0.0144) and days to maturity (0.0020) showed positive and negligible indirect effects. Shelling per cent (-0.0628), harvest index (-0.0049), plant height (-0.0012) and number of primary branches plant^{-1} (-0.0006) demonstrated negative and negligible indirect influence. However, Kumar *et al.* (2019) observed negative and negligible direct effects on pod yield plant^{-1}. The findings of Bhakal and Lal (2017) were consistent with the results found in the current study for shelling per cent and number of primary branches plant^{-1}.

4.6.1.5 Harvest index (%)

Harvest index showed a strong positive correlation with pod yield plant^{-1} (0.3801**). Direct effect on pod yield plant^{-1} was favourable and negligible (0.0190). Additionally, it had moderate positive indirect effect on shelling per cent (0.2372); low positive indirect effects *via* kernel yield plant^{-1} (0.1270) whereas negligible positive indirect effects *via* sound mature kernel per cent (0.0029) and days to maturity (0.0014). SPAD chlorophyll meter reading at 60 DAS (-0.0038), plant height (-0.0022) and number of primary branches plant^{-1} (-0.0013) showed indirect negative negligible effects.

With contrast to this Korat *et al.* (2010) observed high positive direct effect. Reddy *et al.* (2017) found that plant height had negligible negative indirect effect.

4.6.1.6 SPAD chlorophyll meter reading at 60 DAS

Readings from the SPAD chlorophyll meter at 60 DAS (0.4661**) showed a highly significant positive correlation with pod yield plant^{-1}. The direct impact of this feature on pod yield plant^{-1} was favourable

and low (0.1634). Kernel yield plant^{-1} (0.4115) exhibited high positive indirect effect. Plant height (0.0049) demonstrated positive and negligible indirect impacts. It showed negative and low indirect effect *via* shelling per cent (-0.1094). This trait exhibited negative and negligible indirect effects *via* days to maturity (-0.0018), harvest index (-0.0004), number of primary branches plant^{-1} (-0.0010) and sound mature kernel per cent (-0.0010). These findings were in line with the reports of Bhargavi *et al.* (2017b). However, Alam (2014) reported negative negligible indirect effects of plant height *via* this trait.

The phenotypic residual impact was 0.192 indicating that the traits that were considered in the study contributed to the pod yield plant^{-1}.

The path analysis described the relevance of each character in association to the pod yield plant^{-1} as well as the effective measure of direct and indirect relationships. According to the path analysis, the kernel yield plant^{-1} (0.9688) had highest positive direct effect on pod yield plant^{-1} followed by SPAD chlorophyll meter reading at 60 DAS (0.1634), the harvest index (0.0190) and plant height (0.0144).

For majority of the traits such as kernel yield plant^{-1}, SPAD chlorophyll meter reading at 60 DAS, plant height and harvest index the indirect effects are positive. From the analysis of correlation and path co-efficient, kernel yield plant^{-1}, SPAD chlorophyll meter reading at 60 DAS, harvest index and plant height all showed high positive correlations and favourable direct and indirect influences on pod yield plant^{-1}. Therefore, the yield will be greatly increased by maintaining the other traits constant and increasing kernel yield plant^{-1}, SPAD chlorophyll meter reading at 60 DAS, harvest index and decreasing the plant height. The selection of parents in the hybridization programme that will contribute to a rise in the pod yield plant^{-1} in groundnut should therefore give adequate consideration to these characters.

Chapter - V

Summary & Conclusions

Chapter – V

SUMMARY AND CONCLUSIONS

The present investigation entitled “Genetic analysis of yield, yield attributes and water use efficiency related traits in groundnut (*Arachis hypogaea* L.)” was taken up in 36 genotypes of groundnut. The experiment was laid out in a Randomized Block Design (RBD) with three replications and 36 genotypes of groundnut were evaluated at dry land farm of S. V. Agricultural College, Tirupati, during *rabi*, 2021-2022. The present investigation was formulated with the following objectives.

1. To identify the promising genotypes for yield, yield attributes and water use efficiency (WUE) related traits.
2. To study genetic variability, heritability and genetic advance for yield, yield attributes and WUE related traits.
3. To study correlations among the yield, yield attributes and WUE related traits.
4. To study the genetic diversity among the genotypes using D^2 statistics for the yield, yield attributes and WUE related traits.

The data was recorded on fourteen traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, kernel yield plant^{-1} (g), hundred kernel weight (g), shelling per cent, sound mature kernel per cent, harvest index (%), SPAD chlorophyll meter reading at 60 DAS, specific leaf area at 60 DAS (cm^2 gm^{-1}), relative water content (%) and pod yield plant^{-1} (g).

The analysis of variance was carried out for fourteen yield, yield attributes and water use efficiency related traits and it revealed significant differences for all the characters studied among all the genotypes indicating the presence of considerable variability among the genotypes. Based on *per se* performance; TCGS-2223, TCGS-2040, TCGS-2039, TCGS-2230, TCGS-

2053, TCGS-2055, TCGS-2317, TCGS-2278, TCGS-2233 and TCGS-2052 were identified as the promising genotypes.

The genotype TCGS-2223 showed better performance for days to 50% flowering, days to maturity, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, shelling per cent, sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS, specific leaf area at 60 DAS, relative water content and pod yield plant^{-1}. The increase in pod yield plant^{-1} in the genotype TCGS-2040 was mainly due to days to 50% flowering, days to maturity, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, kernel yield plant^{-1}, shelling per cent, sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS and specific leaf area at 60 DAS. The genotype TCGS-2039 came to flowering early and exhibited higher values for plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, sound mature kernel per cent, SPAD chlorophyll meter reading at 60 DAS, relative water content and pod yield plant^{-1}.

The increase in pod yield plant^{-1} in genotype TCGS-2230 was mainly due to days to 50% flowering, days to maturity, plant height, number of secondary branches plant^{-1}, hundred kernel weight, harvest index, SPAD chlorophyll meter reading at 60 DAS and relative water content. The genotype TCGS-2053 exhibited better performance for plant height, number of primary branches plant^{-1}, kernel yield plant^{-1}, sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS, relative water content and pod yield plant^{-1}. The genotype TCGS-2055 recorded higher values for plant height, kernel yield plant^{-1}, sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS, specific leaf area at 60 DAS, relative water content and pod yield plant^{-1}.

The genotype TCGS-2317 came to maturity early and showed better performance for number of secondary branches plant$^{-1,}$ kernel yield plant^{-1}, hundred kernel weight, sound mature kernel per cent, specific leaf area at 60 DAS, relative water content and pod yield plant^{-1}. The genotype TCGS-2278 exhibited early flowering and maturity and also showed better performance for plant height, number of primary branches plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, shelling per cent, sound mature kernel per cent, specific leaf area at 60 DAS and pod yield plant^{-1}. TCGS-2233 reached flowering and maturity earlier and shown superior performance in terms of number of secondary branches plant^{-1}, kernel yield plant^{-1} and relative water content. A higher value in pod yield plant^{-1} in the genotype TCGS-2052 was mainly contributed by the characters number of primary branches plant^{-1}, harvest index and SPAD chlorophyll meter reading at 60 DAS.

TCGS-2223 performed better for all the traits examined except for plant height. TCGS-2053 exhibited high pod yield plant^{-1}, high kernel yield plant^{-1} and also stay green variety. As both these genotypes exhibited high yield, these two genotypes could be recommended for multi evaluation trails in multi environments.

Higher estimates of GCV and PCV was observed for the number of secondary branches plant^{-1} and number of primary branches plant^{-1}. Moderate GCV and high PCV values were exhibited by the traits harvest index and sound mature kernel per cent. Moderate GCV and PCV values were recorded for pod yield plant^{-1}, kernel yield plant^{-1}, specific leaf area at 60 DAS and plant height.

High heritability coupled with high genetic advance as per cent of mean were exhibited by number of primary branches plant^{-1}, number of secondary branches plant^{-1}, pod yield plant^{-1}, kernel yield plant^{-1}, plant height and specific leaf area at 60 DAS which indicates preponderance of additive gene action in expression of these characters and the selection would be effective for improvement of these characters. High heritability coupled with moderate

genetic advance as per cent of mean was exhibited by shelling per cent. Harvest index and sound mature kernel per cent recorded moderate heritability and high genetic advance as per cent of mean.This indicates that these characters were under additive genetic control and selection for genetic improvement will be worthwhile and may rapidly contribute to yield.

By using D^2 analysis, 36 genotypes of groundnut were grouped into nine clusters. The character *viz.,* shelling per cent contributed maximum towards genetic divergence followed by pod yield plant^{-1}, SPAD chlorophyll meter reading at 60 DAS, kernel yield plant^{-1}, number of secondary branches plant^{-1} and specific leaf area at 60 DAS.

Based on inter cluster distances, the clusters VI × IX, VI × VIII, I × IX, V × IX and VII × VIII were found to be more divergent in decreasing order of their magnitude. Hence, genotypes of these clusters could be utilized as parents and crossing among them would result in transgressive segregants in the hybridization programme.

TCGS-2053, K-6, TCGS-2235, Greeshma, TCGS-2223 and TCGS-2230 were found to be better performing in terms of yield, yield attributes and water use efficiency related traits. Hence hybridization programme with them as one of the parents may result in simultaneous improvement of yield, yield attributes and water use efficiency related traits.

Studies on character association analysis revealed highly significant positive association of kernel yield plant^{-1}, number of primary branches plant^{-1}, SPAD chlorophyll meter reading at 60 DAS, harvest index and sound mature kernel per cent with pod yield plant^{-1} as well as among themselves at both phenotypic and genotypic levels. Hence due emphasis should be given to these traits as improvement of these characters would result in increase in the pod yield plant^{-1}.

The results of path co-efficient analysis indicated that kernel yield plant^{-1} exhibited high positive direct effect on pod yield plant^{-1} followed by SPAD chlorophyll meter reading at 60 DAS, harvest index and plant height.

Hence it is suggested that preference should be given to the above characters in the selection programme to isolate superior lines with genetic potential for improving pod yield plant^{-1}.

Critical analysis of results obtained from character association and path analysis indicated that kernel yield plant^{-1} had strong positive association with pod yield plant^{-1} which also had high magnitude of positive direct effect on pod yield plant^{-1}. This revealed the importance of this component trait in selection of superior genotypes for higher yield in groundnut.

Overall analysis of the present study revealed that the genotypes TCGS-2053, K-6, TCGS-2235, Greeshma, TCGS-2223 and TCGS-2230 were found promising for yield, yield attributes and water use efficiency related traits. Hence, these genotypes can be further utilized in the breeding programmes for the development of high yielding varieties with high water use efficiency.

Future line of work

TCGS-2223 was found to be superior for most of the yield, yield attributes and water use efficiency related traits *viz.,* days to 50% flowering, days to maturity, primary branches plant^{-1}, number of secondary branches plant^{-1}, kernel yield plant^{-1}, hundred kernel weight, shelling per cent, sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS, specific leaf area at 60 DAS, relative water content and pod yield plant^{-1}.TCGS-2053 outperformed all the other genotypes in terms of pod yield plant^{-1}. Germplasm lines from diverse clusters showing complementarity for traits of interest could be selected as parents for hybridization programme to produce heterotic effect. By comparing the genetic divergence between clusters and *per se* performance of genotypes, the cross combinations K-6 ×

TCGS-2053 and TCGS-2235 × TCGS-2053 could be recommended to increase water use efficiency related traits in groundnut. Whereas, the cross combinations Greeshma × TCGS-2053 and TCGS-2223 × TCGS-2230 could be recommended to obtain transgressive segregants for yield, yield attributes.

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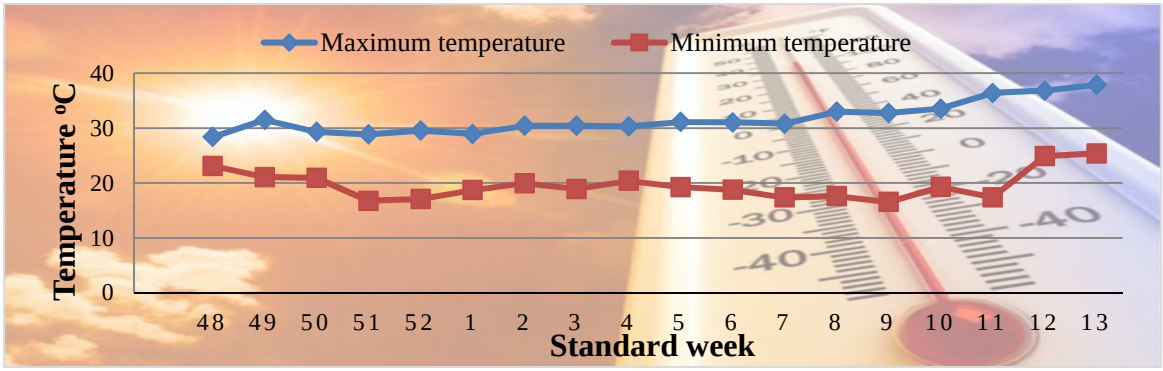
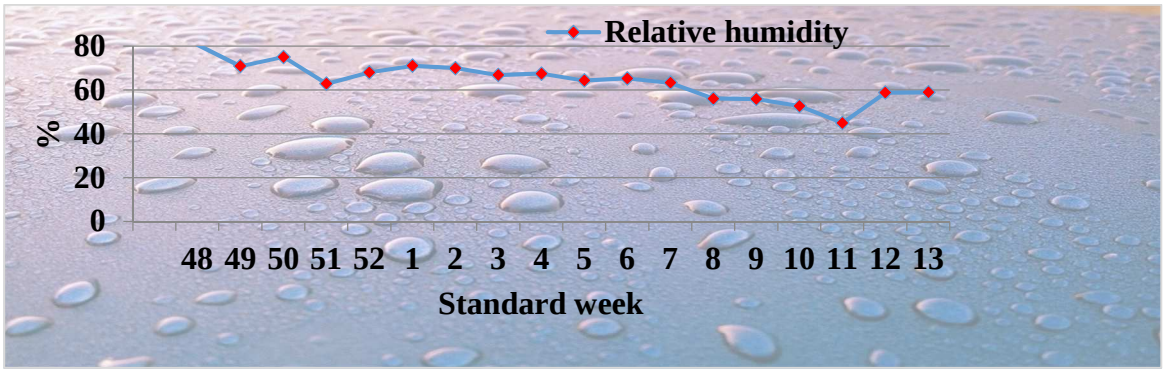
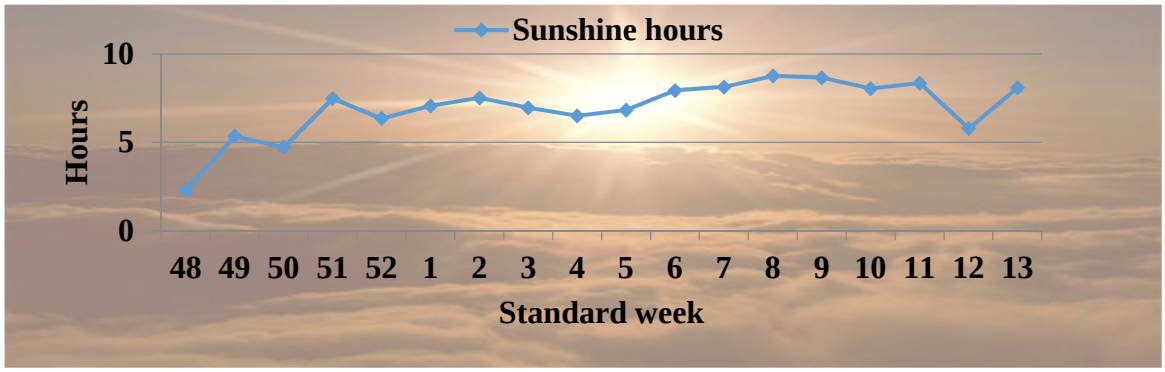
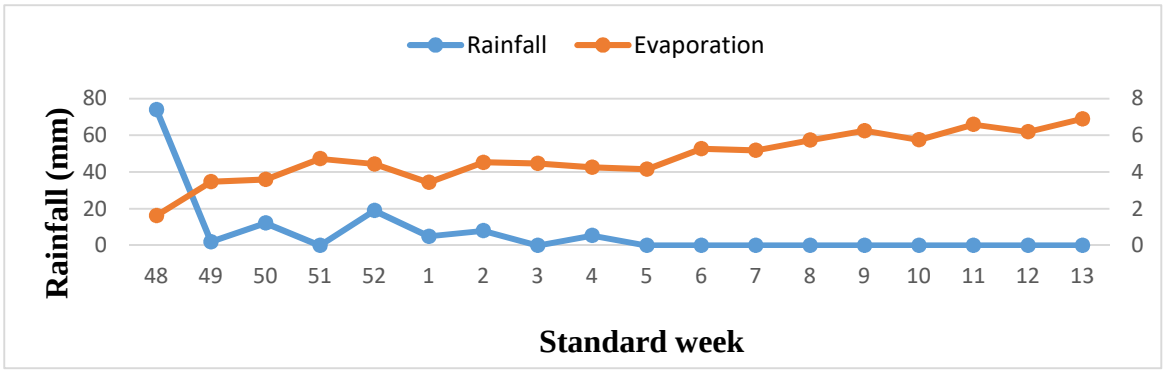
Appendices

APPENDIX


Maximum temperature
Minimum temperature
Temperature ºC
40
30
20
10
0
48 49 50 51 52 1 2 3 4 5 6 7 8 9 10 11 12 13
Standard week


Relative humidity
%
80
60
40
20
0
48 49 50 51 52 1 2 3 4 5 6 7 8 9 10 11 12 13
Standard week


Sunshine hours
Hours
10
5
0
48 49 50 51 52 1 2 3 4 5 6 7 8 9 10 11 12 13
Standard week


Rainfall
Evaporation
Rainfall (mm)
80
60
40
20
0
8
6
4
2
0
48 49 50 51 52 1 2 3 4 5 6 7 8 9 10 11 12 13
Standard week

GENETIC ANALYSIS OF YIELD, YIELD ATTRIBUTES AND WATER USE EFFICIENCY RELATED TRAITS IN GROUNDNUT (*Arachis hypogaea* L.)

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ABSTRACT

The present study named "Genetic analysis of yield, yield attributes and water use efficiency related traits in groundnut (*Arachis hypogaea* L)" for fourteen traits was carried out at the dry land farm of the S. V. Agricultural College, Tirupati, during *rabi* in 2021–2022. Five randomly selected plants were choosen to take the data in order to determine the most promising genotypes, evaluate genetic diversity among genotypes, estimate genetic parameters and analyse genetic correlations and path co-efficients. Analysis of variance (ANOVA) results showed highly significant differences for each character under study proving that genotypes vary greatly. *Per se* performance analysis revealed that the genotypes TCGS-2223, TCGS-2040, TCGS-2039, TCGS-2230 and TCGS-2053 were superior for the majority of parameters related to yield, yield attributes and water use efficiency. The number of secondary branches plant^{-1} and the number of primary branches plant^{-1} displayed greater GCV and PCV values. Number of primary branches plant^{-1}, number of secondary branches plant^{-1}, pod yield plant^{-1}, kernel yield plant^{-1}, plant height and specific leaf area at 60 DAS demonstrated high heritability coupled with high genetic advance as per cent of mean suggesting that additive gene action predominates in the expression of these characters and that selection would be successful in enhancing these traits. Using D^2 analysis, 36 genotypes of groundnut were divided into nine groups. Based on the distances between the clusters, it was found that the clusters VI-IX, VI-VIII, I-IX, V-IX and VII-VIII were increasingly divergent in their magnitudes. In order to produce transgressive segregants, the genotypes of these clusters might be employed as parents in the hybridization scheme. To enhance features associated with water use efficiency, the cross combinations K-6 × TCGS-2053 and TCGS-2235 × TCGS-2053 may be suggested. By analysing the genetic divergence between clusters and genotype *per se* performance; Greeshma × TCGS-2053 and TCGS-2223 × TCGS-2230 could be recommended to obtain transgressive segregants for yield and yield attributes. The most significant contribution to diversity was made by shelling per cent followed by pod yield plant^{-1}, SPAD chlorophyll meter reading at 60 DAS, kernel yield plant^{-1}, number of secondary branches plant^{-1} and specific leaf area at 60 DAS. Character association study demonstrated a highly substantial positive correlation between the sound mature kernel per cent, harvest index, SPAD chlorophyll meter reading at 60 DAS, kernel yield plant^{-1} with pod yield plant^{-1} and between these traits at both the phenotypic and genotypic levels. Hence, it is important to place the appropriate emphasis on these qualities in order to enhance them and increase pod yield plant^{-1}. The path analysis showed that the direct effect of the kernel yield plant^{-1} on the pod yield plant^{-1} was extremely positive and it was followed by SPAD chlorophyll meter reading at 60 DAS, harvest index and plant height. The genotypes TCGS-2053, K-6, TCGS-2235, Greeshma, TCGS-2223 and TCGS-2230 were found to be promising for yield, yield related attributes and traits linked to water use efficiency by the overall analysis of the current study. These genotypes can therefore be used in the crossing programme to create high yielding cultivars with great water use efficiency.