GENETIC STUDIES FOR EARLY MATURITY, YIELD AND YIELD ATTRIBUTES IN GROUNDNUT (*Arachis hypogaea* L.)

By

GUMMA VINEELA NEEHARIKA

B.Sc. (Hons.) Ag.

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

MASTER OF SCIENCE IN AGRICULTURE

(GENETICS AND PLANT BREEDING)

CHAIRPERSON: Dr. C. KIRAN KUMAR REDDY

ANGRAU

DEPARTMENT OF GENETICS AND PLANT BREEDING
SRI VENKATESWARA AGRICULTURAL COLLEGE, TIRUPATI
ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY
GUNTUR- 522 034, A.P.

DECLARATION

I, **Ms. GUMMA VINEELA NEEHARIKA** hereby declare that the thesis entitled **"GENETIC STUDIES FOR EARLY MATURITY, YIELD AND YIELD ATTRIBUTES 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.

Place : Tirupati

Date :

(G. VINEELA NEEHARIKA)
ID. No. TAM/2020-16

CERTIFICATE

Ms. GUMMA VINEELA NEEHARIKA has satisfactorily prosecuted the course of research and that thesis entitled **"GENETIC STUDIES FOR EARLY MATURITY, YIELD AND YIELD ATTRIBUTES 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.

Date:

(Dr. C. KIRAN KUMAR REDDY)
Chairperson

CERTIFICATE

This is to certify that the thesis entitled **"GENETIC STUDIES FOR EARLY MATURITY, YIELD AND YIELD ATTRIBUTES IN GROUNDNUT (*Arachis hypogaea* L.)"** submitted in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** of the Acharya N.G. Ranga Agricultural University, Lam, Guntur is a record of bonafide original research work carried out by **GUMMA VINEELA NEEHARIKA** under our guidance and supervision.

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

Thesis approved by the Student's Advisory Committee:

Chairperson : Dr. C. KIRAN KUMAR REDDY _____
Senior Scientist
Dept. of Genetics and Plant Breeding
R.A.R.S
Tirupati – 517 502, A.P.

Member : Dr. B. RUPESH KUMAR REDDY _____
Assistant Professor
Dept. of Genetics and Plant Breeding
S.V. Agricultural College
Tirupati – 517 502, A.P.

Member : Dr. P. LAVANYA KUMARI _____
Assistant Professor & Head
Dept. of Statistics and Computer Applications
S.V. Agricultural College
Tirupati – 517 502, A.P.

Date of final viva-voce:

ACKNOWLEDGEMENTS

At the outset, I submit that it is by the blessings of ***The Almighty,*** *I have been able to complete my studies successfully hitherto and present this humble piece of work, for which I am eternally indebted.*

With endless pleasure, deep sense of gratitude and honorable respect, I bestow my earnest and wholehearted thanks to my esteemed Chairperson of Advisory Committee ***Dr. C. Kiran Kumar Reddy,*** *Senior Scientist, Department of Genetics and Plant Breeding, Regional Agricultural Research station, Tirupati, for his perspicuous nature, valuable guidance, impeccable logic, untiring help, constant encouragement and constructive criticism which have instilled in me the script of confidence to successfully complete the thesis for which I will be grateful for the rest of my life.*

I humbly place on record my respect and gratitude to ***Dr. B. Rupesh Kumar Reddy,*** *Assistant Professor, Department of Genetics and Plant Breeding, S.V. AgriculturalCollege, Tirupati and member of my Advisory Committee for his valuable guidance, affectionate attitude, healthy criticism, patience, understanding and constant encouragement at every stage which has contributed in making this modest endeavor a reality.*

I sincerely accentuate my everlasting gratitude to the revered memberof my Advisory Committee ***Dr. P. Lavanya Kumari****, Assistant Professor & Head, Department of Statistics and Computer Applications, S.V. Agricultural College, Tirupati, for her encouragement, valuable suggestions, amenable and stupendous guidance during the course of investigation.*

With profound respect, I extend my gratitude to ***Dr. R. P. Vasanthi,*** *Associate Dean and University Head, Department of Genetics and Plant Breeding, S.V. Agricultural college, Tirupati for her help and guidance for successful completion of my investigation.*

I respectfully acknowledge my gratitude to ***Dr. M. Reddi Sekhar****, Professor and Head, Department of Genetics and Plant Breeding,* ***Dr. D. Lokanadha Reddy,*** *Retired Professor and Head, Department of Genetics and Plant Breeding,* ***Dr. P. Shanthi,*** *Associate Professor, Department of Genetics and Plant Breeding,* ***Dr. M. Sreevalli Devi,*** *Assistant Professor, Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati for their help and guidance during the period of my study which enabled the successful completion of my work.*

I express my heartfelt thanks to ***Smt Lakshmi, Mahesh, Vasu, Surya, Tony*** *and other field staff and farm labour for their timely co-operation in the field operations.*

Diction is not at all enough to express my feelings towards my most venerable beloved parents ***Smt. A. Madhavi Latha,*** *and* ***Sri. G. Srinivasarao,*** *my grandmother* ***Smt. A. Koteswaramma*** *and my brother* ***Vineel Vihar*** *for their constant inspiration,*

encouragement, guidance, prayers, love and efforts in shaping my career since childhood and bring out the best in each of my endeavors with boundless affection and moulded me to reach every foot step of my life with full of confidence and attention.

It's my privelage to extend heartful thanks to my best friends ***Geetha and Yamini*** *who helped and encouraged me to reach foot step of my Msc (Ag) career with full of confidence and to my special friends* ***Vineesha, Navya, Akshitha and Pallavi*** *for their support and help in carrying out the entire research work smoothly.*

I cordially concede my gratitude to my colleagues ***Divya, Dinesh, Jyothirmai, Hema Sai, Mounika, Pawan, Praveen, Soumya and Srikanth*** *for their cooperation during study.*

I express my heartfelt gratitude and thanks to my seniors ***Amarnath, Sravani, Kalpana, Hema Sree, Deepthi, Pallavi, Deepika, Sasikala, and Yashwant*** *for their valuable guidance. I have immense pleasure to extend my whole hearted thanks to my juniors* ***Vidya, Anil, Venkat, Nagendra, Praveen, Gireesh, Lokesh, Manasa, Swarna, Vishnu, Bhanu, Sai Teja and Sowmya.***

It is a pleasure to acknowledge the affection and help rendered by Non-teaching staff ***Venkatalakshmi, Munirathnam, Thyagaraju Naidu and Ramesh,*** *Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati.*

I am highly thankful to ***Acharya N.G. Ranga Agricultural University****, Guntur for all the facilities extended during the period of my post-graduation programme and financial assistance provided during my study.*

Finally, I thank ***Sai Graphics*** *for their services in printing the thesis.*

Vineela…

LIST OF CONTENTS

LIST OF TABLES

LIST OF ILLUSTRATIONS

LIST OF PLATES

LIST OF APPENDICES

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
CD	:	Critical difference
Contd.	:	Continued
CoV_g	:	Genotypic covariance
CoV_p	:	Phenotypic covariance
CTT	:	Cumulative Thermal Time
CV	:	Co-efficient of variation
D	:	Intra cluster distances
D^2	:	Inter cluster distances
DAS	:	Days after sowing
DA25E	:	Days to accumulation of 25 flowers from emergence
DA40E	:	Days to accumulation of 40 flowers from emergence
DA50E	:	Days to accumulation of 50 flowers from emergence
Df	:	Degrees of freedom
DFF	:	Days to 50% flowering
DIFE	:	Days from emergence to initial flowering
DM	:	Days to maturity

DOF25	:	Days from opening of first flower to opening of 25 number of flowers
DOF40	:	Days from opening of first flower to opening of 40 number of flowers
DOF50	:	Days from opening of first flower to opening of 50 number of flowers
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
HPW	:	Hundred pod weight
i.e.,	:	That is
IMP	:	Number of immature pods plant^{-1}
Kg	:	Kilogram
M	:	Meters
Max.	:	Maximum
Min.	:	Minimum
MP	:	Number of mature pods plant^{-1}
Mt	:	Million tonnes
No.	:	Number
NSMK	:	Number of sound mature kernels

P_p	:	Phenotypic path coefficient
P_g	:	Genotypic path coefficient
PB	:	Number of primary 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
RP%	:	Percentage of ripe pods
S. No.	:	Serial Number
SB	:	Number of secondary branches plant^{-1}
SE(d)	:	Standard error difference
SE(m)	:	Standard error of mean
SP	:	Shelling per cent
SYP	:	Seed yield plant^{-1}
t ha^{-1}	:	Tonnes per hectare
Via	:	Through
viz.,	:	Namely
vs.	:	Against

Name of the author	:	**GUMMA VINEELA NEEHARIKA**
Title of the thesis	:	**GENETIC STUDIES FOR EARLY MATURITY, YIELD AND YIELD ATTRIBUTES IN GROUNDNUT (*Arachis hypogaea* L.)**
Degree to which thesis is submitted	:	**MASTER OF SCIENCE**
Faculty	:	**AGRICULTURE**
Department	:	**GENETICS AND PLANT BREEDING**
Chairperson	:	**Dr. C. KIRAN KUMAR REDDY**
University	:	**ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY**
Year of submission	:	**2022**

ABSTRACT

The present study entitled "Genetic studies for early maturity, yield and yield attributes in groundnut (*Arachis hypogaea L.)*" was carried out to estimate the extent of genetic variability, genetic divergence and trait associations for high yield, earliness and their contributing traits in groundnut. Thirty six genotypes were evaluated in alpha lattice design with two replications at Regional Agricultural Research Station, Tirupati, during *Rabi*, 2021-22.

The variability among all the 36 genotypes is highly significant for the traits *viz.*, days to first flower from emergence, days to 50% flowering, days from opening of 1st flower to opening of 25, 40 and 50 flowers, days to accumulation of 25, 40 and 50 flowers from emergence, days to maturity, harvest index, percentage of ripe pods, shelling percentage, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of mature pods plant^{-1}, number of immature plant^{-1}, pod yield plant^{-1}, seed yield plant^{-1}, 100 kernel weight, 100 pod weight and number of sound mature kernels. Of all the thirty six entries tested, TAG 24, TCGS 2339, TCGS 2326, UBEK 21-40, UBEK 21-43 and UBEK 21-74 were noteworthy early maturing entries (90 days) with superior agronomic characters. Studies on flowering traits in all the genotypes revealed maximum number of flowers opening on a single day was achieved on 5th day from 1st day of flower opening. Number of flowers opening on fifth day was higher in genotypes maturing in 90days rather than the genotypes maturing at 100 and 110 days. For all the early maturing genotypes, 100 pod weight (g), 100 kernel weight (g) and harvest index (%) was below 90g, 40g and 50%, respectively.

Study of genetic variability revealed high PCV and GCV for characters *viz.,* days from opening of 1st flower to opening of 25 number of flowers, number of primary branches plant^{-1} and number of secondary branches plant^{-1}. High heritability coupled with high genetic advance as per cent of mean were recorded for days from opening of 1st flower to opening of 25, 40, 50 number of flowers, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of mature pods plant^{-1}, harvest index, 100 pod weight and 100 kernel weight.

Genetic divergence studies revealed grouped the 36 genotypes into six clusters. Genotypes from cluster III (TAG 24, TCGS 2339, TCGS 2326, UBEK 21-40, UBEK 21-43, UBEK 21-74 and ISK-II-2020-12) targeting characters *viz.,* days to accumulation of 25 and 40 flowers from 1st flower and days to maturity and genotype (UBEK 21-67) from cluster IV for 100 pod weight and 100 kernel weight might be selected for developing genotypes with early maturity of 90 days. To develop genotypes with higher pod yields, genotypes from cluster II and V with high mean values for pod yield plant^{-1}(UBEK 21-68, UBEK 21-70) and TCGS 2233, TCGS 2348, UBEK 21-68, ISK-II,2020-4 for number of mature pods plant^{-1} are to be utilized in hybridization programs.

Character association studies revealed two phenological traits *viz.*, days to accumulation of 25 and 40 flowers from emergence contributed significantly to days to maturity. Even though other traits exhibited significant inter-se correlations among them, their association with days to maturity was negligible. Therefore, for developing early maturing genotypes, selection for early accumulation of 25 and 40 flowers from emergence would be advantageous. For pod yield plant^{-1}, significant positive correlations were observed with days to maturity, seed yield plant^{-1}, number of mature pods plant^{-1}, 100 pod weight, 100 kernel weight and harvest index but number of immature pods plant^{-1} was observed to be negatively correlated. Thus, for developing high yielders, selection should be focused on number of mature pods plant^{-1}, days to maturity, harvest index, 100 pod weight, 100 kernel weight and seed yield plant^{-1}. For developing early maturing genotypes with optimum yield levels, selection criteria could be days to accumulation of 25 flowers and 40 flowers from emergence with optimal number of ripened pods at 90 days duration with a harvest index (<50%), 100 pod weight (90g) and 100 kernel weight (<40g).

Chapter - I

Introduction

Chapter I

INTRODUCTION

Cultivated groundnut (*Arachis hypogaea L.*) commonly known as peanut, is an annual legume and is widely grown in the tropics and subtropics between latitudes 40°N and 40°S. It is a segmental allotetraploid (2n = 4x = 40) and belongs to the family Fabaceae. It is native of South America with its cultivation distributed over a wide range of environments in more than 100 countries.

Botanically, groundnut can be classified into two sub-species (*hypogaea* and *fastigiata*), which mainly differs in their branching pattern. Both the sub-species are again divided into two botanical forms. Sub-species *hypogaea* is classified into *var. hypogaea* (Virginia) and *var. hirsuta* whereas, sub-species *fastigiata* is divided into *var. fastigiata* (Valencia) and *var. vulgaris* (Spanish) **(**Krapovickas and Gregory 1994).

Groundnut kernels are an incredible source of high-quality edible oil (45-56%), easily digestible protein (13-36%) and carbohydrates (10-20%) (Nageswara and Nigam, 2003). It has a distinct position among the oilseeds, as it can be consumed and utilized in various ways. Groundnut ranks first among oilseed crops in India and is considered as the world's third and fourth largest source of vegetable protein and edible oil, respectively (Agricultural Market Intelligence Centre, ANGRAU, 2021).

Major groundnut producing countries are China, India and Nigeria. Among the Indian states, Gujarat, Andhra Pradesh, Madhya Pradesh and Karnataka are the major peanut growing states. Globally, it is cultivated in an area of 31.5 million hectares with production and productivity of 53.6 million tonnes and 1699 kg ha^{-1}, respectively (FAOSTAT, 2020). India ranks second among the groundnut producing countries in the world with an area of 6.09

million hectares, production of 10.21 million tonnes and productivity of 1676 kg ha^{-1}. In Andhra Pradesh, it is cultivated in an area of 0.87 million hectares with a production of 0.78 million tonnes and an average productivity of 894 kg ha^{-1} (Directorate of Economics and Statistics, Govt. of A.P, India, 2020-2021).

Groundnut is characterized with indeterminate flowering pattern. Thus, at any point of harvest, a wide range of pod maturity patterns are observed. Thus, pod maturity percentage with promising shelling percentage, number of sound mature kernel commands the duration of groundnut. Groundnut is being grown in varied situations from rainfed to irrigated and resource rich to marginal conditions. As such, many varieties with varied durations in spanish bunch and valencia types are under cultivation. Most of the agro-ecological situations are subjected to short growing seasons, end of season droughts, early frosts and late-season diseases and insect pests affecting the productivity of late maturing varieties. Further, short growing seasons which prevails in semi-arid regions prevent peanut from maturing synchronously thus reducing the yield and quality of produce and enhances the growth of toxin producing molds during storage (N'Doye and Smith, 1993). Adoption of early maturing and high yielding cultivars is expected to mitigate the above-mentioned lacunae and also offer less competition to the late maturing crops in groundnut based intercropping systems.

Short duration of a genotype is a relative term that differs from region to region and season to season (Virmani and Singh,1986). A 140-day cultivar in USA or a 120-day cultivar in China or a <100-day cultivar in Southeast Asia or a < 90-day cultivar in Northern fringes of West Africa may be classified as short duration cultivar in these countries. A cultivar maturing in 90 days during summer may turn to maturity in >100days during cold seasons. Thus, duration in groundnut is determined using various criteria like shelling percentage, percentage of ripe pods, stability of pod yields at varied dates of harvest (like 90, 100 and 110 days).

Breeding for earliness in groundnut is always an integral objective in many crop improvement programs across the globe. Due to the subterranean nature of fruiting and indeterminate flowering habit, assessment of maturity is difficult. Many studies indicate that inheritance of maturity is not simple, however components affecting early maturity are highly heritable which include phenological stages such as days to flowering, days to produce first 25, 40 and 50 flowers (Bailey and Bear, 1973; Krishna Sastry *et al.*,1985 and Khalfaoui, 1990b). Limited information is available on genetic diversity for early maturity and its components coupled with yield and desirable seed attributes. Till date, no coherent studies are available to screen for early maturity coupled with yield, promising pod and kernel characters when the maturity duration requirement is 100 and less than 100 days.

Therefore, there is a need to identify characters that contributes to early maturity. Phenology of stable and agronomically superior sources of groundnut genotypes need to be studied in detail to identify genotypes differing in various components of early maturity. Studies on identifying sources for early maturity was earlier reported by Bera *et al.* (2004), Upadhyaya *et al.* (2006) and Coulibaly *et al.* (2017). However, limited information is available on sources of early maturity in agronomically superior lines generated at Regional Agricultural Research Station, Tirupati. Therefore, quantification of variability, heritability, analysis of genetic advance, nature of gene action, genetic diversity and character association will sum up as a functionality and sound criteria can be formulated to improve trait of interest *i.e.,* earliness.

Keeping in view the above perspectives, the present research work is formulated with the following objectives.

OBJECTIVES OF INVESTIGATION

1. To quantify genetic variability and genetic parameters for traits contributing to early maturity, yield and yield components in groundnut.
2. To study genetic diversity among groundnut genotypes.
3. To elucidate information on trait associations among phenological traits contributing to earliness, yield and yield components.

Chapter - II

Review of Literature

Chapter – II

REVIEW OF LITERATURE

Attempts are made to review the published literature to identify the genetic parameters, genetic divergence, correlation and path analysis for traits contributing to earliness, yield and yield components in groundnut. The review of literature is presented below under different sub-headings.

2.1 Genetic variability, heritability and genetic advance

2.2 Genetic divergence

2.3 Character association

2.4 Path coefficient analysis

2.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The exploitation of the genetic variability in the available germplasm is a prerequisite in the breeding programme for increasing yield and other components. The effectiveness of selection is dependent upon nature, extent and magnitude of genetic variability present in the material and the extent to which it is heritable.

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

heritability and genetic advance have an immense value in identifying superior genotypes.

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

Bailey *et al.* (1973) reported the usefulness of two characters *viz.,* days to first flowering and days to accumulation of given number of flowers as important components of early maturity in groundnut. They also demonstrated the high proportion of first 25 flowers developing into mature pods.

Chiow *et al.* (1983) evaluated the selection potential for early maturity in 39 progeny lines of advanced generations from a cross between an early maturing spanish and a large fruited virginia type. Substantial variability was observed for yield, seed weight/20 fruits, while less variability was observed for 20-fruit weight and maturity index. Heritability estimates were found to be highest for yield, intermediate for fruit weight, seed weight/20 fruits and lowest for maturity index.

Khalfaoui (1990b) studied heredity of extreme precocity in a cross between ‘73-30’ and ‘Chico’ using days from sowing to emergence, days from emergence to first flowering, number of flowers produced during first four days of flowering and percentage of ripe pods at 80 days after sowing as parameters which recorded medium to high estimates of broad sense heritability. They recorded that pod ripening precocity is determined by duration of intense flowering and the time taken by fertilized flower to develop into ripe pod.

N’Doye and Smith (1993) crossed five early maturing lines of diverse origin in complete diallel to estimate the heritability of factors producing differential earliness among the lines and to determine if new recombinants could be developed for use as germplasm or cultivars. Measures were made on a plant basis for the number of days from planting to emergence, number of days to first, fifth, tenth, fifteenth, twentieth and twenty-fifth flower, number of full-size pods, mature pods, and percent mature pods. Mean broad sense

heritability estimates for the traits examined ranged from 36 to 45%. Heritability estimates for specific reproductive stages on individual crosses ranged from 4 to 65%, with no cross recording high measures for all traits under study.

Ali *et al.* (1994) conducted a study in two peanut crosses to determine the potential effectiveness of selection for early maturity and seed size by estimating heritability for each trait and correlations among them. Both narrow sense and broad sense heritability estimates were found high for seed weight, maturity index and pod length in both crosses suggesting selection for these traits can be practiced in early segregating generations.

Upadhyaya *et al.* (1994) studied the inheritance of two components of early maturity in diverse crosses belonging to Spanish, Valencia and Virginia types and observed that their inheritance was not simple. Days to first flower being controlled by single gene with additive gene action, whereas, the days to accumulation of 25 flowers was controlled by three genes with two types of epistatic interactions.

Bera *et al.* (2004) screened 768 Spanish bunch groundnut germplasm for earliness using 8 short duration elite cultivars as checks. The results showed wide range of variation for pod weight plant^{-1}, kernel weight plant^{-1}, shelling percent, 100 kernel weight and pod maturity percent at 80 days after germination. Forty two genotypes showed higher pod maturity percent at 80 days after germination than at 100 days after germination which were further evaluated in next season. 16 accessions out of these 42 genotypes repeated their earliness over better performing check and recorded 60 and above more shelling percent.

Jogloy *et al.* (2011) evaluated two hundred groundnut lines of 10 crosses in a randomized complete block design with two replications under fully irrigated conditions. It was inferred that selection would be more effective for maturity than for pod yield and seed size because of higher heritability estimates.

Zaman *et al.* (2011) assessed thirty four genotypes of groundnut and recorded highest genetic coefficient of variation for kernel yield ha^{-1} followed by kernel yield $plant^{-1}$, branches $plant^{-1}$, immature and mature nuts $plant^{-1}$, 100 kernel weight and plant height.

John *et al.* (2013) evaluated thirty seven 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 100 kernel weight. The traits days to 50% flowering, plant height, 100 pod weight, 100 kernel weight, shelling per cent and harvest index showed moderate to high heritability coupled with moderate to high genetic advance.

Rao *et al.* (2014) studied the genetic variability and association of important agronomic characters in fifty groundnut genotypes. They reported high heritability coupled with high genetic advance as per cent of mean for 100 kernel weight, dry pod yield, kernel yield, plant height and number of pods $plant^{-1}$.

Gupta *et al.* (2015a) evaluated sixty diverse genotypes of virginia groundnut for variability parameters and observed high PCV and GCV for plant height, number of primary branches $plant^{-1}$, number of mature pods $plant^{-1}$, 100 pod weight, 100 kernel weight, kernel yield $plant^{-1}$ and harvest index. The traits 100 kernel weight, 100 pod weight, biological yield $plant^{-1}$ and kernel yield $plant^{-1}$ showed high heritability coupled with high genetic advance indicating the preponderance of additive gene action and these traits possess high selection value.

Patil *et al*. (2015) reported the genetic variability for yield and its related traits in 49 groundnut genotypes. They observed the highest genetic coefficient of variation for secondary branches plant^{-1} followed by immature pods, mature pods, pod bearing nodes, pod yield and kernel weight plant^{-1}. The highest heritability was observed for matured pods plant^{-1} and days to 50% flowering (99.0%) followed by kernel weight plant^{-1} (98.0%), 100 kernel weight (98.0%), pod bearing nodes (98.0%), immature pods plant^{-1} (97.0%), plant height (96.0%), oil content (96.0%) and secondary branches (96.0%).

Vasanthi *et al.* (2015) evaluated 29 released and pre-release groundnut cultures for heritability. They reported high GCV, heritability and GAM for length of main axis and primary branches, 100 kernel weight and harvest index which were under the influence of additive gene action. The traits, weight of immature pods plant^{-1} and pod yield plant^{-1} exhibited moderate heritability coupled with high genetic advance, indicating predominant influence of additive gene action. The trait days 50% flowering recorded low GCV, high heritability and high GAM which was influenced by both additive and non-additive gene action.

Bhargavi *et al.* (2017a) evaluated twenty diverse genotypes of spanish bunch groundnut and reported high PCV and GCV for harvest index and pod yield ha^{-1}. High heritability accompanied with high genetic advance as per cent of mean was recorded for number of mature pods plant^{-1}, biological yield plant^{-1}, pod yield plant^{-1}, biological yield ha^{-1}, pod yield ha^{-1} and harvest index.

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}, 100 kernel weight, plant height, 100 pod weight, biological yield plant^{-1}, harvest index and number of branches plant^{-1} indicating the preponderance of additive gene action.

Hampannavar *et al.* (2018a) studied the genetic parameters in 144 groundnut genotypes and observed high GCV, PCV, heritability in addition to genetic advance as percent of mean for characters *viz.,* 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} indicating the presence of considerable genetic variation and additive gene effects.

Raza *et al.* (2018) carried out variability studies in 40 groundnut accessions for 13 characters. The number of primary branches plant^{-1}, 100 seed weight, pod yield plant^{-1} and kernel yield plant^{-1} recorded high PCV, GCV, heritability (broad sense) and genetic advance as percent of mean indicating that these characters were governed by additive gene action and simple selection could be used for their improvement. Days to 50% flowering, days to maturity, plant height, number of pods plant^{-1}, number of seeds pod^{-1}, shelling %, harvest index, protein per cent and oil per cent exhibited moderate to low GCV, PCV, high heritability and moderate to low genetic advance.

Mitra *et al.* (2021) assessed genetic parameters in 31 groundnut accessions and observed higher level of coefficient of variation both at phenotypic and genotypic level for number of pods plant^{-1}, secondary branches, kernel width and pod yield. Genetic advance with higher heritability indicated preponderance of additive variance for pod length, pod yield, and number of pods plant^{-1}. Low GCV and PCV values were documented for the traits namely, days to first flowering, days to maturity and days to 50% flowering, which indicate that there is hardly any opportunity for genetic enhancement of these characters via selection.

Shrotri *et al.* (2021) estimated genetic variability for pod yield and components in thirty groundnut genotypes. High heritability coupled with high genetic advance as per cent of mean was recorded by the kernel yield plant^{-1}, pod yield plant^{-1}, number of mature pods plant^{-1} and 100 kernel weight indicating that these characters are under additive genetic control.

2.2 GENETIC DIVERGENCE

Genetic divergence is an important factor and a prerequisite in any hybridization programme because hybrids between lines of diverse origin displays a greater heterosis than those between closely related parents. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right type parents for purposeful hybridization (Arunachalam, 1981).

The concept of D^2 statistics for measuring the divergence between the two populations was introduced by Mahalanobis, 1936. Rao, 1952 suggested the application of this technique for the assessment of genetic diversity in plant breeding. Crosses between divergent parents usually produce greater heterosis than those between closely related ones. Use of diverse parents in hybridization programme can serve the purpose of combining desirable genes or to obtain recombination.

A brief resume of work done on genetic diversity in peanut is presented below:

Upadhyaya *et al.* (2006) evaluated a groundnut core collection in two seasons to identify 21 early maturing landraces. Phenotypic diversity of these 21 landraces was assessed in three rainy and five post-rainy seasons, along with the three known sources of early maturity (Chico, Gangapuri, and JL 24). Principal component analysis (PCA) using the first 10 PC scores delineated the 21 landraces into three clusters. Landraces in clusters 2 and 3 showed a wide range of variability for several agronomic traits, indicating their usefulness in breeding programs for developing early maturing high yielding culitvaras with broad base.

Zaman *et al.* (2010) studied multivariate analysis using Mahalanobis D^2 statistic in order to group 34 groundnut genotypes into five clusters. The highest intra cluster distance was observed in cluster V and the lowest in cluster II. The highest inter cluster distance was observed between the clusters IV and III and

the lowest between clusters V and I. The characters days to 50% flowering, days to maturity, number of branches plant^{-1}, number of matured nuts plant^{-1} and kernel size contributed maximum towards divergence.

Kumar *et al.* (2010) evaluated 64 germplasm lines of groundnut using Mahalanobis D^2 statistics and grouped them into seven clusters. Maximum inter-cluster distance was recorded between IV and VI representing wide divergence among these clusters, indicating that genotypes from these clusters may be considered for future breeding programmes.

Venkateswarulu *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.,* 100 kernel weight, shelling per cent and harvest index contributed maximum towards genetic divergence.

Suneetha *et al.* (2013) evaluated 29 groundnut genotypes and grouped into 9 clusters using D^2 analysis and reported that maximum contribution to diversity was by harvest index, days to emergence, length of main axis and minimum contribution by number of mature pods plant^{-1}.

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. The maximum intra-cluster distance was observed in cluster V and minimum intra-cluster distance was recorded in cluster II.

Bhakal and Lal (2015) studied genetic divergence using D^2 analysis for 40 groundnut genotypes and grouped them into seven clusters where cluster VI was the largest with 12 genotypes followed by cluster V containing seven genotypes, cluster I and VII consisted of six genotypes each, cluster III, IV and III consisted four, three and two genotypes respectively. The maximum inter-

cluster distance was found between cluster IV and VII followed by cluster I and VII and cluster V and VII.

Gupta *et al.* (2015b) carried out divergence studies among 60 groundnut genotypes using D^2 statistic and grouped them into 13 clusters. Maximum inter-cluster distance was observed between clusters III and V, followed by clusters IV and V and clusters II and IV, indicating that the genotypes in these clusters can be used as parents for yield improvement.

Chavadhari *et al.* (2017a), using D^2 analysis grouped 70 groundnut genotypes into 11 clusters where maximum inter-cluster distance was found between clusters IV and XI, followed by clusters VIII and IX and clusters II and VIII indicating that the genotypes of these groups are divergent from each other. The genotypes in above clusters revealed substantial difference in the means for important yield contributing characters suggesting that they can be used as parents for improvement in groundnut.

Gantait *et al.* (2017) studied genetic divergence among 21 groundnut genotypes using Mahalanobis D^2 statistic and grouped them into four distinct clusters. The maximum inter-cluster distance was observed between clusters II and III, followed by II and IV, whereas, it was minimum between cluster I and IV. It was suggested that using genotypes from clusters II, III and IV as parents could result in wide spectrum of promising genetic variability aiming at enhancement of groundnut yield.

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

Saini *et al.* (2020) estimated genetic diversity among 149 RILs of groundnut using D^2 analysis and classified them into 15 clusters. The maximum inter-cluster distance was observed between clusters III and VIII indicating existence of high variability. They suggested that genotypes in clusters III, VIII, XV, XIII and VII can be exploited as parents in the hybridization programme.

Mitra *et al.* (2021) assessed genetic divergence in 31 groundnut accessions using D^2 statistics and grouped them into 13 clusters. Clusters X and XII showed the largest distance suggesting that hybridization between them can be helpful to achieve high level of heterosis for their exploitation in trait improvement.

2.3 CHARACTER ASSOCIATION

Genetic improvement of yield is the primary concern to the plant breeder. But yield being a complex, quantitatively inherited character and is highly influenced by the environment. Pod yield being a complex character, the direct selection for this character would not be a reliable approach. Hence, a sound knowledge on the extent of association for yield components among themselves and with yield is essential for improving yield. Character association analysis measures the actual relationship between various plant characters and helps the plant breeder in fixing selection criteria for pod yield. 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 is subjected to changes in the environment. It measures the environmental deviations together with non-additive gene action. Genotypic correlation is the correlation of breeding values *i.e.,* additive × additive gene action. Assessing the association of yield components with each other and with yield is helpful in improvement of yield for which direct selection is not effective. A brief review of literature on the association of characters in groundnut is presented here under.

Pattee *et al.* (1977) developed a method to determine maturity based on seed-hull ratio. The ratio or maturity index was determined for fresh as well as air-dried pods and these ratios correlated well with physiological maturity index. The relationship between arginine maturity index and the air-dried seed-hull maturity index was also determined and the two indices were negatively correlated. They concluded that groundnut seed weight increased with maturity then decreased after full maturity.

Chiow *et al.* (1983) observed low phenotypic correlation for the maturity index with yield and yield components indicating the possible recovery of favourable recombinants with early maturity and high yields.

Khalfaoui (1990a) conducted experiments with 7 pure lines and one multiline representing the full range of harvesting dates. Earliness depended on the time taken for flowering and pod maturation. A marked negative correlation ($r = -0.87$) was found between pod maturity (percentage of ripe pods $stem^{-1}$ at day 90) and the interval between sowing and cumulated production of 50 flowers.

Rao *et al.* (1992) developed a procedure to select early-maturing, high-yielding peanut cultivars based on thermal time accumulation where cultivars were harvested when the crop was exposed to a predetermined cumulative thermal time (CTT) and were selected for high yield with acceptable levels of maturity-related traits in a no-stress environment. The predetermined CTT values used in selection for early-maturity represented a 20-day shorter crop duration than for the medium-maturing lines. The two predetermined CTTs, 1240 and 1470 °Cd (degree days) equate to 75 and 90 day durations, respectively.

N'Doye and Smith (1993) observed that days from planting to emergence and to a specified flower number (1^{st}, 5^{th}, 10^{th}, 15^{th}, 20^{th} and 25^{th} flower) were negatively correlated with number of full-size pods, mature pods and percent mature pods. The negative correlation means that fewer days to a given flower number resulted in larger numbers of full-size and mature pods at

harvest. The low number of significant coefficients in first date compared to the other dates is attributed to the low number of mature pods at the time of first harvest.

Ali *et al*. (1994) studied correlation among traits in two peanut crosses to determine effectiveness of selection for earliness. Significant positive correlation was observed between maturity and shelling percentage in both crosses. Pod length was highly correlated with seed weight, but correlation with maturity was non-significant indicating that selection for larger fruit and heavier seed could result in higher seed yield but may not favour early maturity.

Islam and Rasul (1998) observed significant positive correlation between days to 50% flowering and days to maturity, and between shelling percentage and seed yield.

Mahalakshmi *et al.* (2005) revealed that kernel yield per plant showed significant and positive association with days to 50% flowering, plant height, number of secondary branches, number of unproductive pegs, number of immature pods, number of mature pods, sound mature kernel weight, NSMK, total number of pods, total number of gynophores, shelling percentage, 100 kernel weight and pod yield indicating them as selection indices for improvement of kernel yield plant^{-1}.

Kotzamanidis *et al*. (2006) reported that early maturity is closely associated with narrow pod distance from the main stem promoting synchronous maturity of pods.

Korat *et al*. (2010) reported that pod yield plant^{-1} exhibited significant positive association with biological yield per plant, 100 kernel weight and harvest index.

Jogloy *et al.* (2011) evaluated two hundred groundnut lines of 10 crosses in a randomized complete block design with two replications under fully irrigated conditions. No association was observed between maturity and seed size. Maturity was negatively correlated with pod yield and harvest index,

suggesting the possibility to select for early maturing genotypes without detrimental effect on pod yield and harvest index. Selection for early maturity, high pod yield, large seeds, and high harvest index in the studied populations would be successful.

Zaman *et al.* (2011) indicated that seed yield plant^{-1} showed highly significant and positive association with pod size, number of pods plant^{-1}, kernel size and days to 50 % flowering.

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). On contrary, days to maturity showed the largest direct negative effect of -0.33 and -0.36. They observed significant genotype and genotype × environment interactions on yield plant^{-1}.

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}, 100 kernel weight and dry haulms yield.

The pod yield plant^{-1} showed highly significant positive association with number of pod bearing nodes, number of matured pods plant^{-1}, kernel weight plant^{-1} and days to 50% flowering. The number of branches plant^{-1}, height of main axis, pods plant^{-1}, days to 50% flowering, kernel weight plant^{-1}, shelling per cent and days to maturity were identified to be the important characters which could be used in selection for yield as reported by Patil *et al.* (2015).

Vasanthi *et al*. (2015) documented correlation and path co-efficient analysis and indicated that the number of mature pods plant^{-1}, number of primary branches plant^{-1} and 100 kernel weight should be given major emphasis for the development of high yielding genotypes.

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 days after sowing and 100 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.

Oppong-Sekyere *et al.* (2018) observed significant but negative correlation ($p \leq 0.05$) between days to emergence and days to 50% flowering ($r = -0.7962$). Pod yield was correlated positively and significantly with pod weight and harvest index. Shelling percentage had positive correlation with seed weight and negative correlation with pod weight and harvest index.

Hampannavar *et al.* (2018a) observed that kernel yield plant^{-1}, mature pods plant^{-1}, sound mature kernels and haulm yield plant^{-1} had significant positive phenotypic and genotypic correlation with dry pod yield plant^{-1}.

Correlation analysis reported 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}, 100 pod weight, 100 sound mature kernel, kernel yield and harvest index, while negative and significant for days to 50% flowering.

Mitra *et al*. (2021) observed significant positive correlation between number of secondary branches, pod length, number of pods plant^{-1} as well as kernel width, individually with pod yield suggesting simultaneous improvement in both the characters. Alternatively, a significant negative correlation was observed both for plant height and shelling per cent with pod yield.

2.4 PATH COEFFICIENT ANALYSIS

For rational improvement of yield and its components, knowledge of mechanism of association, cause and effect relationship, direct and indirect effects of component characters provide a basis in framing suitable selection methods. Simple correlation does not give the direct and indirect effects towards yield. Therefore, Path coefficient analysis is a useful method of estimating the direct and indirect contribution of an attribute.

The concept of path analysis was initially suggested by Wright (1921) but was applied for the first time in plant breeding by Dewey and Lu (1959). A path coefficient is a standardized partial regression coefficient. It measures the direct and indirect effects of independent variable on dependent variable and allows partitioning of the total correlation coefficient between two variables into direct and indirect components. Hence, path analysis is of much importance in any plant breeding programme.

The available literature on path coefficient analysis carried out in groundnut is furnished 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 100 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 nut size, shelling per cent, days to 50% flowering and days to maturity on seed yield ha^{-1}. 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 100 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}.

Pavan *et al.* (2013) evaluated 66 groundnut genotypes for path analysis studies and revealed high positive direct effect of pod yield plant^{-1} and shelling per cent on kernel yield. They also reported that pod yield plant^{-1} also had positive indirect effects through number of mature pods plant^{-1}, harvest index, shelling per cent and sound mature kernel per cent, whereas shelling per cent had positive indirect effects through sound mature kernel per cent.

Alam (2014) carried 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}. 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 100 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 100 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}. 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 for selection to improve the yield.

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 of pod yield plant^{-1}.

Reddy *et al.* (2017) carried out path analysis for kernel yield and its component characters in six parents and their 15 F_1 crosses in groundnut and inferred that pod yield exerted the highest positive direct effect on kernel yield followed by shelling percentage and pegs 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 100 kernel weight.

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.

Hampannavar *et al.* (2018a) 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.

Rathod and Toprope (2018) studied path analysis of 18 spanish bunch groundnut genotypes and revealed that total sugar, kernel yield, test weight, 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, 100 kernel weight and number of well filled and mature pods plant^{-1}. Hence direct selection for these traits would be effective.

Chapter - III

Material and Methods

Chapter III

MATERIAL AND METHODS

The experimental material used and methods followed pertaining to the present investigation entitled “Genetic studies for early maturity, yield and yield attributes in groundnut (*Arachis hypogaea* L.)” are briefly described here.

3.1 LOCATION OF THE EXPERIMENTAL SITE

The field experiment was conducted at Regional Agricultural Research Station (RARS), 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 material used in the present study consisted of thirty six genotypes of groundnut provided by Regional Agricultural Research Station, Tirupati, Acharya N.G Ranga Agricultural University, Andhra Pradesh. The list of thirty six groundnut genotypes and their pedigree are furnished in Table 3.1.

3.3 METHOD

3.3.1 Field Layout

The experiment was laid out according to alpha lattice design with incomplete blocks with two replications comprising of thirty-six genotypes, four blocks within a replicate and nine plots per block in each replication. Randomization of thirty-six genotypes was done manually. In each replication every genotype was sown in four rows of 4 m length with a spacing of 30 X 10 cm.

Table 3.1 List of 36 groundnut genotypes studied and their pedigree

S. No	Entry	Pedigree
1	TAG 24	TGS 2 X TGE 1
2	ROHINI	Tirupati 4 X TIR 45
3	TCGS 2223	Dharani X ICGV 06188
4	TCGS 2233	Dharani X ICGV 06100
5	TCGS 2339	TAG 24 X Dharani
6	TCGS 2347	TAG 24 X K. Harithandhra
7	TCGS 2348	TAG 24 X TCGS 1157
8	TCGS 2350	TAG 24 X Dharani
9	TCGS 2351	TAG 24 X Dharani
10	TCGS 2352	TAG 24 X Dharani
11	TCGS 2353	TAG 24 X Dharani
12	TCGS 2354	TAG 24 X Dharani
13	TCGS 2357	TAG 24 X K. Amaravathi
14	UBEK 21-39	TAG 24 X TCGS 1694
15	UBEK 21-40	TAG 24 X TCGS 1694
16	UBEK 21-43	TAG 24 X TCGS 1694
17	UBEK 21-61	TAG 24 X TCGS 1694
18	UBEK 21-67	TAG 24 X TCGS 1694
19	UBEK 21-68	TAG 24 X TCGS 1694
20	UBEK 21-70	TAG 24 X TCGS 1694
21	UBEK 20-32	TAG 24 X Dharani
22	UBEK 20-24	TAG 24 X Dharani
23	TCGS 2326	TAG 24 X Dharani
24	TCGS 2333	TAG 24 X TCGS 1173
25	JL 24	JL 86 X NcAc 343-75
26	UBEK 21-35	TAG 24 X TCGS 1694
27	UBEK 21-38	TAG 24 X TCGS 1694
28	UBEK 21-42	TAG 24 X TCGS 1694
29	UBEK 21-60	TAG 24 X TCGS 1694
30	UBEK 21-74	TAG 24 X TCGS 1694
31	UBEK 21-76	TAG 24 X TCGS 1694
32	ISK-II-2020-4	AICRP test entry. Pedigree not provided.
33	SB-I-2021-7	AICRP test entry. Pedigree not provided.
34	ISK-I-2021-8	AICRP test entry. Pedigree not provided.
35	ISK-II-2020-12	AICRP test entry. Pedigree not provided.
36	ISK-I-2021-21	AICRP test entry. Pedigree not provided.

Plate 1. General Field view of the experimental plot

3.3.2 Crop Husbandry

Field preparation was done till a fine tilth was obtained. FYM @ 10 t ha^{-1} was applied at the time of field preparation. The crop was raised under sprinkler irrigation and recommended dose of chemical fertilizers at the rate of 20 kg N, 40 kg P_2O_5 and 50 kg K_2O ha^{-1} in the form of Urea, Single Super Phosphate and Muriate of Potash and 500 kg of Gypsum ha^{-1} was applied at 35 days after sowing. Cultural practices like weeding were taken up to maintain good crop growth and need based plant protection measures were adopted to manage the pests and diseases.

3.3.3 Data Recording

Observations were recorded at 90 DAS, 100 DAS and 110 DAS 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, which was recorded on plot basis. For, days to accumulation of 25, 40 and 50 flowers from seedling emergence and days to accumulation of 25, 40 and 50 flowers from appearance of 1st flower, data was continuously recorded on same five plants which were numbered from 1 to 5 in each plot. The details of the data recorded are as follows.

3.3.3.1 Days from emergence to first flowering

Number of days required from seedling emergence to day on which first flower appeared on the plants was recorded as days from emergence to first flowering.

3.3.3.2 Days to accumulation of 25, 40 and 50 flowers from opening of first flower

Number of days required from opening of first flower to opening of 25, 40 and 50 flowers on each plant were recorded continuously on same plants numbered from 1 to 5.

3.3.3.3 Days to accumulation of 25, 40 and 50 flowers from emergence

Number of days required from seedling emergence to opening of 25, 40 and 50 flowers on each plant were recorded continuously on same plants with numbering done from 1 to 5.

3.3.3.4 Days to 50 % flowering

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

3.3.3.5 Days to maturity

Harvesting of single row in each entry for both the replications was done at 90 days followed by 100 days and 110 days after sowing. To fix days to maturity, double factorial ANOVA was performed on data collected for pod yield row^{-1} (converted to kg ha^{-1}) at three dates of harvesting *viz.*, 90 DAS, 100 DAS and 110 DAS. Pair wise comparisons were made for pod yields at two successive dates of harvesting, and the date on which significant higher pod yield was recorded was chosen to compute corresponding days to maturity for each genotype.

3.3.3.6 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.

3.3.3.7 Number of primary branches $plant^{-1}$

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

3.3.3.8 Number of secondary branches $plant^{-1}$

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

3.3.3.9 Number of mature pods plant^{-1}

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

3.3.3.10 Number of immature pods plant^{-1}

The number of underdeveloped pods were counted from randomly selected five plants at the time of harvest.

3.3.3.11 Percentage of ripe pods

Percentage of ripe pods were recorded based on the number of mature and immature pods plant^{-1}. This was calculated by using the formula,

$$\% \text{ of ripe pods} = \frac{\text{Number of mature pods per plant}}{\text{Total number of pods per plant}} \times 100$$

3.3.3.12 Hundred pod weight (g)

Randomly 100 dried pods were counted and weighed for each genotype per replication and was recorded as hundred pod weight using electronic top pan balance (precision of 0.001 g).

3.3.3.13 Shelling per cent

The shelling per cent was recorded based on the weight of the kernels recovered from 100 g of pods at 90 DAS, 100 DAS and 110 DAS, respectively, using the following formula,

$$\text{Shelling per cent} = \frac{\text{Kernel weight recovered from 100 g pods}}{\text{pod weight}\,(100\ \text{g})} \times 100$$

3.3.3.14 Hundred kernel weight (g)

The weight of randomly selected hundred kernels from each genotype and replication was recorded using electronic top pan balance and expressed in grams (precision of 0.001 g).

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

The pods obtained from each individual plant harvested at 90 DAS, 100 DAS and 110 DAS, respectively, were weighed in grams using electronic top pan balance (precision of 0.001 g).

3.3.3.16 Pod yield row^{-1} (kg)

The pods obtained from the plants in each row harvested at different dates were weighed in kilograms using electronic top pan balance (precision of 0.001 kg).

3.3.3.17 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,

$$HI = \frac{\text{Economic yield per row}}{\text{Biological yield per row}} \times 100$$

3.3.3.18 Kernel (Seed) 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).

3.3.3.19 Number of sound mature kernels (NSMK)

The number of good, sound mature kernels separated from 100 random kernels for each genotype in each replication were recorded.

3.4 Construction of final data sets

Data on plant height, number of primary and secondary branches plant^{-1}, number of mature and immature pods plant^{-1}, percentage of ripe pods, 100 pod weight, 100 kernel weight, pod yield plant^{-1}, pod yield row^{-1}, shelling percentage, harvest index, seed yield plant^{-1} and number of sound mature kernels were recorded for all the entries in both replications at all the three dates of harvesting. Days to maturity was finalized based on pod yield comparisons

at three dates of harvesting. Final data set of all 36 genotypes was constructed by including the corresponding data of each entry at its maturity.

3.5 STATISTICAL ANALYSIS

The treatment means for each character over two replications were subjected to the following statistical analysis.

3.5.1 Analysis of Variance

The data collected on individual characters were subjected to method of analysis of variance commonly applicable to alpha lattice design as per mathematical model proposed by Patterson and Williams (1976) using R packages (version 3.1.1).

$$Y_{ijk} = \mu + t_i + r_j + b_{k(j)} + e_{ijk}$$

Where,

Y_{ijk} = Phenotypic observation on 'i'th genotype in 'kth' block in the 'j'th replication.

μ = General mean

t_i = Fixed effect of ith genotype (i=1,2,…..t)

r_j = Effect of jth replication (j=1,2,…..r)

$b_{k(j)}$ = Effect of kth block within jth replicate (k=1,2,…..s)

e_{ijk} = Experimental error associated with the observation of ith genotype in kth block within jth replication.

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

Source of variation	***df***	**S.S**	**M.S.S**	**F Ratio**
Replications(r)	r-1	SS_r	$MSS_r=SS_r/r-1$	$F_r = MSS_r/MSS_e$
Blocks (within replications ignoring treatments) (b)	rs-r	SS_b	$MSS_b=SS_b/rs-r$	$F_b = MSS_b/MSS_e$
Treatments (adjusted with blocks) (t)	t-1	SS_t	$MSS(\sigma^2_e+ r\sigma^2_g) =SS_t/t-1$	$F_t = MSS_t/MSS_e$
Experimental error (e)	rt-rs-t+1	SS_e	$MSS_e(\sigma^2_e) = SS_e/rt-rs-t+1$	
Total	tr-1	SS_T		

Where,

df = Degrees of freedom

r = Number of replications

b = Number of blocks within a replication

t = Number of genotypes

e = Experimental error

S.S = Sum of squares

M.S.S = Mean sum of squares

F_r = F ratio for replications

F_b = F ratio for blocks

F_t = F ratio for treatments

The significance test was carried out by referring to standard 'F' table values given by Fisher and Yates (1967), at $P \leq 0.05$ and $P \leq 0.01$.

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)

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

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

σ_g^2 = Genotypic variance

σ_e^2 = Error variance

3.4.2.2 Genotypic and phenotypic coefficient of variation

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

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

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

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 (h^2_b)

The proportion of genotypic variance to the total variance of the population is referred to as heritability in broad sense (h^2_b) and was calculated by the formula given by Lush (1940).

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

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

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

σ^2_e = Environmental variance

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

Less than 30 % - Low

30 – 60 % - Moderate

More than 60 % - High

3.4.2.4 Genetic advance

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

$$GA = \sigma_p Hk$$

Where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

H = Heritability (broad sense)

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

3.4.2.5 Genetic advance as percent of mean (GAM)

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

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

Where,

GA = Genetic advance

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

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

Less than 10% - Low

10 – 20 % - Moderate

More than 20 % - High

3.4.3 Genetic Divergence Analysis

3.4.3.1 Mahalanobis's generalized distance (D^2)

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

3.4.3.1.1 Test of significance

Variances were calculated for all the characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1961). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried

out using ‘V’ statistic, which in turn utilizes Wilk’s criterion (Wilks, 1932). The sum of squares and sum of products of error and error + variety, variance – covariance matrix were used for this purpose.

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

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

Where,

λ = Wilk’s criterion

(E) = Determinant of error matrix

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

The significance of λ was tested by

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

Where,

χ^2_{pq} = estimation χ^2 value at ‘pq’ degrees of freedom

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

n = degrees of freedom of error + varieties

p = Number of characters

q = Number of genotypes – 1

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

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

3.4.3.1.2 Transformation of correlated variables

Transformation was done using pivotal condensation method. Transformation of correlated variables into standardized uncorrelated ones was done before working out the D^2 values because computation of D^2 values was

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

3.4.3.1.3 Computation of D^2 values

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

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

Where,

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

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

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

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 Chaudhary (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

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

Where,

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

3.4.3.1.7 Average inter cluster distance

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

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

Where, n_1 and n_2 are number of genotypes for each cluster.

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 ($d_i = Y_{it} - Y_{ij}$). 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 genotypes concerned

3.4.4. Character Association

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

3.4.4.1 Genotypic correlation coefficient (r_g)

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

where,

$r_g\,(x_i x_j)$ = Genotypic correlation between '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)

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

Where,

$V_p\,(x_i)$ = Phenotypic variance of 'i^{th}' character

$V_p\,(x_j)$ = Phenotypic variance of 'j^{th}' character

$CoV_p\,(x_i x_j)$ = Phenotypic covariance between 'i^{th}' and 'j^{th}' characters.

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

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.

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

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

. . . . . .

. . . . . .

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

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:

$$A = C \cdot B$$

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

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

Where,

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

Then, direct effects were calculated as follows

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

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

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

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

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

where, P_{RY} = Residual effect

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

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

The scales for path coefficients as proposed by Lenka and Mishra (1973) was adopted in the present investigation and 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

In the present investigation, thirty six groundnut genotypes were evaluated for genetic variability, genetic parameters, genetic divergence, trait associations and path analysis for traits contributing to early maturity, yield and yield components. The data recorded for these traits was subjected to statistical analysis and the results are presented and discussed here under.

4.1 ANALYSIS OF VARIANCE

Mean sum of squares due to different sources for twenty two traits are presented in Table 4.1. Highly significant differences were observed among the genotypes for all the traits under investigation indicating the presence of sufficient variability in the material under study.

Table 4.1. Analysis of variance for phenological and quantitative traits for earliness, yield and yield components among 36 groundnut genotypes

S.No	Traits	Mean sum of squares			
		Replications	Genotypes	Blocks	Error
		df=1	df=35	df=6	df=29
1	Days from emergence to first flowering	2.00	7.56**	1.23	0.57
2	Days to 50% flowering	0.13	5.90**	0.38	0.76
3	Days from opening of 1st flower to opening of 25 flowers	0.50	7.35**	1.55	0.90
4	Days from opening of 1st flower to opening of 40 flowers	0.13	13.30**	4.86	0.80
5	Days from opening of 1st flower to opening of 50 flowers	0.35	18.58**	5.16	1.80
6	Days to accumulation of 25 flowers from emergence	0.50	3.82**	0.13	0.65
7	Days to accumulation of 40 flowers from emergence	0.35	8.09**	1.94	0.64
8	Days to accumulation of 50 flowers from emergence	0.13	10.85**	2.67	1.18
9	Days to maturity	0.06	95.64**	0.51	1.54
10	Plant height (cm)	13.52	54.08**	2.29	2.51
11	Primary branches plant^{-1}	0.68	1.56**	0.21	0.25
12	Secondary branches plant^{-1}	0.50	1.89**	0.14	0.09
13	Mature pods plant^{-1}	1.24	13.85**	0.82	1.37
14	Immature pods plant^{-1}	0.28	1.55**	0.44	0.25
15	Percentage of ripe pods	23.35	39.84**	8.52	6.04
16	Pod yield plant^{-1} (g)	0.11	12.45**	2.84	3.70
17	Seed yield plant^{-1} (g)	0.61	7.39**	2.12	1.81
18	Shelling percentage	22.22	46.20**	17.15	7.17
19	Harvest index (%)	15.73	129.94**	19.80	29.21
22	100 pod weight (g)	30.94	394.27**	2.10	21.68
21	100 kernel weight (g)	1.68	66.70**	4.28	2.19
22	Number of sound mature kernels	0.06	39.42**	7.02	7.41

** Significant at 1% LoS, *Significant at 5% LoS

4.2 *PER SE* PERFORMANCE

The *per se* performance for phenological and quantitative traits contributing to early maturity, yield and yield components are furnished in Tables 4.3 and 4.4.

Classification of genotypes based on duration at an earlier point of time improves the efficacy of breeding program. Classification of genotypes should be fast and non-destructive to hasten the process of ascertaining relative growth duration during early generations. Here, an attempt was made to study the pattern of flowering behaviour (4.3.1 to 4.3.8) among genotypes under study.

4.2.1 Days from emergence to first flowering

The *per se* performance for days from emergence to first flowering ranged from 17.00 days (TCGS 2352 and UBEK 21-70) to 23.50 days (ISK-II-2020-4, SB-I-2021-7 and ISK-I-2021-21). Eighteen genotypes recorded early initial flowering when compared to general mean (20.14 days).

4.2.2 Days to 50% flowering

The mean performance for days to 50% flowering ranged from 29.00 days (Rohini, TCGS 2352, UBEK 21-70, TCGS 2333, UBEK 21-60 and ISK-I-2021-8) to 35.00 days (TCGS 2347). Seventeen genotypes came to flowering earlier when compared to general mean (30.99 days).

4.2.3 Days from opening of 1st flower to opening of 25 number of flowers

Mean values varied from 5.50 days (UBEK 21-35) to 12.00 days (TCGS 2223, TCGS 2351, TCGS 2352, TCGS 2353, UBEK 21-70 and UBEK 20-24). For eighteen genotypes opening of 25 number of flowers from 1st flower was earlier than the general mean (8.81 days).

4.2.4 Days from opening of 1st flower to opening of 40 number of flowers

Mean performance of genotypes ranged from 8.50 days (UBEK 21-35) to 18.50 days (UBEK 20-24). Eighteen genotypes recorded opening of 40 number of flowers earlier when compared to general mean (12.79 days).

4.2.5 Days from opening of 1st flower to opening of 50 number of flowers

Mean values from 10.50 days (UBEK 21-35) to 23.50 days (UBEK 20-24). Days to opening of 50 number of flowers from 1st flower were earlier in 17 genotypes compared to general mean (15.88 days).

4.2.6 Days to accumulation of 25 flowers from emergence

Mean values ranged between 27.00 days (TCGS 2333, UBEK 21-35, UBEK 21-38 and ISK-I-2021-8) to 33.50 days (TCGS 2223). Eleven genotypes were observed to be earlier for this trait than the general mean performance (28.94).

4.2.7 Days to accumulation of 40 flowers from emergence

Mean values varied from 29.50 days (TCGS 2333) to 38.50 days (TCGS 2223). Data on days to accumulation of 40 flowers from emergence was observed to be earlier than the general mean (32.88) in fifteen genotypes.

4.2.8 Days to accumulation of 50 flowers from emergence

Mean values for days to accumulation of 50 flowers from emergence ranged from 32.00 days (TCGS 2333, UBEK 21-35) to 42.00 days (TCGS 2223 and UBEK 20-24). Twelve genotypes showed recorded lesser number of days for this trait than the general mean (35.90).

To understand the pattern of flowering in different groups of maturity (90, 100 and 110 DAS), mean data on number of flowers opening in each day was calculated for 6 genotypes in 90 DAS group, 16 genotypes in 100 DAS group and 14 genotypes in 110 DAS groups. A line graph (Fig. 4.1.) was constructed and it clearly shows that maximum number of flowers opened within 5 days (on 5th day) from the date of opening of 1st flower in all the duration groups. But the number of flowers opening in early group (90 DAS) genotypes was observed with a significant peak when compared with genotypes of 100 DAS and 110 DAS. Second peak was observed in early group (90 DAS) genotypes at 13th day from opening of 1st flower whereas, the peak was observed at 17th day from opening of 1st flower in late (110 DAS) group.

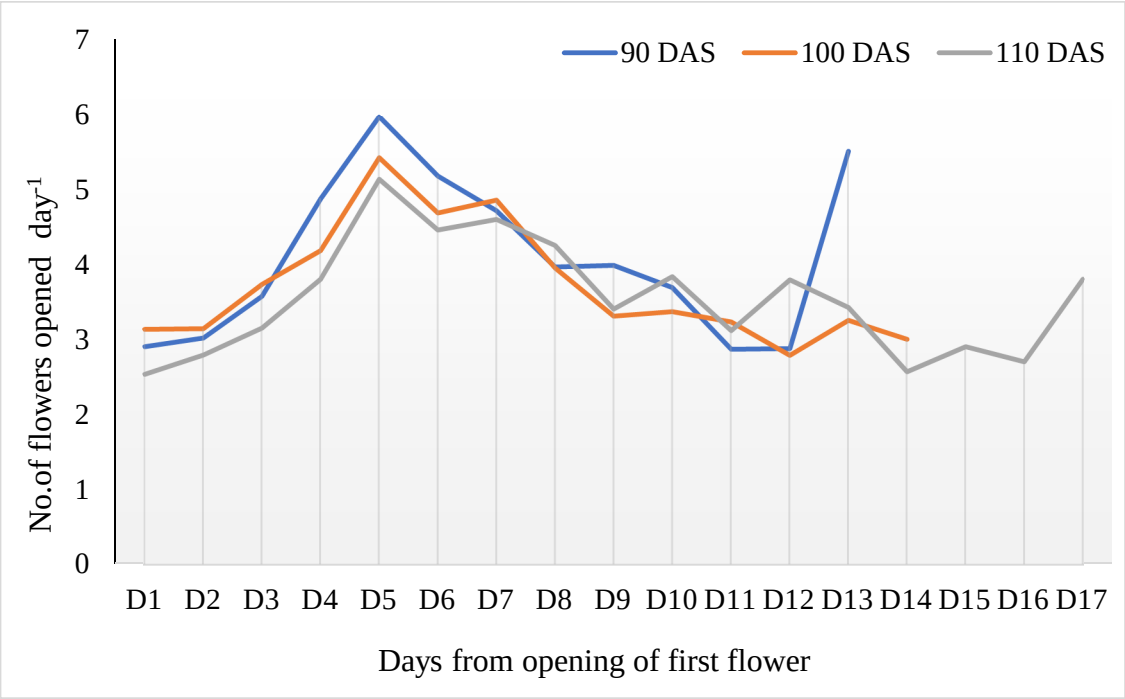


Fig. 4.1. Line graph depicting trend for number of flowers opened day^{-1} among genotypes with duration 90, 100 and 110 DAS

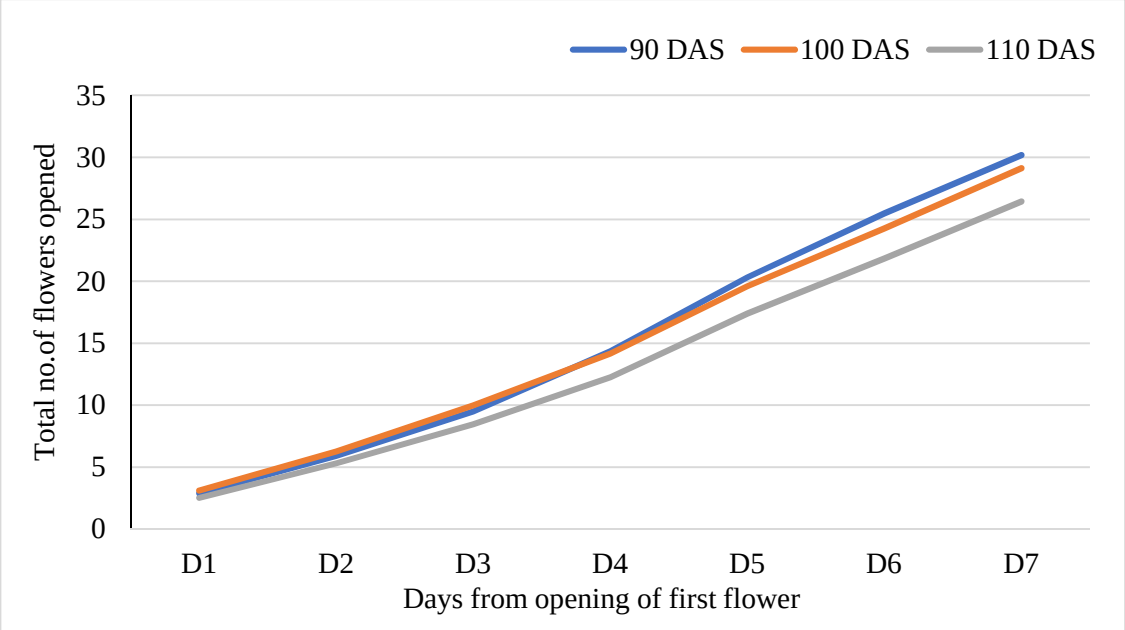


Fig. 4.2. Line graph depicting trend for days to accumulation of 25 flowers from opening of first flower among groundnut genotypes with duration of 90, 100 and 110 DAS

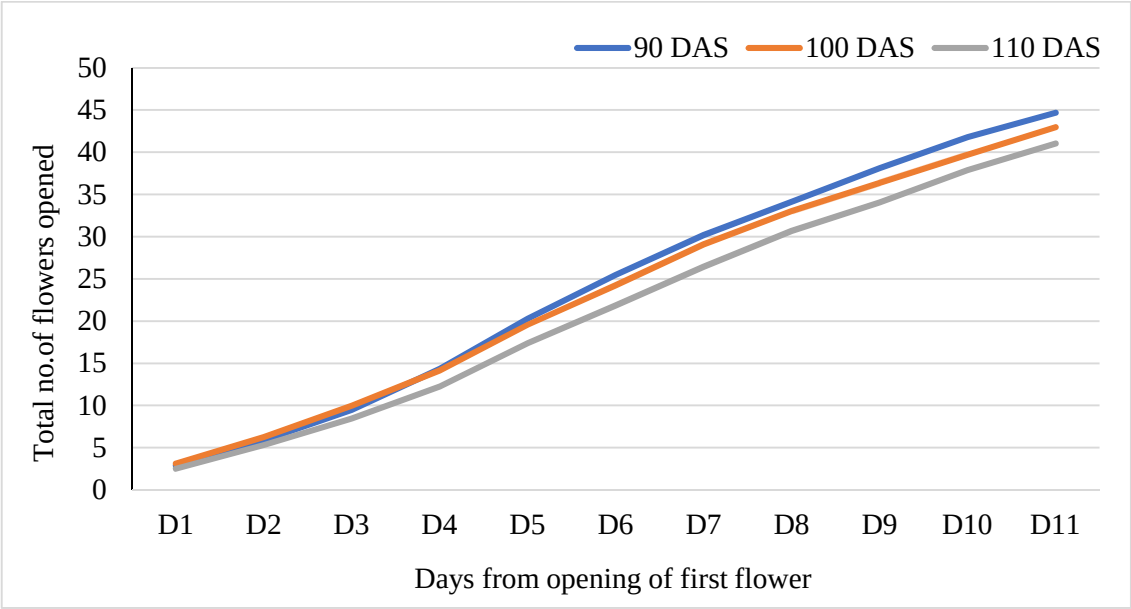


Fig. 4.3. Line graph depicting trend for days to accumulation of 40 from opening of first flower among groundnut genotypes with duration of 90, 100 and 110 DAS

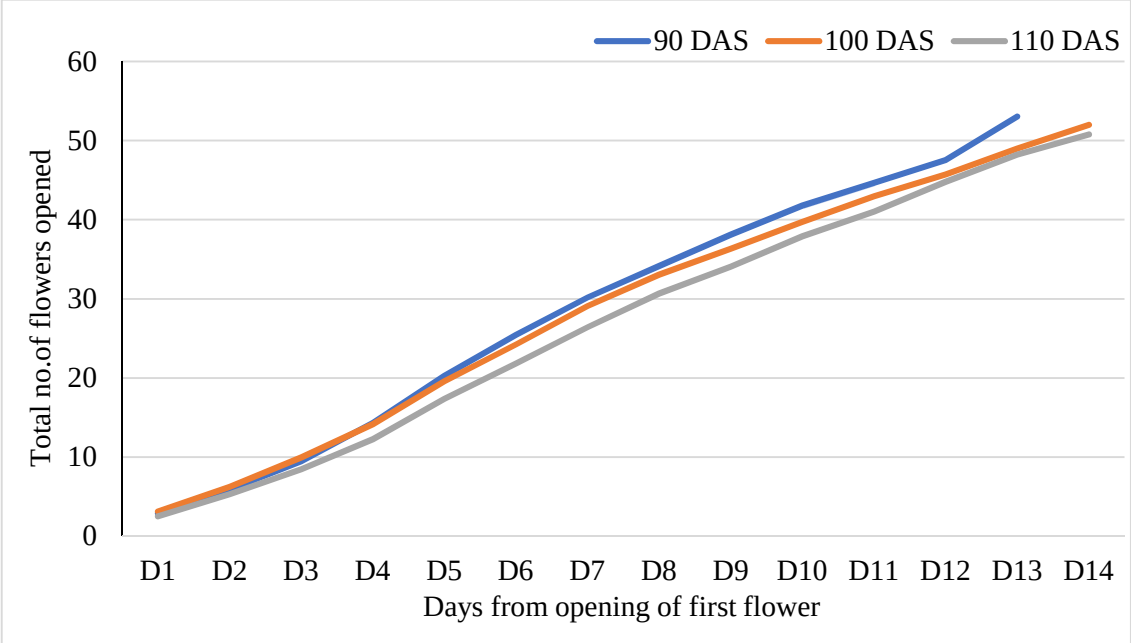


Fig. 4.4. Line graph depicting trend for days to accumulation of 50 from opening of first flower among groundnut genotypes with duration of 90, 100 and 110 DAS

The information is further supported from the Fig. 4.2, Fig. 4.3 and Fig. 4.4 which clearly illustrates the accumulation of 25, 40 and 50 flowers from 1st flower in early group genotypes at a faster pace than the genotypes maturing at 100 and 110 DAS. The information supports the finding of Khalfaoui (1990b) reporting the precocity of pod ripening is determined by duration of intense flowering and the time taken by fertilized flower to develop into ripe pod.

4.2.9 Days to maturity

Early maturity is preferred in agro-ecological situations which are characterized by short growing seasons and often subjected to terminal moisture stress. Also, it is the most sought after character in any crop for high intensity cropping systems. To fix days to maturity, double factorial ANOVA was performed on data collected for pod yield row^{-1} (converted to kg ha^{-1}) at three dates of harvesting *viz.*, 90 DAS, 100 DAS and 110 DAS. Pair wise comparisons were made for pod yields at two successive dates of harvesting, and the date where higher pod yield was recorded was chosen to compute the corresponding days to maturity for each genotype. Days to maturity obtained for each genotype is depicted in the Table 4.2.

Mean performance for days to maturity ranged from 89.50 days (UBEK 21-40, UBEK 21-43) to 111.0 days (TCGS 2348). Twenty two genotypes exhibited earliness when compared to general mean (102.08 days). A total of 16 and 13 genotypes were observed to be matured in 100 days and 110 days respectively. Meanwhile, six genotypes *viz.*, TAG 24, TCGS 2339, TCGS 2326, UBEK 21-40, UBEK 21-43 and UBEK 21-74 came to maturity at 90 DAS. Therefore, these genotypes can be utilized in the hybridization programme as donor parents to develop short duration genotypes.

Decreasing trend in pod yield in some of the genotypes (maturing at 90 and 100 DAS) at latter harvest dates could be due to pod losses in soil and also due to decrease in seed weight after attaining full maturity as reported by Pattee *et al.* (1977).

Table 4.2. Determination of days to maturity by comparing mean yields at different dates of harvesting

Genotypes	Mean pod yield at different dates of harvesting (kg ha^{-1})			Days to maturity
	90 DAS	100 DAS	110 DAS	
TAG 24	2,271^{a}	2,113^{b}	1,829^{c}	90
TCGS 2339	2,608^{a}	2,246^{b}	2,508^{c}	90
UBEK 21-40	2,830^{a}	2,563^{b}	2,692^{c}	90
UBEK 21-43	1,696^{a}	1,171^{b}	1,725^{a}	90
TCGS 2326	2,246^{a}	1,938^{b}	2,042^{c}	90
UBEK 21-74	2,421^{a}	2,480^{a}	2,355^{a}	90
ROHINI	2,208^{a}	2,759^{b}	2,738^{b}	100
TCGS 2350	2,867^{a}	3,254^{b}	3,088^{c}	100
TCGS 2351	2,350^{a}	2,842^{b}	2,750^{c}	100
TCGS 2352	2,017^{a}	2,975^{b}	2,821^{c}	100
TCGS 2353	2,746^{a}	3,221^{b}	3,225^{b}	100
TCGS 2354	3,000^{a}	3,379^{b}	3,379^{b}	100
UBEK 21-39	2,821^{a}	2,933^{b}	2,938^{b}	100
UBEK 21-61	2,438^{a}	3,908^{b}	2,509^{a}	100
UBEK 20-24	2,404^{a}	3,488^{b}	3,138^{c}	100
TCGS 2333	2,667^{a}	3,338^{b}	3,067^{c}	100
JL 24	2,050^{a}	2,446^{b}	2,476^{b}	100
UBEK 21-38	2,500^{a}	3,730^{b}	2,933^{b}	100
UBEK 21-42	2,238^{a}	2,405^{b}	1,717^{c}	100
SB-I-2021-7	2,930^{a}	3,175^{b}	3,083^{c}	100
ISK-I-2021-8	3,196^{a}	3,629^{b}	2,783^{c}	100
ISK-II-2020-12	2,900^{a}	3,142^{b}	3,125^{b}	100
TCGS 2223	2,608^{a}	3,250^{b}	4,050^{c}	110
TCGS 2233	2,825^{a}	3,575^{b}	4,204^{c}	110
TCGS 2347	3,271^{a}	3,596^{b}	5,571^{c}	110
TCGS 2348	2,833^{a}	2,613^{b}	3,567^{c}	110
TCGS 2357	2,375^{a}	2,088^{b}	3,117^{c}	110
UBEK 21-67	2,625^{a}	4,105^{b}	4,279^{c}	110
UBEK 21-68	2,175^{a}	3,046^{b}	3,846^{c}	110
UBEK 21-70	1,871^{a}	2,609^{b}	3,996^{c}	110
UBEK 20-32	1,796^{a}	2,763^{b}	2,904^{c}	110
UBEK 21-35	1,642^{a}	1,850^{b}	2,796^{c}	110
UBEK 21-60	1,225^{a}	2,142^{b}	2,313^{c}	110
UBEK 21-76	2,725^{a}	3,409^{b}	3,675^{c}	110
ISK-II-2020-4	2,958^{a}	3,163^{b}	3,905^{c}	110
ISK-I-2021-21	2,617^{a}	3,121^{b}	3,996^{c}	110

C.D (@5% level of significance) for yield at different dates of harvesting = 74.64

Table 4.3. Mean performance of 36 groundnut genotypes for earliness and its contributing traits

Genotypes	DIFE	DFF	DOF25	DOF40	DOF50	DA25E	DA40E	DA50E	DM	HI(%)	RP%	SP(%)
UBEK 21-40	20.00	29.50	8.00	12.00	15.00	28.00	32.00	35.00	89.50	47.20	82.00	64.00
UBEK 21-43	21.50	29.50	6.50	9.50	12.50	28.00	31.00	34.00	89.50	25.30	76.00	64.00
UBEK 21-74	21.50	30.00	6.50	10.50	14.00	28.00	32.00	35.50	90.00	42.50	68.50	63.00
TAG 24	20.00	31.00	8.50	13.00	17.50	28.50	32.00	35.00	91.00	47.10	82.00	66.00
TCGS 2339	19.00	31.50	9.00	12.50	15.50	28.00	31.50	34.50	91.50	37.40	79.50	67.00
TCGS 2326	22.00	33.00	8.50	13.00	16.00	30.50	35.00	38.00	91.50	40.40	83.50	68.00
TCGS 2352	17.00	29.00	11.50	16.00	21.00	28.50	33.00	38.00	99.00	49.70	80.00	70.00
ISK-I-2021-8	17.50	29.00	9.50	12.50	15.00	27.00	30.00	32.50	99.00	54.50	79.00	74.00
TCGS 2351	17.50	30.00	12.00	15.50	18.00	29.50	33.00	35.50	99.50	39.40	80.50	70.50
TCGS 2333	20.00	29.00	7.00	9.50	12.00	27.00	29.50	32.00	99.50	55.30	80.50	75.50
UBEK 21-38	21.00	29.50	6.00	9.00	11.50	27.00	30.00	32.50	99.50	51.80	81.00	77.00
ROHINI	17.50	29.00	10.00	14.00	17.00	27.50	31.00	34.00	100.00	48.10	83.50	76.00
TCGS 2350	20.50	30.00	7.00	9.50	12.00	27.50	30.00	32.50	100.00	44.50	83.00	76.50
JL 24	20.00	30.00	8.50	13.50	16.50	28.50	33.50	36.50	100.00	35.40	82.50	65.00
UBEK 21-42	20.50	30.00	8.00	11.50	15.00	28.50	32.00	35.50	100.00	47.10	80.50	68.50
TCGS 2353	18.00	30.50	11.50	17.00	21.50	29.50	35.00	39.50	100.50	43.50	77.00	68.50
UBEK 21-39	21.00	30.50	7.50	11.00	14.00	28.50	32.00	35.00	100.50	52.40	73.00	75.50
TCGS 2354	18.00	32.50	11.00	15.50	18.00	29.00	33.00	36.00	101.00	45.50	78.50	73.50
UBEK 21-61	22.00	31.00	7.00	10.50	14.00	29.00	32.50	36.00	101.00	56.00	80.00	77.00
UBEK 20-24	18.50	31.00	11.50	18.50	23.50	30.00	37.00	42.00	101.00	49.70	82.00	72.50
ISK-II-2020-12	23.00	33.50	8.00	13.00	16.50	31.00	36.00	38.50	101.00	44.10	78.00	69.50
SB-I-2021-7	23.50	34.00	7.50	11.00	13.50	31.00	34.50	37.00	101.50	48.60	76.00	66.00
UBEK 21-76	21.00	30.00	9.00	14.00	17.00	30.00	35.00	38.00	109.00	57.60	86.50	78.00
TCGS 2223	22.50	34.00	11.00	16.00	19.00	33.50	38.50	41.50	109.50	59.00	87.50	73.00

Cont.

Table 4.3. (cont.).

TCGS 2347	20.50	35.00	8.00	12.00	15.00	28.50	32.50	35.50	109.50	55.40	85.00	72.00
TCGS 2357	18.00	32.00	11.00	14.50	18.50	29.00	32.50	36.50	109.50	41.50	82.00	75.00
UBEK 21-68	19.00	30.00	10.00	15.00	17.50	29.00	34.00	36.50	109.50	61.70	87.00	63.00
UBEK 21-70	17.00	29.00	11.50	16.00	19.00	28.50	33.00	36.00	109.50	56.00	84.50	66.00
UBEK 21-60	20.00	29.00	8.00	12.00	16.00	28.00	32.00	36.00	109.50	33.50	86.50	71.00
ISK-I-2021-21	23.50	32.00	6.50	10.00	12.50	30.00	33.50	36.00	109.50	43.00	85.00	74.00
UBEK 21-35	21.50	30.00	5.50	8.50	10.50	27.00	30.00	32.00	110.00	50.80	86.00	71.50
ISK-II-2020-4	23.50	34.00	7.00	10.50	12.50	30.50	34.00	36.00	110.00	39.50	85.50	75.00
TCGS 2233	18.00	30.50	12.00	16.50	19.50	30.00	34.50	37.50	110.50	48.70	89.50	60.00
UBEK 21-67	21.00	33.00	9.50	12.50	15.00	30.50	33.50	36.00	110.50	49.40	84.00	74.50
UBEK 20-32	21.50	32.00	7.00	10.00	12.00	28.50	31.50	33.50	110.50	34.00	82.00	70.50
TCGS 2348	18.50	32.00	10.50	15.00	18.00	29.00	33.50	36.50	111.00	54.30	90.00	66.50
General mean	**20.14**	**30.99**	**8.81**	**12.79**	**15.88**	**28.94**	**32.88**	**35.90**	**102.08**	**46.93**	**81.88**	**70.50**
Minimum	**17.00**	**29.00**	**5.50**	**8.50**	**10.50**	**27.00**	**29.50**	**32.00**	**89.50**	**25.30**	**68.50**	**60.00**
Maximum	**23.50**	**35.00**	**12.00**	**18.50**	**23.50**	**33.50**	**38.50**	**42.00**	**111.00**	**61.70**	**90.00**	**78.00**
C.D. 5%	**1.68**	**1.69**	**2.04**	**2.48**	**3.13**	**1.52**	**1.88**	**2.44**	**2.38**	**10.67**	**5.16**	**6.05**
S.E.(m)	**0.59**	**0.59**	**0.71**	**0.87**	**1.09**	**0.53**	**0.66**	**0.85**	**0.83**	**3.71**	**1.80**	**2.11**
C.V.(%)	**3.80**	**2.80**	**10.80**	**7.00**	**8.40**	**2.80**	**2.40**	**3.00**	**1.20**	**11.50**	**3.00**	**3.80**

DIFE : Days from emergence to initial flowering
DFF : Days to 50% flowering
DOF25 : Days from opening of first flower to twenty-five number of flowers
DOF40 : Days from opening of first flower to forty number of flowers
DOF50 : Days from opening of first flower to fifty number of flowers
DA25E : Days to accumulation of twenty-five flowers from emergence
DA40E : Days to accumulation of forty flowers from emergence
DA50E : Days to accumulation of fifty flowers from emergence
DM : Days to maturity
HI : Harvest index
RP% : Percentage of ripe pods
SP : Shelling percentage

4.2.10 Harvest index (%)

Harvest index (HI) is a measure of success in partitioning assimilated photosynthates. Very often high yields are associated with high harvest index (Pilbeam, 1996). Understanding HI among different genotypes would be informative to select ideal genotypes for improving productivity. Harvest index varied from 25.30% (UBEK 21-43) to 61.70% (UBEK 21-68). Twenty one genotypes registered higher harvest index than the general mean of 46.93%. All the early maturing genotypes (90 DAS) recorded harvest index < 50%.

4.2.11 Percentage of ripe pods

Mean values for percentage of ripe pods ranged between 68.50% (UBEK 21-74) to 90.00% (TCGS 2348). Twenty one genotypes recorded higher percentage of ripe pods than the general mean of 81.88%.

4.2.12 Shelling percentage

Shelling percentage varied from 60.00% (TCGS 2233) to 78.00% (UBEK 21-74). Eighteen genotypes exhibited higher shelling percentage than the general mean of 70.50%.

4.2.13 Plant height (cm)

Mean values for plant height ranged between 25.90 cm (TCGS 2233) to 44.60 cm (UBEK 21-74). Fifteen genotypes expressed short stature against the general mean of 36.86 cm.

4.2.14 Number of primary branches plant^{-1}

Number of primary branches plant^{-1} varied from 2.00 (UBEK 21-68, UBEK 21-35) to 6.00 (TCGS 2352). Twenty one genotypes produced more primary branches than their general mean value (3.86).

Table 4.4. Mean Performance of 36 groundnut genotypes for yield and yield components

Genotypes	PH (cm)	PB	SB	MP	IMP	PYP (g)	HPW (g)	HKW (g)	SYP (g)	NSMK
UBEK 21-40	33.20	4.00	0.50	18.10	3.90	12.15	85.50	34.40	7.79	78.00
UBEK 21-43	40.30	4.00	1.00	12.10	3.90	8.45	70.00	32.60	5.41	85.00
UBEK 21-74	36.90	3.50	1.50	13.00	6.00	9.50	90.00	35.40	6.02	81.00
TAG 24	32.45	4.00	1.00	15.60	3.40	10.85	92.00	40.00	7.15	84.00
TCGS 2339	38.75	3.50	2.50	13.50	3.50	12.60	80.50	38.40	8.43	78.00
TCGS 2326	38.85	4.00	1.00	18.40	3.60	12.20	84.00	37.20	8.30	77.00
TCGS 2352	37.90	6.00	2.00	13.20	3.30	12.90	105.00	44.80	9.04	85.00
ISK-I-2021-8	34.10	5.00	1.00	15.40	4.10	14.15	113.10	42.10	10.43	95.00
TCGS 2351	38.60	4.50	3.00	14.90	3.60	11.05	108.50	45.10	7.78	84.00
TCGS 2333	38.60	3.50	2.00	15.70	3.80	11.65	99.00	39.10	8.80	85.00
UBEK 21-38	35.10	5.00	1.00	15.40	3.60	13.20	97.00	41.60	10.16	86.50
ROHINI	32.40	4.00	0.50	14.20	2.80	14.95	111.00	44.60	11.42	91.00
TCGS 2350	42.00	4.00	1.00	20.80	4.30	14.45	111.50	47.50	11.07	94.00
JL 24	45.40	3.50	1.00	12.00	2.50	8.85	92.80	38.90	5.75	88.00
UBEK 21-42	26.65	2.50	3.00	13.30	3.20	8.65	89.00	38.80	5.92	84.00
TCGS 2353	42.95	4.00	1.00	16.20	4.80	11.60	107.00	48.00	7.94	84.00
UBEK 21-39	37.35	4.00	1.50	12.40	4.60	10.00	88.00	39.10	7.56	82.00
TCGS 2354	39.45	3.50	1.00	13.40	3.60	13.55	103.20	45.50	9.97	92.00
UBEK 21-61	41.85	4.00	1.00	14.80	3.70	14.65	97.20	45.10	11.29	89.00
UBEK 20-24	32.60	3.00	0.50	12.30	2.70	13.05	105.00	43.40	9.46	84.00
ISK-II-2020-12	33.50	5.00	3.00	15.60	4.40	11.20	89.30	37.30	7.78	91.00
SB-I-2021-7	37.50	3.50	2.00	13.00	4.10	9.95	84.50	36.20	6.62	83.00

Cont

Table 4.4. (cont.).

UBEK 21-76	33.70	3.00	1.00	16.00	2.50	14.85	102.60	46.30	11.58	88.00
TCGS 2223	35.50	4.00	4.50	15.70	2.30	14.00	126.00	53.90	10.21	87.00
TCGS 2347	41.45	5.00	2.00	14.00	2.50	17.75	140.00	58.60	12.83	82.00
TCGS 2357	43.35	5.00	2.00	12.30	2.70	9.65	100.00	40.00	7.24	86.00
UBEK 21-68	35.85	2.00	2.00	18.70	2.80	16.25	118.60	46.20	10.26	86.50
UBEK 21-70	41.00	3.50	1.00	13.50	2.50	16.35	101.50	46.60	10.71	82.00
UBEK 21-60	25.90	2.50	1.00	9.90	1.60	11.50	89.40	37.50	8.21	85.00
ISK-I-2021-21	28.15	4.00	1.00	15.30	2.70	14.75	96.20	41.60	10.93	78.00
UBEK 21-35	29.05	2.00	0.50	15.90	2.60	12.85	84.70	39.50	9.13	85.00
ISK-II-2020-4	39.30	4.00	2.50	19.20	3.30	12.25	112.50	49.40	9.20	88.00
TCGS 2233	43.60	4.50	2.00	18.80	2.20	17.05	116.00	49.70	10.23	83.00
UBEK 21-67	28.10	3.00	4.00	15.10	2.90	16.40	93.20	39.70	12.21	84.00
UBEK 20-32	44.60	3.50	1.00	15.60	3.50	11.25	101.70	49.50	7.94	77.00
TCGS 2348	40.85	5.00	1.50	22.00	2.50	15.80	115.50	50.90	10.49	83.00
General mean	**36.86**	**3.86**	**1.61**	**15.14**	**3.33**	**12.79**	**100.03**	**42.90**	**9.04**	**84.86**
Minimum	**25.90**	**2.00**	**0.50**	**9.90**	**1.60**	**8.45**	**70.00**	**32.60**	**5.41**	**77.00**
Maximum	**44.60**	**6.00**	**4.50**	**22.00**	**6.00**	**16.40**	**140.00**	**58.60**	**12.83**	**95.00**
C.D. 5%	**3.19**	**1.00**	**0.87**	**2.29**	**1.08**	**3.83**	**8.69**	**3.28**	**2.77**	**5.50**
S.E.(m)	**1.11**	**0.35**	**0.23**	**0.80**	**0.37**	**1.33**	**3.03**	**1.13**	**0.96**	**1.92**
C.V.(%)	**4.30**	**12.90**	**19.20**	**7.70**	**15.00**	**15.00**	**4.70**	**3.40**	**14.90**	**3.20**

PH : Plant height
MP : Number of mature pods plant^{-1}
HPW : Hundred pod weight
NSMK : Number of sound mature kernels
PB : Number of primary branches plant^{-1}
IMP : Number of immature pods plant^{-1}
HKW : Hundred kernel weight
SB : Number of secondary branches plant^{-1}
PYP : Pod yield plant^{-1} (g)
SYP : Seed yield plant^{-1} (g)

4.2.15 Number of secondary branches plant^{-1}

Mean values for number of secondary branches plant^{-1} varied from 0.50 (Rohini, UBEK 21-40, UBEK 20-24 and UBEK 21-35) to 4.50 (TCGS 2223). Fourteen genotypes recorded higher number of secondary branches plant^{-1} against general mean value (1.61).

4.2.16 Number of mature pods plant^{-1}

The character number of mature pods plant^{-1} is one of the most important yield components directly influencing the pod yield. Mean values for number of mature pods plant^{-1} ranged between 9.90 (UBEK 21-60) to 22.00 (TCGS 2348). Fifteen genotypes recorded more number of mature pods plant^{-1} against the general mean (15.14).

4.2.17 Number of immature pods plant^{-1}

Presence of immature pods is not desirable as they promote *Aspergillus flavus* contamination. Number of immature pods plant^{-1} varied from 1.60 (UBEK 21-60) to 6.00 (UBEK 21-74). Twenty one genotypes recorded lower number of immature pods plant^{-1} than the general mean (3.33).

4.2.18 Pod yield plant^{-1}

Mean pod yield plant^{-1} ranged between 8.45g (UBEK 21-43) to 16.40g (TCGS 2347). Sixteen genotypes recorded higher pod yield plant^{-1} against the general mean of 12.79g.

4.2.19 Hundred pod weight (g)

Hundred pod weight ranged from 70.00g (UBEK 21-43) to 140.00g (TCGS 2347). Seventeen genotypes recorded higher 100 pod weight than the general mean (100.03g). All the early maturing genotypes (90 DAS) recorded 100 pod weight of < 90g.

4.2.20 Hundred kernel weight (g)

Mean 100 kernel weight ranged between 32.60g (UBEK 21-43) to 58.60g (TCGS 2347). Seventeen genotypes registered higher 100 kernel weight

than the general mean (42.90g). All the early maturing genotypes (90 DAS) recorded 100 kernel weight of < 40g.

4.2.21 Seed yield plant^{-1}

Mean seed yield plant^{-1} varied from 5.41g (UBEK 21-43) to 12.83g (TCGS 2347). Eighteen genotypes recorded higher seed yield plant^{-1} when compared to the general mean of 9.04g.

4.2.22 Number of sound mature kernels

Number of Sound mature kernels ranged from 77.00 (UBEK 20-32 and TCGS 2326) to 95.00 (ISK-I-2021-8). Eighteen genotypes registered higher number of sound mature kernels than the general mean value (84.86).

To sum up the most relevant findings of the present study, genotypes *viz.,* UBEK 21-74, UBEK 21-40, UBEK 21-43, TAG 24, TCGS 2339 and TCGS 2326 recorded early maturity at 90 DAS. Among these genotypes, UBEK 21-43 and UBEK 21-74 also recorded earlier opening of 25 number of flowers from opening of 1st flower. UBEK 21-40 and TCGS 2326 recorded more number of mature pods plant^{-1}. Looking comprehensively at the trend for different traits in early maturing genotypes, it can be visualized that 100 pod weight, 100 kernel weight and harvest index were below 90g, 40g and 50%, respectively. Employing these traits while selecting the lines for early maturity might yield good results in developing early maturing cultivars with optimum yields. These traits are to be confirmed in future studies and in designing ideal plant type for early maturity. Seventeen genotypes were observed to be having a maturity duration of 100 days. Of them, UBEK 21-61 and ISK-I-2021-8 were the most promising entries with respect to pod yield plant^{-1}, shelling percentage, 100 pod weight and 100 kernel weight and harvest index. Among 13 entries that matured at 110 days after sowing, TCGS 2347 followed by UBEK 21-67 produced more pod yield plant^{-1} and the corresponding traits *viz.,* harvest index, shelling percentage, percentage of ripe pods, 100 pod weight and 100 kernel weight. The entry, Rohini registered higher seed yield plant^{-1}, shelling percentage, and number of sound mature kernels along with earlier initial

flowering and accumulation of 25 flowers from emergence. Considering *per se* performance, top five genotypes for each character were identified and listed in Table 4.5. Promising genotypes identified for pod yield in all the duration groups can be evaluated at station level and multilocation testing to check for consistency and stability to promote them for commercial cultivation. Genotypes identified as early maturing can be involved in hybridization program to assess the combining ability for traits of interest along with their contributing traits. Most promising combiners could be put to use in breeding program for evolving short duration and high yielding groundnut cultivars.

4.3 STUDY OF VARIABILITY

Genetic variability is the basic prerequisite for any plant breeding programme as it provides wider scope for selection. The amount of variability present in the material under study can be determined with the help of genetic parameters *viz.*, mean, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability estimates and genetic advance. The estimates of all the above mentioned parameters for the all the traits among thirty six genotypes are furnished in the Table 4.6.

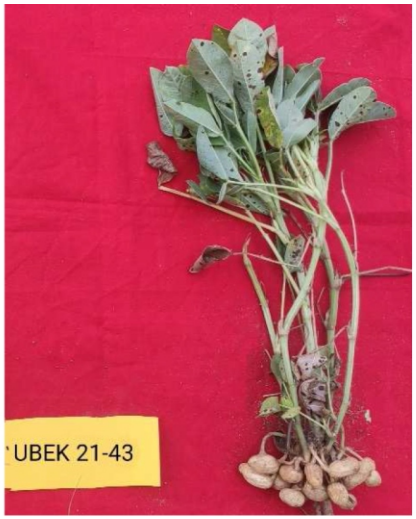
4.3.1 Variability studies (PCV and GCV)

Variability estimates provides a preliminary idea on the extent of variability for the traits under study. All the estimates were observed to be significant for all the traits studied (Table.4.6). Variation measured in terms of PCV and GCV as low (<10%), moderate (10 – 20%) and high (>20%) proposed by Sivasubramanian and Madhavamenon (1973) was followed.

Phenotypic coefficient of variation was found to be greater than genotypic coefficient of variation for all the traits under study, indicating the effect of environment on these traits. Narasimhulu *et al.* (2012), John *et al.* (2013), Rao *et al*. (2014), Singh *et al.* (2017), Hampannavar *et al*. (2018a), Mitra *et al*. (2021) and Shrotri *et al.* (2021) reported similar trends in groundnut.

TAG 24

TCGS 2339



UBEK 21-43

UBEK 21-74

UBEK 21-40

TCGS 2326

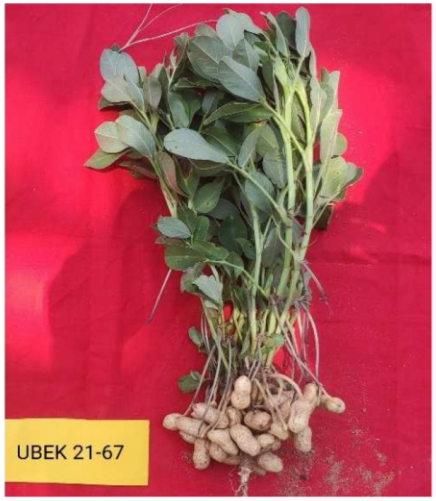
Plate 2. Promising genotypes for earliness (90 DAS) and its contributing traits based on *per se* performance (Photographs taken at 90 DAS)

TCGS 2347

TCGS 2223

TCGS 2233

UBEK 21-76



UBEK 21-67

UBEK 21-70

Plate 3. Promising genotypes for yield and yield components based on *per se* performance (Photographs taken at 90 DAS)

Table 4.5. List of top five genotypes based on mean performance in groundnut

S.No	Characters	Genotypes
1	Days from emergence to initial flowering	TCGS 2352, UBEK 21-70, Rohini, TCGS 2351, ISK-I-2021-8
2	Days to 50% flowering	Rohini, TCGS 2352, UBEK 21-70, TCGS 2333, UBEK 21-60, ISK-I-2021-8
3	Days from opening of 1st flower to opening of 25 number of flowers	UBEK 21-35, UBEK 21-38, UBEK 21-43, UBEK 21-74, ISK-I-2021-21
4	Days from opening of 1st flower to opening of 40 number of flowers	UBEK 21-35, UBEK 21-38, TCGS 2333, TCGS 2350, UBEK 21-43
5	Days from opening of 1st flower to opening of 50 number of flowers	UBEK 21-35, UBEK 21-38, TCGS 2333, TCGS 2350, UBEK 20-32
6	Days to accumulation of 25 flowers from emergence	UBEK 21-35, UBEK 21-38, TCGS 2333, ISK-I-2021-8, Rohini, TCGS 2350
7	Days to accumulation of 40 flowers from emergence	UBEK 21-35, UBEK 21-38, TCGS 2333, ISK-I-2021-8, TCGS 2350
8	Days to accumulation of 50 flowers from emergence	UBEK 21-35, UBEK 21-38, TCGS 2333, ISK-I-2021-8, TCGS 2350
9	Days to maturity	UBEK 21-74, UBEK 21-40, UBEK 21-43, TAG 24, TCGS 2339, TCGS 2326
10	Plant height (cm)	UBEK 21-60, UBEK 21-42, UBEK 21-67, ISK-I-2021-21, UBEK 21-35
11	Number of primary branches plant^{-1}	TCGS 2352, TCGS 2347, TCGS 2348, TCGS 2357, UBEK 21-38, ISK-I-2021-8, ISK-II-2020-12
12	Number of secondary branches plant^{-1}	TCGS 2223, UBEK 21-67, TCGS 2351, UBEK 21-42, ISK-II-2020-12
13	Number of mature pods plant^{-1}	TCGS 2348, TCGS 2350, TCGS 2233, UBEK 21-68, ISK-II-2020-4, UBEK 21-40, TCGS 2326
14	Number of immature pods plant^{-1}	UBEK 21-60, UBEK 21-76, UBEK 21-70, TCGS 2223, TCGS 2233, TCGS 2347, TCGS 2348
15	Percentage of ripe pods	TCGS 2348, TCGS 2233, TCGS 2223, UBEK 21-68, UBEK 21-60, UBEK 21-76
16	Pod yield plant^{-1} (g)	TCGS 2347, TCGS 2233, UBEK 21-67, UBEK 21-70, UBEK 21-68
17	Seed yield plant^{-1} (g)	TCGS 2347, UBEK 21-67, UBEK 21-76, Rohini, UBEK 21-61
18	Shelling percentage	UBEK 21-76, UBEK 21-38, UBEK 21-61, Rohini, TCGS 2350
19	Harvest index (%)	UBEK 21-68, TCGS 2223, UBEK 21-76, UBEK 21-61, UBEK 21-70
22	100 pod weight (g)	TCGS 2347, TCGS 2223, UBEK 21-68, TCGS 2233, TCGS 2348
21	100 kernel weight (g)	TCGS 2347, TCGS 2223, TCGS 2348, TCGS 2233, UBEK 20-32, ISK-II-2020-4
22	Number of sound mature kernels	ISK-I-2021-8, TCGS 2350, TCGS 2354, Rohini, ISK-II-2020-12

The traits, days from opening of 1st flower to opening of 25 flowers (PCV = 23.23, GCV = 20.21), number of primary branches plant^{-1} (PCV = 24.58, GCV = 21.03) and number of secondary branches plant^{-1} (PCV = 74.81, GCV = 63.36) recorded higher PCV and GCV estimates suggesting the presence of sufficient amount of variation in the genotypes under study for which these traits can be improved through selection. The results of Zaman *et al.* (2011), Hampannavar *et al.* (2018a) are in accordance with the present report of high PCV and GCV for number of primary branches plant^{-1} whereas, Korat *et al.* (2009) and Mahalakshmi *et al.* (2005) reported similar findings of high PCV and GCV for number of secondary branches plant^{-1}.

High PCV and moderate GCV was recorded for pod yield plant^{-1} (PCV = 22.12, GCV = 16.49), seed yield plant^{-1} (PCV = 23.80, GCV = 18.40), days from opening of 1st flower to 40 flowers (PCV = 21.26, GCV = 18.99) and days from opening of 1st flower to 50 flowers (PCV = 20.39, GCV = 17.93) indicating that these traits are sensitive to environmental fluctuations. Traits *viz.*, plant height (PCV = 14.43, GCV = 13.78), number of mature pods plant^{-1} (PCV = 18.16, GCV = 16.55), harvest index (PCV = 18.91, GCV = 15.24), 100 pod weight (PCV = 14.36, GCV = 13.71) and 100 kernel weight (PCV = 13.71, GCV = 13.20) exhibited moderate PCV and GCV. Meanwhile, moderate PCV (10.08) and low GCV (9.21) was observed for days from emergence to first flowering.

The results of Yusuf *et al.* (2017) and Hampannavar *et al.* (2018a) are supporting the findings of current study where high PCV and moderate GCV was observed for pod yield plant^{-1} and seed yield plant^{-1}. Moderate PCV and GCV for plant height, number of mature pods plant^{-1}, harvest index, 100 pod weight and 100 kernel weight were observed earlier by Patil *et al.* (2014). The findings of moderate PCV and GCV for plant height, 100 pod weight and 100 kernel weight were in accordance with the observations of Gupta *et al.* (2015a) and for harvest index is supported by the reports of Raza *et al.* (2018) and Kumar *et al.* (2019). Low GCV and moderate PCV was obtained for days from

emergence to first flowering in the current study, whereas Mitra *et al.* (2021), John *et al.* (2009) previously observed low PCV and GCV.

Traits *viz.*, days to 50% flowering, days to accumulation of 25 flowers from emergence, days to accumulation of 40 flowers from emergence, days to accumulation of 50 flowers from emergence, days to maturity, percentage of ripe pods, shelling percentage and number of sound mature kernels exhibited low PCV and GCV. Similar findings were reported for shelling percentage and number of sound mature kernels by Patil *et al.* (2014) and Shrotri *et al.* (2021). Low PCV and GCV for days to 50% flowering was in accordance with the results of John *et al.* (2009) and Bhakal and Lal (2017), whereas, for days to maturity it was earlier reported by John *et al.* (2008), Bhakal and Lal (2017) and Mitra *et al.* (2021).

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

The ratio of genotypic variance to the phenotypic variance or total variance is defined as heritability and is generally expressed in per cent. Falconer (1996) described heritability as a good measure of the transmission of traits from parents to their offspring. Genotypic coefficient of variation together with heritability should be considered in plant breeding programs as they would provide a better picture of the amount of genetic advance to be expected by the phenotypic selection (Burton, 1952). Classification of heritability into low (<30%), medium (30-60%) and high (>60%) given by Johnson *et al*. (1955a) is followed.

High estimates of heritability were recorded for days to maturity (97.18%), 100 kernel weight (92.65%), plant height (91.26%), 100 pod weight (91.12%), days to first flowering from emergence (83.37%), number of mature pods plant^{-1} (83.14%), days to 50% flowering (78.88%), days from opening of 1st flower to 25, 40 and 50 flowers (75.75%, 79.77% and 77.33%, respectively), days to accumulation of 25, 40 and 50 flowers from emergence (74.56%, 80.77% and 76.58%, respectively), number of primary branches plant^{-1}

(73.21%), percentage of ripe pods (72.09%), number of secondary branches plant^{-1} (71.21%), number of immature pods plant^{-1} (69.35%), number of sound mature kernels (68.60%), shelling percentage (67.76%) and harvest index (64.96%).

Moderate heritability was observed for seed yield plant^{-1} (59.74%) and pod yield plant^{-1} (55.57%).

4.3.1.3 Genetic Advance as per cent of Mean (GAM)

Genetic advance is the improvement in the mean of selected families over the base population (Lush, 1940). It is the measure of genetic gain under selection. Since, magnitude of genetic advance is influenced by units of measurement, genetic advance as per cent of mean was computed.

High genetic advance as per cent of mean was registered for the traits *viz.,* number of secondary branches plant^{-1} (110.53%), number of immature pods plant^{-1} (41.07%), number of primary branches plant^{-1} (37.07%), days from opening of 1st flower to 25, 40 and 50 flowers (36.24%, 34.94% and 32.48%, respectively), number of mature pods plant^{-1} (31.10%), seed yield plant^{-1} (29.29%), plant height (27.12%), 100 pod weight (26.95%), 100 kernel weight (26.17%), pod yield plant^{-1} (25.32%), harvest index (25.31%) and shelling percentage (10.39%).

Days to initial flowering from emergence (17.32%), days to accumulation of 40 flowers from emergence (10.71%), days to accumulation of 50 flowers from emergence (10.89%), days to maturity (13.66%) and shelling percentage (10.39%) recorded moderate genetic advance as per cent of mean.

Low genetic advance as per cent of mean was exhibited by days to 50% flowering (9.52), days to accumulation of 25 flowers from emergence (7.85%), percentage ripe pods (8.73%) and number of sound mature kernels (8.05%).

Table 4.6. Estimates of mean, range and genetic parameters for earliness and its contributing traits, yield and yield components among 36 groundnut genotypes

S. No	Characters	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advance as percent of mean (%)
			Min.	Max.	Phenotypic	Genotypic	Phenotypic	Genotypic			
1	Days from emergence to initial flowering	20.14	17.00	24.00	4.12	3.44	10.08	9.21	83.37	3.49	17.32
2	Days to 50% flowering	30.99	29.00	35.00	3.30	2.60	5.86	5.21	78.88	2.95	9.52
3	Days from opening of 1st flower to opening of 25 number of flowers	8.81	5.00	12.00	4.18	3.17	23.23	20.21	75.75	3.19	36.24
4	Days from opening of 1st flower to opening of 40 number of flowers	12.79	8.00	19.00	7.40	5.90	21.26	18.99	79.77	4.47	34.94
5	Days from opening of 1st flower to opening of 50 number of flowers	15.88	10.00	24.00	10.48	8.10	20.39	17.93	77.33	5.16	32.48
6	Days to accumulation of 25 flowers from emergence	28.94	27.00	34.00	2.19	1.63	5.11	4.41	74.56	2.27	7.85
7	Days to accumulation of 40 flowers from emergence	32.88	29.00	39.00	4.48	3.62	6.44	5.79	80.77	3.52	10.71
8	Days to accumulation of 50 flowers from emergence	35.90	31.00	43.00	6.15	4.71	6.90	6.04	76.58	3.91	10.89
9	Days to maturity	102.08	89.00	112.00	48.51	47.14	6.82	6.73	97.18	13.94	13.66

Cont.

Table 4.6. (cont.).

S. No	Characters	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advance as percent of mean (%)
			Min.	Max.	Phenotypic	Genotypic	Phenotypic	Genotypic			
10	Plant height (cm)	36.86	23.60	46.80	28.28	25.80	14.43	13.78	91.26	10.00	27.12
11	Number of primary branches plant^{-1}	3.86	2.00	6.00	0.90	0.66	24.58	21.03	73.21	1.43	37.07
12	Number of secondary branches plant^{-1}	1.42	0.00	5.00	1.12	0.81	74.81	63.36	71.73	1.57	110.53
13	Number of mature pods plant^{-1}	15.14	9.79	22.41	7.56	6.29	18.16	16.55	83.14	4.71	31.10
14	Number of immature pods plant^{-1}	3.33	1.21	6.93	0.92	0.63	28.75	23.75	69.35	1.37	41.07
15	Percentage of ripe pods	81.88	67.00	92.00	23.15	16.69	5.88	4.99	72.09	7.15	8.73
16	Pod yield plant^{-1} (g)	12.79	7.60	20.40	7.99	4.45	22.12	16.49	55.57	3.24	25.32
17	Seed yield plant^{-1} (g)	9.04	4.86	15.10	4.62	2.76	23.80	18.40	59.74	2.65	29.29
18	Shelling percentage	70.50	60.00	79.00	27.54	18.66	7.44	6.13	67.76	7.33	10.39
19	Harvest index (%)	46.93	24.47	65.13	78.77	51.17	18.91	15.24	64.96	11.88	25.31
20	100 pod weight (g)	100.03	68.00	150.00	206.30	187.97	14.36	13.71	91.12	26.96	26.95
21	100 kernel weight (g)	42.90	32.00	59.40	34.62	32.07	13.71	13.20	92.65	11.23	26.17
22	Number of sound mature kernels	84.86	76.00	96.00	23.38	16.04	5.70	4.72	68.60	6.83	8.05

High heritability in broad sense does not essentially mean better response to selection as it includes non-additive genetic factors as well. Therefore, estimation of genetic advance coupled with heritability further narrows down the response to selection. Traits studied in the present study were categorized into following three groups to reap their merit in crop improvement program.

1. High heritability and high genetic advance
2. High heritability and moderate genetic advance
3. High heritability and low genetic advance

High heritability coupled with high genetic advance as per cent of mean were recorded for days from opening of 1st flower to opening of 25, 40 and 50 flowers, plant height and 100 kernel weight [Mitra *et al.* (2021), Patil *et al.* (2014), Hampannavar *et al.* (2018a) and Yusuf *et al.* (2017)], number of primary branches plant^{-1} [Raza *et al.* (2018)], number of secondary branches plant^{-1}[John *et al.* (2009) and Mitra *et al.* (2021)], number of mature pods plant^{-1} [Patil *et al.* (2014), Yusuf *et al.* (2017) and Shrotri *et al.* (2021)], number of immature pods plant^{-1} [Mahalakshmi *et al.* (2005), John *et al.* (2009) and Hampannavar *et al.* (2018a)], harvest index [Vasanthi *et al.* (2015), Yusuf *et al.* (2017) and Raza *et al.* (2018). Patil *et al.* (2014)], 100 pod weight [Gupta *et al.* (2015a) and Kumar *et al.* (2019)] and 100 kernel weight indicating the preponderance of additive gene action in expression of these traits and selection would be effective for improvement of these traits.

High heritability coupled with moderate genetic advance as per cent of mean was observed for days to initial flowering [Mahalakshmi *et al.* (2005) and John *et al.* (2009)], days to accumulation of 40 and 50 flowers from emergence, days to maturity [Patil *et al.* (2014), Singh *et al.* (2017) and Hampannavar *et al.* (2018a)] and shelling percentage [Patil *et al.* (2014), Gupta *et al.* (2015a), Mitra *et al.* (2021) and Shrotri *et al.* (2021)]. The improvement of these traits may not be encouraging if early generation selection is practiced, inspite of high heritability estimates.

High heritability coupled with low genetic advance as per cent of mean was exhibited by days to 50% flowering [Bhakal and Lal (2017) and Mitra *et al.* (2021)], days to accumulation of 25 flowers from emergence (N'Doye and Smith, 1993), percentage of ripe pods (Khalfaoui, 1990b) and number of sound mature kernels [Narasimhulu *et al.* (2012), Patil *et al.* (2014), Singh *et al.* (2017) and Hampannavar *et al.* (2018a)] indicating the presence of non-fixable genetic variance in the expression of these traits and selection for these traits would be ineffective among the genotypes tested.

Moderate heritability coupled with high genetic advance as per cent of mean was recorded for pod yield plant^{-1} and seed yield plant^{-1} indicating that these traits were most likely to be controlled by additive gene action. These results were confirmed by the reports of Shoba *et al.* (2009).

With the available information on extent of genetic variation and genetic parameters like heritability estimates and expected genetic advance for traits contributing to earliness, yield and yield components, it is proposed to consider the traits with moderate GCV and expected genetic advance for realizing targeted maturity groups with break throughs in yield potentials. Selection could be effective for 100 pod weight, 100 kernel weight, number of mature pods plant^{-1}, harvest index, pod yield plant^{-1} and seed yield plant^{-1} to increase the yield and yield components. Among the traits related to earliness, days from opening of 1st flower to 25 flowers and 40 flowers with a focused selection pressure on 100 pod weight, 100 kernel weight, harvest index and pod yield plant^{-1} could lead to good response to selection.

4.4 STUDY OF GENETIC DIVERGENCE

In any crop improvement programme, assessment of genetic diversity is of paramount importance for identifying potential parents for hybridization. Diverse parents are expected to yield high frequency of heterotic hybrids in addition to generation of a broad spectrum of variability in segregating generations. D^2 statistics is a useful multivariate analysis tool for measuring the genetic diversity in germplasm collection with respect to the traits considered together. It also provides a quantitative measure of association between geographic and genetic diversity based on general distances (Mahalanobis, 1936). The data collected for twenty two traits in 36 genotypes was subjected to Mahalanobis D^2 and the results are furnished below. Analysis of dispersion for thirty six groundnut genotypes is presented in Table 4.7.

Table 4.7. Analysis of variance for dispersion of 36 groundnut genotypes

Source of variation	Degree of freedom	Mean sum of squares
Genotype	35	4.8730E-15*
Error	34	-5.0163E-15
Total	69	0.0000E+00

Thirty six genotypes of groundnut were grouped into six clusters by using Tocher's method (Rao, 1952). The distribution of genotypes into various clusters are presented in Table 4.8 and Fig. 4.5. Among the six clusters, cluster I was the largest cluster consisting sixteen genotypes followed by cluster II with ten genotypes and cluster III with seven genotypes and the remaining clusters (IV, V, and VI) are monogenotypic indicating wide range of diversity among the genotypes.

The average intra and inter cluster distances (D^2) were calculated by using the method given by Singh and Chaudhary (1977) and are illustrated in the Table 4.9 and Fig. 4.6.

Table 4.8. Clustering of 36 groundnut genotypes based on Tocher's method

S.No	Cluster number	Number of genotypes	Genotypes
1	I	16	Rohini, TCGS 2333, TCGS 2350, TCGS 2351, TCGS 2352, TCGS 2353, TCGS 2354, TCGS 2357, JL 24, UBEK 21-38, UBEK 21-39, UBEK 21-42, UBEK 21-61, UBEK 20-24, SB-I-2021-7, ISK-I-2021-8
2	II	10	TCGS 2233, TCGS 2348, UBEK 21-35, UBEK 21-60, UBEK 21-68, UBEK 21-70, UBEK 20-32, UBEK 21-76, ISK-II-2020-4, ISK-I-2021-21
3	III	7	TAG 24, TCGS 2339, TCGS 2326, UBEK 21-40, UBEK 21-43, UBEK 21-74, ISK-II-2020-12
4	IV	1	UBEK 21-67
5	V	1	TCGS 2223
6	VI	1	TCGS 2347

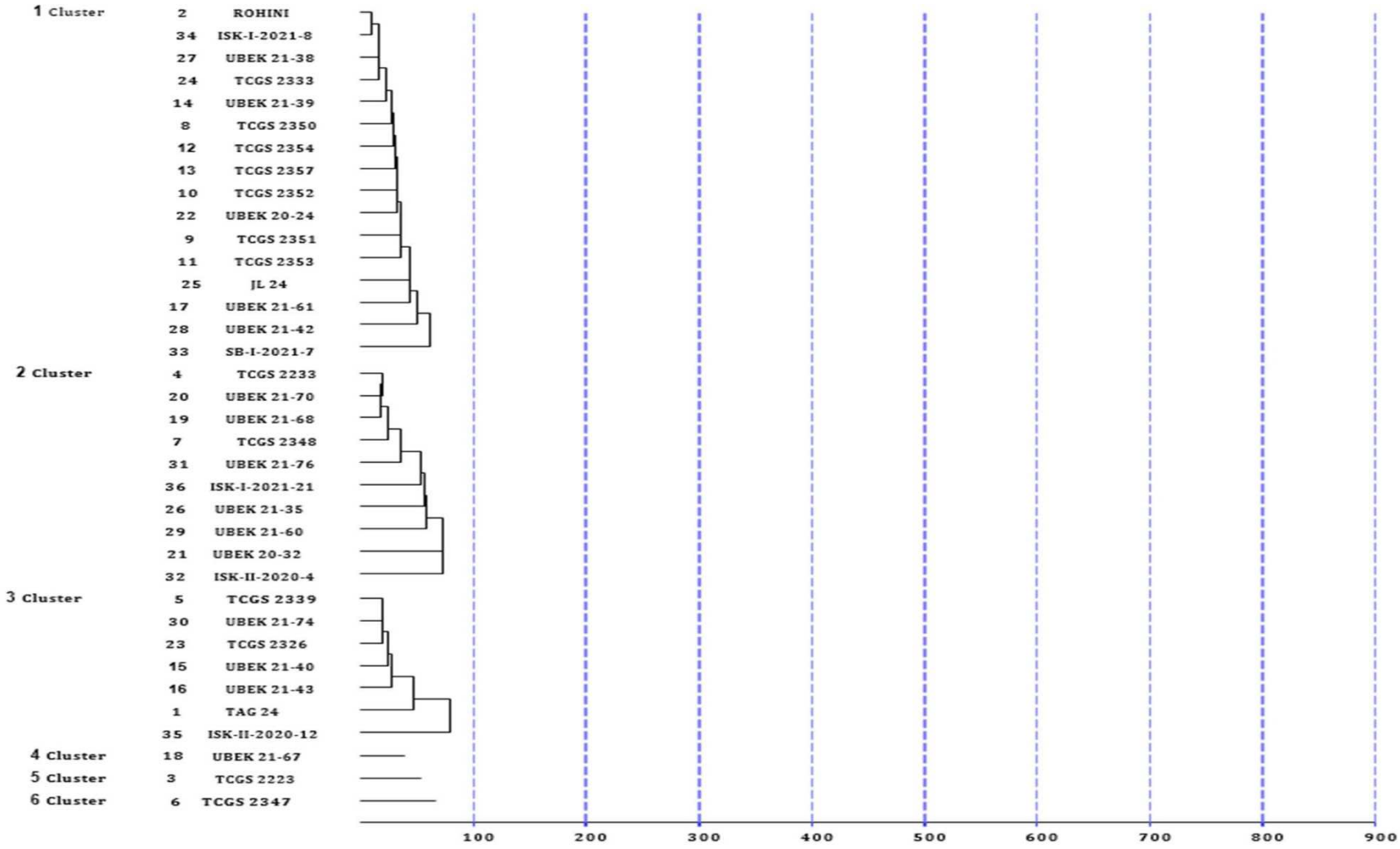


Fig. 4.5. Grouping of 36 groundnut genotypes into six clusters using Tocher's method

Table 4.9. Average inter (above diagonal) and intra cluster (diagonal) D^2 and D values (in parenthesis) among six clusters that included 36 groundnut genotypes

Clusters	I	II	III	IV	V	VI
I	114.84 **(10.72)**	274.25 **(16.56)**	317.13 **(17.81)**	206.72 **(14.38)**	429.96 **(20.74)**	558.57 **(23.63)**
II		171.64 **(13.10)**	774.73 **(27.83)**	237.66 **(15.42)**	420.18 **(20.50)**	440.53 **(20.99)**
III			144.93 **(12.04)**	487.57 **(22.08)**	832.72 **(28.86)**	1125.86 **(33.55)**
IV				0.00 **(0.00)**	399.66 **(19.99)**	696.62 **(26.39)**
V					0.00 **(0.00)**	203.15 **(14.25)**
VI						0.00 **(0.00)**

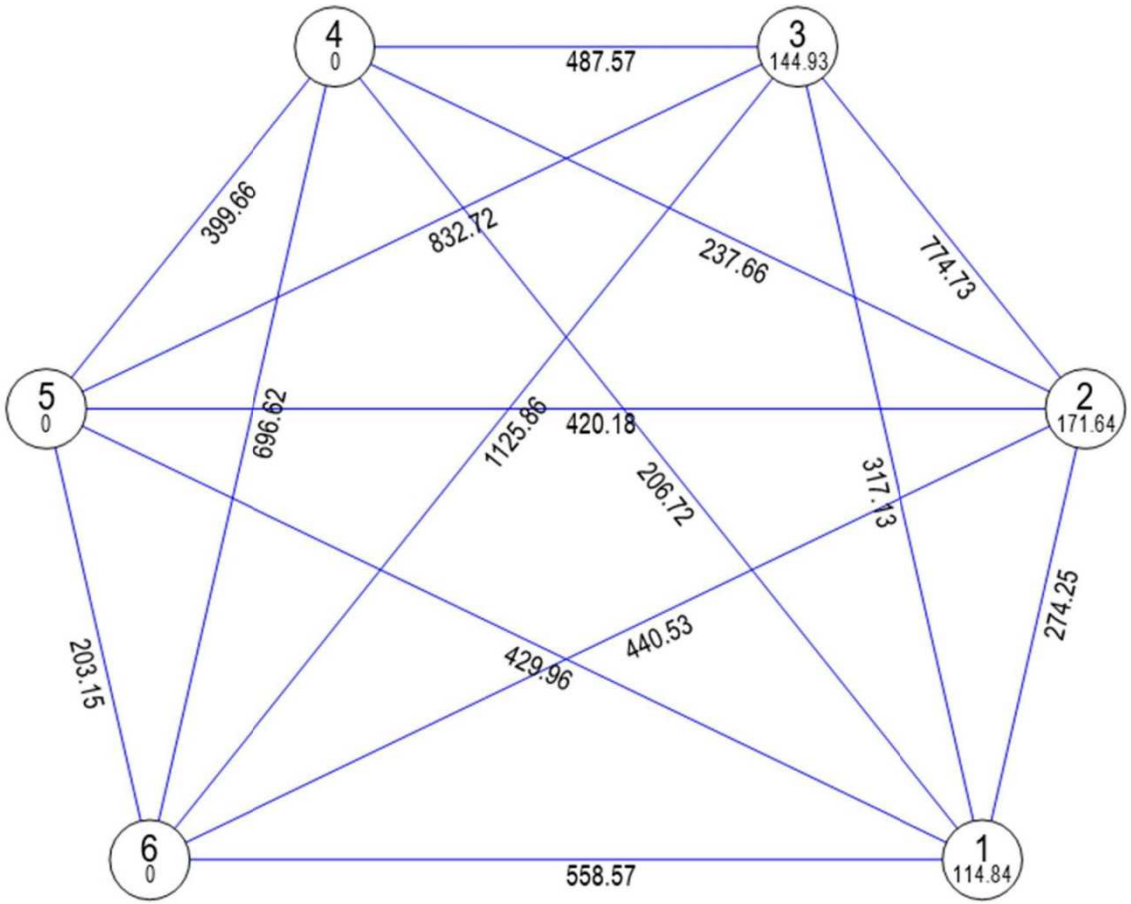


Fig. 4.6. Average intra and inter cluster distances among six clusters that included 36 groundnut genotypes

The intra cluster distances ranged from 0.00 to 171.64. The highest intra cluster distance was observed for cluster II (171.64), followed by cluster III (144.93) and cluster I (114.84). For the other clusters (IV, V and VI), intra cluster distance is zero as they are monogenotypic.

Maximum inter cluster distance was observed between cluster VI and III (1125.86), followed by cluster V and III (832.72), cluster II and III (774.73), cluster IV and VI (696.62) and cluster I and VI (558.57). It indicates the presence of high genetic diversity between these clusters thereby selecting genotypes from these clusters as parents in a hybridizing programme could be fruitful. Minimum inter cluster distance was observed between cluster VI and V (203.15) followed by cluster IV and I (206.72) and cluster 1V and II (237.66) suggesting that these clusters are genetically close with narrow genetic base and could be ineffective to use as parents in a hybridizing programme. Inter-cluster distances were higher than intra-cluster distance indicating the presence of wider genetic diversity between the clusters rather than within the clusters.

The number of times that each of the twenty-two traits appeared in first rank and its respective per cent contribution towards the total diversity is presented in Table 4.10. Among all the traits studied, days to maturity contributed maximum (59.84%) towards genetic diversity by ranking first for 377 times followed by days to initial flowering from emergence (7.62%) ranking first for 48 times and plant height (7.14%) ranking first for 45 times. The traits *viz.*, number of secondary branches plant^{-1} (5.4%), number of mature pods plant^{-1} (4.76%), days to 50% flowering (4.76%), days to accumulation of 40 flowers from emergence (3.33%), days to opening of 1st flower to opening of 50 number of flowers (3.02%), number of primary branches plant^{-1} (1.59%), days to accumulation of 25 flowers from emergence (0.95%), number of sound mature kernels (0.79%), shelling percentage (0.32%), 100 kernel weight (0.32%), number of immature pods plant^{-1} (0.16%), percentage of ripe pods (0.16%) and 100 pod weight (0.16%) contributed less for genetic diversity. Meanwhile, the contribution of days from opening of 1st flower to opening of

25 and 40 number of flowers, days to accumulation of 50 flowers from emergence, pod yield plant^{-1}, seed yield plant^{-1} and harvest index for genetic diversity is negligible.

The cluster means of different characters aids to assess the performance of genotypes with better mean performance against cluster means. The cluster means for each of 22 traits are presented in Table 4.11.

For phenological traits contributing to earliness, cluster I recorded lower mean values for days to initial flowering from emergence (19.41), days to 50% flowering (30.44) and days to accumulation of 40 flowers from emergence (32.41); cluster VI for days to accumulation of 25 flowers from emergence (28.50), days to accumulation of 50 flowers from emergence (35.50) and days from opening of first flower to opening of 50 number of flowers (15.00) followed by cluster III for days from opening of 1st flower to opening of 25 number of flowers (7.86), days from opening of 1st flower to opening of 40 number of flowers (11.93). Cluster III recorded lower mean values for days to maturity (92.00) and all the early maturing genotypes were observed here. Higher cluster means for plant height (41.45), primary branches plant^{-1} (5.00), pod yield plant^{-1} (17.75) seed yield plant^{-1} (12.85), hundred pod weight (140.00) and 100 kernel weight (58.60) were recorded in monogenotypic cluster VI. Cluster V recorded higher cluster mean values for number of secondary branches plant^{-1} (4.50) percentage of ripened pods, harvest index (58.95) and number of sound mature kernels (87.00). Higher cluster mean for shelling percentage (74.50) was recorded in cluster IV.

Table 4.10. Relative contribution of various traits towards genetic diversity among 36 groundnut genotypes

S.No	Characters	Number of times ranked first	Contribution (%)
1	Days from emergence to initial flowering	48	7.62
2	Days to 50% flowering	29	4.60
3	Days from opening of 1st flower to opening of 25 number of flowers	-	-
4	Days from opening of 1st flower to opening of 40 number of flowers	-	-
5	Days from opening of 1st flower to opening of 50 number of flowers	19	3.02
6	Days to accumulation of 25 flowers from emergence	6	0.95
7	Days to accumulation of 40 flowers from emergence	21	3.33
8	Days to accumulation of 50 flowers from emergence	-	-
9	Days to maturity	377	59.84
10	Plant height (cm)	45	7.14
11	Number of primary branches plant^{-1}	10	1.59
12	Number of secondary branches plant^{-1}	34	5.40
13	Number of mature pods plant^{-1}	29	4.60
14	Number of immature pods plant^{-1}	1	0.16
15	Percentage of ripe pods	1	0.16
16	Pod yield plant^{-1} (g)	-	-
17	Seed yield plant^{-1} (g)	-	-
18	Shelling percentage	2	0.32
19	Harvest index (%)	-	-
20	100 pod weight (g)	1	0.16
21	100 kernel weight (g)	2	0.32
22	Number of sound mature kernels	5	0.79

Table 4.11. Cluster means with respect to earliness and its contributing traits, yield and yield components among 36 groundnut genotypes

Clusters	DIFE	DFF	DA25E	DOF25	DA40E	DOF40	DA50E	DOF50	DM	PH	PB	SB
I	19.41	30.44	28.56	9.16	32.41	13.06	35.69	16.31	100.16	37.86	4.06	1.47
II	20.35	30.85	29.05	8.70	33.10	12.75	35.80	15.45	109.90	36.20	3.40	1.35
III	21.00	31.14	28.86	7.86	32.79	11.93	35.79	15.29	92.00	36.28	4.00	1.50
IV	21.00	33.00	30.50	9.50	33.50	12.50	36.00	15.00	110.50	28.10	3.00	4.00
V	22.50	34.00	33.50	11.00	38.50	16.00	41.50	19.00	109.50	35.50	4.00	4.50
VI	20.50	35.00	28.50	8.00	32.50	12.00	35.50	15.00	109.50	41.45	5.00	2.00
Mean	20.79	32.41	29.83	9.04	33.80	13.04	36.71	16.01	105.26	35.90	3.91	2.47

Clusters	MP	IMP	RP%	PYP	SYP	SP	HI	HPW	HKW	NSMK
I	14.38	3.53	79.94	12.02	8.79	72.59	47.68	100.72	42.49	87.03
II	16.50	2.60	86.25	14.29	9.87	69.55	47.90	103.80	45.72	83.55
III	15.29	4.00	78.50	10.99	7.26	65.93	40.56	84.50	36.47	82.00
IV	15.50	2.50	84.00	16.40	12.20	74.50	49.35	93.50	39.70	84.00
V	16.00	2.00	87.50	14.00	10.20	73.00	58.95	126.00	53.90	87.00
VI	14.00	2.50	85.00	17.75	12.85	72.00	55.40	140.00	58.60	82.00
Mean	15.28	2.86	83.53	14.24	10.20	71.26	49.97	108.09	46.15	84.26

DIFE : Days from emergence to initial flowering
DFF : Days to fifty percent flowering
DA25E : Days to accumulation of twenty-five flowers from emergence
DOF25 : Days from opening of first flower to twenty-five number of flowers
DA40E : Days to accumulation of forty flowers from emergence
DOF40 : Days from opening of first flower to forty number of flowers
DA50E : Days to accumulation of fifty flowers from emergence
DOF50 : Days from opening of first flower to fifty number of flowers
DM : Days to maturity
PH : Plant height
PB : Number of primary branches plant^{-1}
SB : Number of secondary branches plant^{-1}
MP : Number of mature pods plant^{-1}
IMP : Number of immature pods plant^{-1}
RP% : Percentage of ripe pods
PYP : Pod yield plant^{-1} (g)
SYP : Seed yield plant^{-1} (g)
SP : Shelling percentage
HI : Harvest index
HPW : Hundred pod weight
HKW : Hundred kernel weight
NSMK : Number of sound mature kernels

Improvement of traits contributing to early maturity

Genotypes from cluster III (TAG 24, TCGS 2339, TCGS 2326, UBEK 21-40, UBEK 21-43, UBEK 21-74 and ISK-II-2020-12) targeting characters *viz.*, days to accumulation of 25 and 40 flowers from 1st flower and days to maturity and genotype (UBEK 21-67) from cluster IV for 100 pod weight and 100 kernel weight might be selected for developing genotypes with early maturity of 90 days.

Improvement of traits related to pod yield

To develop genotypes with higher pod yields, genotypes from cluster II and V with high mean values for pod yield plant^{-1} (UBEK 21-68, UBEK 21-70), number of mature pods plant^{-1} (TCGS 2233, TCGS 2348, UBEK 21-68, ISK-II,2020-4), TCGS 2223 genotype from cluster V for high harvest index and TCGS 2347 genotype from cluster VI with high mean value for 100 pod weight and 100 kernel weight are to be involved in hybridization program.

A perusal of foregoing discussion revealed that, there is no single cluster with all the desirable traits, which ruled out the possibility of direct selection of genotypes for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is suggested for judicious combination of all the targeted traits. Manifestation of heterosis is maximum in cross combinations involving the parents selected from the most divergent clusters and having complementarity for traits of interest. TCGS 2347 from cluster VI, TCGS 2233, TCGS 2348 and UBEK 21-68 from cluster II, Rohini and UBEK 21-76 from cluster I could be selected as parents for hybridization programme as they expressed maximum inter cluster distance and high per se performance for more number of yield traits in respective clusters. It is to conclude that, the crosses viz., TCGS 2347 × UBEK 21-76 (cluster VI × cluster I), TCGS 2347 × Rohini (cluster VI × cluster I), TCGS 2347 × TCGS 2233 (cluster VI × cluster II) and TCGS 2347 × UBEK 21-68 (cluster VI × cluster II) could be recommended for complementarity of traits of interest. Hybridization between genotypes from

cluster III and cluster II, VI is more likely to produce transgressive segregants with both early maturity and high yield like crosses *viz.*, TAG 24 × TCGS 2347, TCGS 2326 × TCGS 2347, UBEK 21-43 × TCGS 2347, UBEK 21-74 × TCGS 2347, TAG 24 × TCGS 2233, TCGS 2326 × TCGS 2348, UBEK 21-43 × UBEK 21-60, UBEK 21-74 × TCGS 2233, TAG 24 × UBEK 21-60, TCGS 2326 × TCGS 2233.

4.5 STUDY OF CHARACTER ASSOCIATION

The present study was made to establish the relationships among the yield, maturity and their corresponding components. The components for yield and maturity exhibit varying degree of association with the trait under study and among themselves. To pyramid optimum number of traits contributing for yield and maturity, it is inevitable to know the relationships among themselves. Correlation analysis provides nature, extent and direction of selection if we need to combine a trait with desirable traits.

In the current study, phenotypic and genotypic correlation among yield and yield components, earliness and its components were computed to know their relationship with yield and maturity. The magnitude of genotypic correlation values was higher than the corresponding phenotypic correlation values. Thus, it can be inferred that the heritable association between the traits and their magnitude got reduced due to the influence of environment.

4.5.1 Correlation between yield and yield components

The phenotypic (r_p) and genotypic (r_g) correlation coefficients for 13 yield and yield attributing traits among 36 genotypes are furnished in Table 4.12.

Pod yield plant^{-1} exhibited highly significant and positive correlation with seed yield plant^{-1} ($r_p = 0.9434^{**}$; $r_g = 0.9354^{**}$) [Narasimhulu *et al.* (2012), Singh *et al.* (2017), Bhakal and Lal (2017), Hampannavar *et al.* (2018a) and Kumar *et al.* (2019)], followed by 100 kernel weight ($r_p = 0.5818^{**}$; $r_g = 0.7702^{**}$) [Shoba *et al.* (2012), Bhargavi *et al.* (2015b), Vasanthi *et al.*

(2015), Singh *et al.* (2017), Hampannavar *et al.* (2018a)], 100 pod weight (r_p = 0.5937**; r_g = 0.7417**) [Prabhu *et al.* (2015)], harvest index (r_p = 0.5380**; r_g = 0.7306**) [Babariya and Dobariya (2012)], days to maturity (r_p = 0.4921**; r_g = 0.7033**) [Bhargavi *et al.* (2015b)] and number of mature pods plant^{-1} (r_p = 0.3868**; r_g = 0.5832**) [Babariya and Dobariya (2012), Bhargavi *et al.* (2015b) and Vasanthi *et al*. (2015)] at both phenotypic and genotypic levels indicating selection for these traits will simultaneously improve pod yield plant^{-1}. On the other hand, pod yield plant^{-1} showed highly significant and negative phenotypic and genotypic correlation with number of immature pods plant^{-1} (r_p = -0.3863**; r_g = -0.4885**) [Hampannavar *et al.* (2018a)].

These results emphasize that selection for late maturing genotypes with more number of mature pods, higher 100 pod weight, higher 100 kernel weight, high harvest index and fewer immature pods plant^{-1} consisting larger kernels would improve pod yield plant^{-1}.

4.5.2 Inter-correlation among yield and yield components

Studies on inter-correlations among yield and yield components reveals the favourable or unfavourable associations among themselves as well as with yield. The inter-correlations among these traits assessed in the present study are described here under.

Significant positive association of plant height was recorded with number of primary branches plant^{-1} (r_p = 0.3794**; r_g = 0.4417**), 100 pod weight (r_p = 0.2634*) and 100 kernel weight (r_p = 0.3439**; r_g = 0.3895*). These results are in harmony with the findings of Prabhu *et al.* (2015) for number of primary branches plant^{-1} and 100 pod weight whereas, similar results were recorded by Meta and Monpara (2010) for 100 kernel weight. Also, number of primary branches plant^{-1} exhibited significant positive association with 100 pod weight (r_p = 0.2491*; r_g = 0.3401*). Thus, selecting for number of primary branches plant^{-1}, 100 pod weight and 100 kernel weight might promote gains in pod yields.

Table 4.12. Correlation analysis for yield and yield components among 36 groundnut genotypes

		PH	PB	SB	MP	IMP	DFF	DM	HI	HPW	HKW	SYP	NSMK	PYP
PH	r_p	1 **	0.3794 **	-0.0834	0.1778	0.1711	0.1208	-0.0666	-0.1378	0.2634 *	0.3439 **	-0.0639	-0.0046	0.0029
	r_g	1 **	0.4417 **	-0.0925	0.1913	0.2023	0.1469	-0.0725	-0.1346	0.2602	0.3895 *	-0.1065	-0.0008	-0.0284
PB	r_p		1 **	0.0804	0.1203	0.1515	0.1453	-0.1829	-0.0122	0.2491 *	0.1967	0.0807	0.0908	0.0662
	r_g		1 **	0.091	0.1662	0.246	0.1439	-0.2094	0.0166	0.3401 *	0.2826	0.1258	0.1496	0.095
SB	r_p			1 **	0.0404	-0.0687	0.435 **	0.2191	0.1298	0.1977	0.1692	0.0064	0.0278	0.0157
	r_g			1 **	0.0274	-0.0809	0.5158 **	0.2291	0.1331	0.2216	0.181	0.0334	-0.0195	0.0446
MP	r_p				1 **	0.0107	0.1515	0.2094	0.2621 *	0.355 **	0.38 **	0.2957 *	0.0477	0.3868**
	r_g				1 **	0.0152	0.1664	0.219	0.3384* *	0.3917 *	0.4092 *	0.4905 **	0.0407	0.5832**
IMP	r_p					1 **	-0.0607	-0.5851 **	-0.119	-0.2873 *	-0.3297 **	-0.3643 **	0.0339	-0.3863**
	r_g					1 **	-0.0858	-0.706 **	-0.215	-0.3711 *	-0.4302 **	-0.4741 **	0.0023	-0.4885**
DFF	r_p						1 **	0.2826 *	0.019	0.2132	0.2752 *	0.1024	-0.1367	0.0948
	r_g						1 **	0.2593	-0.0083	0.2528	0.3815 *	0.2252	-0.1708	0.1893
DM	r_p							1 **	0.3255 **	0.5284 **	0.6129 **	0.4953 **	0.0792	0.4921 **
	r_g							1 **	0.4078 *	0.5609 **	0.6582 **	0.682 **	0.0919	0.7033 **
HI	r_p								1 **	0.4555 **	0.3733 **	0.5244 **	0.1823	0.5380 **
	r_g								1 **	0.5998 **	0.4937 **	0.7424 **	0.2745	0.7306 **
HPW	r_p									1 **	0.8818 **	0.5886 **	0.28 *	0.5938**
	r_g									1 **	0.9398 **	0.7121 **	0.3229	0.7417**
HKW	r_p										1 **	0.5833 **	0.176	0.5818**
	r_g										1 **	0.7366 **	0.1297	0.7702**
SYP	r_p											1 **	0.1622	0.9434**
	r_g											1 **	0.3872 *	0.9354**
NSMK	r_p												1 **	0.0527
	r_g												1 **	0.2117
PYP	r_p													1 **
	r_g													1 **

** Significant at 1% LoS, *Significant at 5% LoS

PH: Plant height
PB: Number of primary branches plant^{-1}
SB: Number of secondary branches plant^{-1}
MP: Number of mature pods plant^{-1}
IMP: Number of immature pods plant^{-1}
DFF: Days to fifty percent flowering
DM: Days to maturity
HI: Harvest index
HPW: Hundred pod weight
HKW: Hundred kernel weight
SYP: Seed yield plant^{-1} (g)
NSMK: Number of sound mature kernels
PYP: Pod yield plant^{-1} (g)

Significant positive association is recorded for number of secondary branches plant^{-1} with days to 50% flowering (r_p = 0.4350*; r_g = 0.5158*). These results are confirmed by the reports of Mahalakshmi *et al.* (2005).

Number of mature pods plant^{-1} showed significant positive correlation with harvest index (r_p = 0.2621*; r_g = 0.3384**) [Bhargavi *et al.* (2015b)], 100 pod weight (r_p = 0.355**; r_g = 0.3917*), 100 kernel weight (r_p = 0.38**; r_g = 0.4092*), seed yield plant^{-1} (r_p = 0.2957*; r_g = 0.4905**). Similar results for 100 kernel weight and seed yield plant^{-1} was reported by Mahalakshmi *et al.* (2005). These results indicate that selection for plants with more number of mature pods and larger seeds would increase economic yield.

Number of immature pods plant^{-1} exhibited significant negative association with days to maturity (r_p = -0.5851**; r_g = 0.706**), 100 pod weight (r_p = -0.2873*; r_g = -0.3711*) [John *et al.* (2019)], 100 kernel weight (r_p = -0.3297**; r_g = -0.4302**) [Hampannavar *et al.* (2018a)] and seed yield plant^{-1} (r_p = -0.3643**; r_g = -0.4741**). It indicates that selection for plants with lesser number of immature pods would improve seed yield.

Significant positive association with days to 50% flowering is exhibited by days to maturity (r_p = 0.2826*) Rao *et al.* (2014) and Bhargavi *et al.* (2015b)] and hundred kernel weight (r_p = 0.2752*; r_g = 0.3815*) [Vasanthi *et al.* (2015)].

Days to maturity exhibited significant positive correlation with harvest index (r_p = 0.3255**; r_g = 0.4078*), 100 pod weight (r_p = 0.5284**; r_g = 0.5609**), 100 kernel weight (r_p = 0.6129**; r_g = 0.6582**), seed yield plant^{-1} (r_p = 0.4953**; r_g = 0.682**). It suggests that selection for late maturing genotypes would increase seed yield plant^{-1}. Bhargavi *et al.* (2015b) reported similar findings for harvest index and 100 kernel weight while significant positive association of days to maturity with seed yield plant^{-1} was earlier reported by Babariya and Dobariya (2012).

Harvest index was observed to be positively associated with 100 pod weight (r_p = 0.4555**; r_g = 0.5998**), 100 kernel weight (r_p = 0.3733**;

r_g = 0.4937**) [Vasanthi *et al.* (2015), Alam *et al.* (2014)] and seed yield plant^{-1} (r_p = 0.5244**; r_g = 0.7424**) [Babariya and Dobariya (2012) and Bhargavi *et al.* (2015b)]. Therefore, selection for larger seeds would increase harvest index.

Hundred pod weight was positively associated with hundred kernel weight (r_p = 0.8818**; r_g = 0.9398**), seed yield plant^{-1}(r_p = 0.5886**; r_g = 0.7121**) and number of sound mature kernels (r_p = 0.2800*) [Prabhu *et al.* (2015)]. Earlier, positive association of 100 pod weight with 100 kernel weight and seed yield plant^{-1} was confirmed by the findings of Zaman *et al.* (2011) and John *et al.* (2019).

Positive association of hundred kernel weight with seed yield plant^{-1} was observed in the present study which was earlier reported by Babariya and Dobariya (2012), Shoba *et al.* (2012), Rao *et al.* (2014) and Vasanthi *et al.* (2015). Positive association of number of sound mature kernels with seed yield plant^{-1} suggests that selection for genotypes with more number of sound mature kernels would increase seed yield [Mahalakshmi *et al.* (2005) and Prabhu *et al.* (2015)].

From the present discussion on character association for pod yield plant^{-1}, it is inferred that number of mature pods plant^{-1}, days to maturity, harvest index, 100 pod weight, 100 kernel weight and seed yield plant^{-1} at both phenotypic and genotypic levels were highly positive and significant with pod yield plant^{-1} and also among themselves, indicating that an increase in the magnitude of any of these traits will lead to subsequent increase in the magnitude of pod yield. Hence, these traits could be used in the further selection programme for improvement of pod yield plant^{-1}.

4.5.3 Correlation between earliness and its components

The phenotypic (r_p) and genotypic (r_g) correlation coefficients for phenological and quantitative traits contributing earliness among 36 genotypes are furnished in Table 4.13.

Table 4.13. Correlation analysis for earliness and its contributing traits among 36 groundnut genotypes

		DIFE	DA25E	DOF25	DA40E	DOF40	DA50E	DOF50	RP%	HI	SP	HPW	HKW	PYP	DM
DIFE	r_p	1 **	0.3545 **	-0.7364 **	0.1443	-0.6426 **	-0.0072	-0.6214 **	-0.0988	-0.0891	0.1131	-0.2859 *	-0.204	-0.1697	0.0736
	r_g	1 **	0.4014 *	-0.7535 **	0.1826	-0.6421 **	0.0123	-0.6431 **	-0.0904	-0.2044	0.1706	-0.3267	-0.2009	-0.3106	0.0679
DA25E	r_p		1 **	0.3716 **	0.8853 **	0.4133 **	0.7725 **	0.3755 **	0.2129	0.0829	-0.0282	0.2029	0.2247	0.0782	0.3052 **
	r_g		1 **	0.2998	0.9518 **	0.4323 **	0.8394 **	0.3735 *	0.2215	0.136	-0.069	0.1942	0.3074	0.1515	0.3184
DOF25	r_p			1 **	0.4973 **	0.9371 **	0.566 **	0.8887 **	0.2521 *	0.1484	-0.1327	0.4307 **	0.3651 **	0.2251	0.1478
	r_g			1 **	0.493 **	0.9791 **	0.5897 **	0.9379 **	0.2531	0.3106	-0.2273	0.4797 **	0.4299 **	0.4323 **	0.1578
DA40E	r_p				1 **	0.6586 **	0.9364 **	0.6302 **	0.2427 *	0.131	-0.1483	0.2398 *	0.25 *	0.0935	0.2681 *
	r_g				1 **	0.6367 **	0.9775 **	0.6215 **	0.2054	0.195	-0.1838	0.259	0.3251	0.1962	0.2745
DOF40	r_p					1 **	0.7261 **	0.9637 **	0.2596 *	0.1691	-0.194	0.3987 **	0.3513 **	0.1965	0.1337
	r_g					1 **	0.7467 **	0.9924 **	0.2295	0.3079	-0.2821	0.452 **	0.3996 *	0.3899 *	0.1423
DA50E	r_p						1 **	0.7732 **	0.1514	0.092	-0.1385	0.2059	0.2011	0.0574	0.1551
	r_g						1 **	0.7447 **	0.1271	0.1796	-0.204	0.2326	0.2812	0.0963	0.1685
DOF50	r_p							1 **	0.1768	0.1321	-0.1915	0.322 **	0.2646 *	0.1338	0.0341
	r_g							1 **	0.1438	0.2565	-0.2896	0.3708 *	0.3232	0.2501	0.0414
RP%	r_p								1 **	0.2261	0.0513	0.4358 **	0.4795 **	0.5302 **	0.6222 **
	r_g								1 **	0.3532 *	0.0642	0.5353 **	0.5874 **	0.7913 **	0.7314 **
HI	r_p									1 **	0.1631	0.4555 **	0.3733 **	0.5375 **	0.3255 **
	r_g									1 **	0.3534 *	0.5998 **	0.4937 **	0.7298 **	0.4078 *
SP	r_p										1 **	0.1859	0.21	0.1468	0.2114
	r_g										1 **	0.2412	0.2312	0.2092	0.2674
HPW	r_p											1 **	0.8818 **	0.5937 **	0.5284 **
	r_g											1 **	0.9398 **	0.7414 **	0.5609 **
HKW	r_p												1 **	0.5818 **	0.6129 **
	r_g												1 **	0.7702 **	0.6582 **
PYP	r_p													1 **	0.4921 **
	r_g													1**	0.7033 **
DM	r_p														1 **
	r_g														1 **

** Significant at 1% LoS, *Significant at 5% LoS

DIFE: Days from emergence to initial flowering
DOF50: Days from opening of first flower to fifty number of flowers
DA50E: Days to accumulation of fifty flowers from emergence
HI: Harvest index
HKW: Hundred kernel weight

DOF25: Days from opening of first flower to twenty-five number of flowers
DA25E: Days to accumulation of twenty-five flowers from emergence
DM: Days to maturity
SP: Shelling percentage
PYP: Pod yield plant^{-1} (g)

DOF40: Days from opening of first flower to forty number of flowers
DA40E: Days to accumulation of forty flowers from emergence
RP%: Percentage of ripe pods
HPW: Hundred pod weight

Days to maturity exhibited highly significant positive correlation with percentage ripe pods ($r_p = 0.6222^{**}$; $r_g = 0.7314^{**}$), harvest index ($r_p = 0.3255^{**}$; $r_g = 0.4078^{*}$), 100 pod weight ($r_p = 0.5284^{**}$; $r_g = 0.5609^{**}$), 100 kernel weight ($r_p = 0.6129^{**}$; $r_g = 0.6582^{**}$) and pod yield plant^{-1} ($r_p = 0.4921^{**}$; $r_g = 0.7033^{**}$) at both phenotypic and genotypic levels.

Days to maturity is also associated phenotypically with days to accumulation of 25 ($r_p = 0.3052^{**}$) and 40 ($r_p = 0.2681^{*}$) flowers from the emergence. These results indicate that days to accumulation of 25 and 40 flowers from emergence can be used as good criteria in selection programmes to improve short duration genotypes. These results are in conformity with the findings of Bailey and Bear (1973) and Khalfaoui (1990b) who demonstrated that the early onset of flowering and early accumulation of a given number of flowers are important components of early maturity in groundnut.

4.5.4 *Inter se* relationship of traits

Days to initial flowering from emergence exhibited significant positive correlation with days to accumulation of 25 flowers from emergence ($r_p = 0.3545^{**}$; $r_g = 0.4014^{*}$) indicating that the fewer days to first flowering from emergence resulted in faster accumulation of 25 flowers from emergence. Days to initial flowering from emergence also exhibited non-significant positive correlation with days to maturity which was in accordance with findings of Khalfaoui (1990a) who concluded that days to start of flowering do not provide a dependable role in selection for early maturity.

Significant negative correlation was observed for days from emergence to first flower with days to opening of 25 flowers from opening of 1st flower ($r_p = -0.7364^{**}$; $r_g = -0.7535^{*}$), days from opening of 1st flower to 40 flowers ($r_p = -0.6426^{**}$; $r_g = -0.6421^{**}$) and days from opening of 1st flower to 50 flowers ($r_p = -0.6214^{**}$; $r_g = -0.6431^{*}$). The trend indicates that the greater number of days it takes to initial flowering from emergence, the lesser days it takes to open 25, 40 and 50 number of flowers from initial flowering. This trend could aid in uniform maturity of pods which is very much essential in groundnut due to its geocarpic nature.

Days to accumulation of 25 flowers from emergence exhibited highly significant positive correlation with days to accumulation of 40 flowers from emergence (r_p = 0.8853**; r_g = 0.9518**), 50 flowers from emergence (r_p = 0.7725**; r_g = 0.8394**) and days from opening of 1st flower to opening of 40 flowers (r_p = 0.4133**; r_g = 0.4323**), days from opening of 1st flower to 50 flowers (r_p = 0.3735**; r_g = 0.3735*). It indicates that lesser the number of days it takes to accumulate 25 flowers from emergence, the fewer days it takes to attain maturity through accumulation of 40 and 50 number of flowers which results in development into ripe pods. This is evident from the significant positive phenotypic correlation of % ripe pods with days to accumulation of 25 flowers from 1st flower opening (r_p = 0.2521*), days to accumulation of 40 flowers from emergence (r_p = 0.2427*) and days from opening of 1st flower to 40 flowers (r_p = 0.2596*). Khalfaoui (1990a) reported strong phenotypic correlations between precocity components and percentage of mature pods at 90 days duration.

Days from opening of 1st flower to 25 number of flowers recorded significant positive correlation with all the phenological traits under study except days to maturity. It was positively associated with 100 pod weight (r_p = 0.4307**; r_g = 0.4797**), 100 kernel weight (r_p = 0.3651**; r_g = 0.4299**) and genotypic correlation was recorded for pod yield plant^{-1} (r_g = 0.4323**). Days from opening of 1st flower to 25 number of flowers could be an important phenology in groundnut which favours optimum 100 pod weight, 100 kernel weight and pod yield plant^{-1}.

Significant positive association of days to accumulation of 40 flowers from emergence with all phenological traits (except days to initial flowering from emergence) was recorded along with 100 pod weight (r_p = 0.2398*) and 100 kernel weight (r_p = 0.2500*). Percentage of ripe pods (r_p = 0.2681*) was positively associated with days to accumulation of 40 flowers from emergence at phenotypic level.

Days from opening of 1st flower to opening of 40 number of flowers recorded significant positive correlation with days to accumulation of 50 flowers from emergence ($r_p = 0.7261^{**}$; $r_g = 0.7467^{**}$), and days from opening of 1st flower to opening of 50 number of flowers ($r_p = 0.9637^{**}$; $r_g = 0.9924^{**}$), 100 pod weight ($r_p = 0.3987^{**}$; $r_g = 0.452^{**}$), 100 kernel weight ($r_p = 0.3513^{**}$; $r_g = 0.3996^{*}$).

Significant positive association was exhibited by days to accumulation of 50 flowers from emergence with all the traits recorded on flowering trends except days to initial flowering from emergence.

Days from opening of 1st flower to opening of 50 number of flowers recorded significant positive correlation with all flowering traits. It also exhibited significant positive correlation with 100 pod weight ($r_p = 0.3220^{**}$; $r_g = 0.3708^{*}$).

Shelling percentage was positively associated with harvest index at genotypic level ($r_g = 0.3534^{*}$). Earlier, similar results were reported by Babariya and Dobariya (2012) and Bhargavi *et al.* (2017b).

From the present discussion on character association, it can be concluded that only two phenological traits *viz.*, days to accumulation of 25 and 40 flowers from emergence contributed significantly to days to maturity. Even though other traits exhibited significant *inter se* correlations among them, their association with days to maturity was negligible. Therefore, for development of early maturing genotypes, selection for early accumulation of 25 and 40 flowers from emergence would be advantageous. Coffelt *et al*. (1989) reported that increased yields in groundnut could be realized by developing cultivars with high reproductive efficiency, harvest index and total flower count. Passioura (1986) predicted that seed yield is function of harvest index, water use efficiency and water transpired. The results of this study indicate that larger the pods and kernels, the more days it takes to attain maturity. From this, it could be inferred that attaining earliness without compromising the yield might be a difficult task to achieve. Thereby, it is suggested that setting an optimum

limit for yield along with 100 pod weight (< 90 g), 100 kerrnel weight (< 40 g) and harvest index (< 50%)could be helpful to breed early maturing lines with optimum yield.

4.6 PATH COEFFICIENT ANALYSIS

Yield and maturity are complex traits which depend upon the interaction of number of components and environment. Due to their complex nature of inheritance, direct selection for pod yield and early maturity is not a reliable approach. Thus, correlation of yield with its components and correlation of days to maturity with its possible components were partitioned into direct and indirect effects of these component traits on corresponding traits was studied.

In the current study, phenotypic and genotypic correlation among yield and yield components, earliness and its components were computed to know their relationship with yield and maturity.

4.6.1 Pod yield and yield attributing traits

Path coefficient analysis was conducted using pod yield plant^{-1} as dependent variable and 13 independent variables, of them seven traits *viz.*, number of mature pods plant^{-1}, number of immature pods plant^{-1}, days to maturity, harvest index, 100 pod weight, 100 kernel weight and seed yield plant^{-1} exhibited significant correlation with pod yield plant^{-1}. The results are presented in the Table 4.14.

Seed yield plant^{-1} showed high and positive direct effect on pod yield plant^{-1} (P_p = 0.8875; P_g = 0.3480). Therefore, direct selection based on this character would be rewarding in increasing pod yield plant^{-1}. Several research workers also demonstrated similar findings [Singh *et al.* (2017), Hampannavar *et al*. (2018a) and Kumar *et al.* (2019)]. Direct selection for number of mature pods plant^{-1} (P_p = 0.0984; P_g = 0.2497) might be useful for improving pod yield plant^{-1} as it exerted moderate positive direct effect on pod yield plant^{-1}. The traits *viz.*, harvest index (P_p = 0.0601; P_g = 0.2264), days to maturity (P_p = 0.0106; P_g = 0.1088) and 100 pod weight (P_p = 0.1032; P_g = -0.1754) exhibited

low positive direct effect on pod yield plant^{-1} indicating direct selection for improving these traits might be ineffective. Direct positive effect of number of mature pods plant^{-1} with pod yield plant^{-1} was earlier reported by Meta and Monpara (2010), Bhargavi *et al.* (2015b), Patil *et al.* (2015), Jain *et al.* (2016), Hampannavar *et al.* (2018a) and John *et al*. (2019).

On the other hand, number of immature pods plant^{-1} (P_p = -0.0572; P_g= -0.1665) and 100 kernel weight (P_p = -0.1067; P_g = 0.3659) depicted low negative direct effects on pod yield plant^{-1}. Positive and significant correlation of 100 kernel weight with pod yield plant^{-1} can be explained by high indirect effect via seed yield plant^{-1} (P_p =0.502; P_g=0.3689) [Singh *et al.* (2017)].

Number of mature pods plant^{-1} exhibited moderate positive direct effect on pod yield plant^{-1} (P_p = 0.0984; P_g = 0.2497). The significant positive association of number of mature pods plant^{-1} was mainly due to the indirect effects of moderate seed yield plant^{-1} (P_p = 0.2734; P_g = 0.1695) along with negligible effects of harvest index (P_p = 0.0303; P_g = 0.0166) and 100 pod weight (P_p = 0.0360; P_g = -0.0668). Similar results were in accordance with the findings of John *et al.* (2019).

Number of immature pods plant^{-1} exerted high negative indirect effect through seed yield plant^{-1} (P_p = -0.3343; P_g = -0.1505) followed by indirect negligible effects of harvest index (P_p = -0.0086; P_g = -0.0547), 100 pod weight (P_p = -0.0245; P_g = 0.0532) and 100 kernel weight (P_p = 0.0279; P_g = -0.1306) thus its correlation with pod yield plant^{-1} is negative. Similar results for negligible indirect effect of immature pods through 100 kernel weight was observed by Kadam *et al.* (2018).

Harvest index had positive indirect effect through seed yield plant^{-1} (P_p = 0.4638; P_g = 0.2585) [Kiranmai *et al.* (2016)] along with negligible effects *via* number of mature pods plant^{-1} (P_p = 0.0273; P_g = 0.0888), number of immature pods plant^{-1} (P_p = 0.0082; P_g = 0.0402) and 100 pod weight (P_p = 0.0472; P_g = -0.1055)

Table 4.14. Phenotypic (P_p) and genotypic (P_g) path coefficient analysis for yield and yield components

		DFF	DM	PH	PB	SB	MP	IMP	HI	HPW	HKW	SYP	NSMK	Correlation with PYP
DFF	P_p	**-0.0402**	0.0030	0.0110	-0.0033	0.0094	0.0145	0.0024	0.0011	0.0221	-0.0294	0.0877	0.0164	0.0948
	P_g	**-0.0218**	0.0282	-0.0118	0.0137	-0.0411	0.0400	0.0093	-0.0019	-0.0448	0.1396	0.0768	0.0032	0.1893
DM	P_p	-0.0114	**0.0106**	-0.0061	0.0041	0.0047	0.0200	0.0305	0.0196	0.0545	-0.0654	0.4404	-0.0095	0.4921**
	P_g	-0.0057	**0.1088**	0.0058	-0.0199	-0.0183	0.0525	0.1089	0.0924	-0.0985	0.2408	0.2380	-0.0017	0.7033**
PH	P_p	-0.0049	-0.0007	**0.0912**	-0.0086	-0.0018	0.0147	-0.0142	-0.0083	0.0272	-0.0367	-0.0557	0.0005	0.0029
	P_g	-0.0032	-0.0079	**-0.0804**	0.0419	0.0074	0.0381	-0.0545	-0.0304	-0.0457	0.1425	-0.0362	0.0000	-0.0284
PB	P_p	-0.0058	-0.0019	0.0346	**-0.0227**	0.0017	0.0091	-0.0128	-0.0007	0.0257	-0.0210	0.0709	-0.0109	0.0662
	P_g	-0.0031	-0.0228	-0.0355	**0.0949**	-0.0073	0.0349	-0.0552	0.0039	-0.0599	0.1034	0.0444	-0.0028	0.0950
SB	P_p	-0.0175	0.0023	-0.0076	-0.0018	**0.0216**	0.0041	0.0038	0.0079	0.0207	-0.0181	0.0036	-0.0033	0.0157
	P_g	-0.0112	0.0249	0.0074	0.0086	**-0.0797**	0.0089	0.0171	0.0303	-0.0394	0.0662	0.0110	0.0004	0.0446
MP	P_p	-0.0059	0.0022	0.0136	-0.0021	0.0009	**0.0984**	-0.0017	0.0166	0.0360	-0.0391	0.2734	-0.0055	0.3868**
	P_g	-0.0035	0.0229	-0.0123	0.0133	-0.0028	**0.2497**	-0.0113	0.0805	-0.0668	0.1447	0.1697	-0.0008	0.5832**
IMP	P_p	0.0017	-0.0056	0.0226	-0.0051	-0.0014	0.0029	**-0.0572**	-0.0086	-0.0245	0.0279	-0.3343	-0.0046	-0.3863**
	P_g	0.0012	-0.0711	-0.0263	0.0315	0.0082	0.0170	**-0.1665**	-0.0547	0.0532	-0.1306	-0.1505	0.0001	-0.4885**
HI	P_p	-0.0008	0.0035	-0.0125	0.0003	0.0028	0.0273	0.0082	**0.0601**	0.0472	-0.0399	0.4638	-0.0219	0.5380**
	P_g	0.0002	0.0444	0.0108	0.0016	-0.0107	0.0888	0.0402	**0.2264**	-0.1055	0.1809	0.2585	-0.0051	0.7306**
HPW	P_p	-0.0086	0.0056	0.0241	-0.0057	0.0043	0.0343	0.0136	0.0275	**0.1032**	-0.0941	0.5233	-0.0337	0.5938**
	P_g	-0.0056	0.0611	-0.0209	0.0324	-0.0179	0.0951	0.0505	0.1362	**-0.1754**	0.3438	0.2485	-0.0060	0.7417**
HKW	P_p	-0.0111	0.0065	0.0314	-0.0045	0.0037	0.0360	0.0150	0.0225	0.0910	**-0.1067**	0.5193	-0.0212	0.5818**
	P_g	-0.0083	0.0716	-0.0313	0.0268	-0.0144	0.0988	0.0594	0.1119	-0.1649	**0.3659**	0.2570	-0.0024	0.7702**
SYP	P_p	-0.0040	0.0053	-0.0057	-0.0018	0.0001	0.0303	0.0216	0.0314	0.0609	-0.0625	**0.8875**	-0.0197	0.9434**
	P_g	-0.0048	0.0744	0.0084	0.0121	-0.0025	0.1218	0.0720	0.1682	-0.1253	0.2703	**0.3480**	-0.0072	0.9354**
NSMK	P_p	0.0055	0.0008	-0.0004	-0.0021	0.0006	0.0045	-0.0022	0.0109	0.0290	-0.0188	0.1451	**-0.1202**	0.0527
	P_g	0.0037	0.0100	0.0001	0.0142	0.0016	0.0112	0.0013	0.0619	-0.0568	0.0475	0.1356	**-0.0185**	0.2117

RESIDUAL EFFECT = 0.2772 (Phenotypic), RESIDUAL EFFECT = 0.2328 (Genotypic)

** Significant at 1% LoS

PH: Plant height
MP: Number of mature pods plant^{-1}
DM: Days to maturity
HKW: Hundred kernel weight
PYP: Pod yield plant^{-1} (g)
PB: Number of primary branches plant^{-1}
IMP: Number of immature pods plant^{-1}
HI: Harvest index
SYP: Seed yield plant^{-1} (g)
SB: Number of secondary branches plant^{-1}
DFF: Days to fifty percent flowering
HPW: Hundred pod weight
NSMK: Number of sound mature kernels

Hundred pod weight exerted high positive indirect effect through seed yield plant^{-1} (P_p = 0.5233; P_g = 0.2485) followed by negligible effects through number of mature pods plant^{-1} (P_p = 0.0343; P_g = 0.0951), number of immature pods plant^{-1} (P_p = 0.0136; P_g = 0.0505) and harvest index (P_p = 0.0275; P_g = 0.1362). Thus, selection for 100 pod weight contributes to realize higher pod yields. Results of harvest index were in accordance with those of Alam *et al.* (2014).

Highly significant and positive correlation of seed yield plant^{-1} with pod yield plant^{-1} was mainly due to its direct effect on pod yield plant^{-1}. Its indirect effects through all the other traits were found to be negligible suggesting direct selection for seed yield plant^{-1} would improve the yield.

The residual effect (P_p = 0.2772; P_g = 0.2328) was low with the traits included in the present study as most of the traits included in the present study established the cause and effect relationships on pod yield plant^{-1}.

Thus, from the above results it becomes clear that the traits *viz.*, seed yield plant^{-1} and number of mature pods plant^{-1} should be given more weightage during selection programme for the improvement of pod yield in groundnut. Traits which contributed indirectly through seed yield plant^{-1} should be carefully considered in breeding programmes for evolving high yielding lines.

4.6.2 Direct effects and indirect effects of earliness and its contributing traits on days to maturity

The phenotypic and genotypic path coefficients are presented in the Table 4.15.

Table 4.15. Phenotypic (P_p) and genotypic (P_g) path analysis for earliness and its contributing traits

		DIFE	DA25E	DOF25	DA40E	DOF40	DA50E	DOF50	RP%	HI	SP	HPW	HKW	PYP	Correlation with DM
DIFE	P_p	**-2.9282**	0.5234	1.3679	0.0856	0.3928	-0.0052	0.7414	-0.0405	-0.0102	0.0076	0.0251	-0.0864	0.0005	0.0736
	P_g	**-1.6371**	0.4829	1.0574	-0.1808	-0.4594	0.0168	0.9073	-0.0357	0.0005	0.0126	0.0702	-0.0849	-0.0818	0.0679
DA25E	P_p	-1.0380	**1.4765**	-0.6903	0.5248	-0.2526	0.5608	-0.4480	0.0873	0.0095	-0.0019	-0.0179	0.0952	-0.0002	0.3052**
	P_g	-0.6571	**1.2030**	-0.4207	-0.9420	0.3093	1.1427	-0.5269	0.0876	-0.0003	-0.0051	-0.0419	0.1300	0.0399	0.3184
DOF25	P_p	2.1563	0.5487	**-1.8577**	0.2948	-0.5727	0.4110	-1.0603	0.1034	0.0170	-0.0089	-0.0379	0.1547	-0.0006	0.1478
	P_g	1.2335	0.3606	**-1.4034**	-0.4879	0.7005	0.8028	-1.3233	0.1001	-0.0007	-0.0168	-0.1031	0.1818	0.1139	0.1578
DA40E	P_p	-0.4226	1.3072	-0.9238	**0.5928**	-0.4025	0.6799	-0.7519	0.0995	0.0149	-0.0100	-0.0212	0.1059	-0.0003	0.2681*
	P_g	-0.2990	1.1451	-0.6919	**-0.9897**	0.4556	1.3307	-0.8768	0.0812	-0.0004	-0.0136	-0.0558	0.1375	0.0517	0.2745
DOF40	P_p	1.8818	0.6102	-1.7407	0.3904	**-0.6112**	0.5271	-1.1498	0.1065	0.0193	-0.0130	-0.0351	0.1489	-0.0005	0.1337
	P_g	1.0512	0.5201	-1.3741	-0.6302	**0.7154**	1.0165	-1.4002	0.0908	-0.0007	-0.0209	-0.0972	0.1690	0.1027	0.1423
DA50E	P_p	0.0210	1.1406	-1.0515	0.5551	-0.4438	**0.7260**	-0.9225	0.0621	0.0105	-0.0093	-0.0181	0.0852	-0.0002	0.1551
	P_g	-0.0202	1.0098	-0.8275	-0.9675	0.5342	**1.3614**	-1.0507	0.0502	-0.0004	-0.0151	-0.0500	0.1189	0.0254	0.1685
DOF50	P_p	1.8196	0.5545	-1.6509	0.3736	-0.5890	0.5613	**-1.1931**	0.0725	0.0151	-0.0129	-0.0283	0.1121	-0.0004	0.0341
	P_g	1.0528	0.4493	-1.3163	-0.6151	0.7100	1.0138	**-1.4109**	0.0568	-0.0006	-0.0214	-0.0796	0.1366	0.0659	0.0414
RP%	P_p	0.2894	0.3143	-0.4684	0.1439	-0.1587	0.1099	-0.2109	**0.4100**	0.0258	0.0034	-0.0383	0.2032	-0.0014	0.6222**
	P_g	0.1480	0.2664	-0.3552	-0.2033	0.1642	0.1730	-0.2028	**0.3954**	-0.0008	0.0048	-0.1150	0.2483	0.2084	0.7314**
HI	P_p	0.2624	0.1225	-0.2768	0.0775	-0.1035	0.0666	-0.1576	0.0927	**0.1143**	0.0109	-0.0401	0.1584	-0.0015	0.3258**
	P_g	0.3359	0.1633	-0.4368	-0.1927	0.2205	0.2439	-0.3620	0.1399	**-0.0023**	0.0261	-0.1294	0.2090	0.1925	0.4081**
SP	P_p	-0.3311	-0.0416	0.2464	-0.0879	0.1186	-0.1006	0.2285	0.0210	0.0186	**0.0671**	-0.0162	0.0890	-0.0004	0.2114
	P_g	-0.2794	-0.0830	0.3190	0.1819	-0.2018	-0.2777	0.4086	0.0254	-0.0008	**0.0741**	-0.0517	0.0978	0.0551	0.2674
HPW	P_p	0.8369	0.3016	-0.8017	0.1429	-0.2443	0.1500	-0.3851	0.1790	0.0522	0.0124	**-0.0877**	0.3734	-0.0016	0.5280**
	P_g	0.5339	0.2343	-0.6729	-0.2567	0.3232	0.3162	-0.5223	0.2115	-0.0014	0.0178	**-0.2151**	0.3973	0.1954	0.5612**
HKW	P_p	0.5973	0.3317	-0.6782	0.1482	-0.2147	0.1460	-0.3157	0.1966	0.0427	0.0141	-0.0773	**0.4237**	-0.0016	0.6129**
	P_g	0.3289	0.3698	-0.6033	-0.3218	0.2859	0.3828	-0.4559	0.2323	-0.0011	0.0171	-0.2021	**0.4228**	0.2029	0.6582**
PYP	P_p	0.4970	0.1155	-0.4181	0.0554	-0.1201	0.0417	-0.1597	0.2174	0.0615	0.0099	-0.0521	0.2465	**-0.0027**	0.4921
	P_g	0.5085	0.1823	-0.6067	-0.1942	0.2790	0.1310	-0.3529	0.3129	-0.0017	0.0155	-0.1595	0.3256	**0.2634**	0.7033

RESIDUAL EFFECT = 0.6097 (Phenotypic), RESIDUAL EFFECT = 0.5455 (Genotypic)

** Significant at 1% LoS, *Significant at 5% LoS

DIFE: Days from emergence to initial flowering
DOF25: Days from opening of first flower to twenty-five number of flowers
DOF40: Days from opening of first flower to forty number of flowers
DOF50: Days from opening of first flower to fifty number of flowers
DA25E: Days to accumulation of twenty-five flowers from emergence
DA40E: Days to accumulation of forty flowers from emergence
DA50E: Days to accumulation of fifty flowers from emergence
DM: Days to maturity
RP%: Percentage of ripe pods
HI: Harvest index
SP: Shelling percentage
HPW: Hundred pod weight
HKW: Hundred kernel weight
PYP: Pod yield plant^{-1} (g)

4.6.2.1 Days to accumulation of 25 flowers from emergence and days to accumulation of 40 flowers from emergence

Days to accumulation of 25 flowers from emergence (r_p = 0.3052**) and days to accumulation of 40 flowers from emergence (r_p=0.2681*) recorded positive significant correlation at phenotypic level with days to maturity. Days to accumulation of 25 flowers from emergence (P_p = 1.4765) and days to accumulation of 40 flowers from emergence (P_p = 0.5928) with their high positive direct effect on days to maturity indicates that direct selection will be rewarding for these traits. The significant positive association of days to accumulation of 25 flowers from emergence with days to maturity was further contributed by positive indirect effects through days to accumulation of 40 flowers from emergence (P_p = 0.5248), days to accumulation of 50 flowers from emergence (P_p = 0.5608), 100 kernel weight (P_p = 0.0952) followed by percentage of ripe pods (P_p = 0.0873) and harvest index (P_p = 0.0095). With respect to days to accumulation of 40 flowers from emergence, the significant positive correlation was due to the high direct effect (P_p = 0.5928) and through indirect effects of days to accumulation of 50 flowers from emergence (P_p = 0.6799), 100 kernel weight (P_p = 0.1059) and percentage ripe pods (P_p = 0.0995).

4.6.2.2 Percentage of ripe pods

Percentage of ripe pods showed positive significant correlation (r_p = 0.6222**; r_g = 0.7314**) and high positive direct effect (P_p = 0.4100; P_g = 0.3954) on days to maturity at both phenotypic and genotypic levels. It showed highest positive indirect effect through days to initial flowering from emergence (P_p = 0.2894; P_g = 0.1480), days to accumulation of 25 flowers from emergence (P_p = 0.3143; P_g = 0.2664), days to accumulation of 40 flowers from emergence (P_p = 0.1439; P_g = -0.2033), days to accumulation of 50 flowers from emergence (P_p = 0.1099; P_g = 0.1730) and 100 kernel weight (P_p = 0.2032; P_g = 0.2483).

4.6.2.3 Harvest index

Positive significant correlation (r_p = 0.3258**; r_g = 0.4081**) of harvest index with days to maturity is due to the positive low direct effect (P_p = 0.1143; P_g = -0.0023) coupled with indirect effects via moderate effects of days to initial flowering from emergence (P_p = 0.2624; P_g = 0.3359), days to accumulation of 25 flowers from emergence (P_p = 0.1225; P_g = 0.1633), days to accumulation of 50 flowers from emergence (P_p = 0.0666; P_g = 0.2439), percentage of ripe pods (P_p = 0.0927; P_g = 0.1399) and 100 kernel weight (P_p = 0.1584; P_g = 0.2090).

4.6.2.4 Hundred pod weight

Hundred pod weight recorded positive significant correlation (r_p = 0.5280**; r_g = 0.5612**) with days to maturity. But its negligible negative direct effect (P_p = -0.0877; P_g = -0.2151) on days to maturity implies that direct selection of this trait would not lead to improvement of earliness. The positive correlation could be via high indirect effects of days to initial flowering from emergence (P_p = 0.8369; P_g = 0.5339), days to accumulation of 25 flowers from emergence (P_p = 0.3016; P_g = 0.2343) and 100 kernel weight (P_p = 0.3734; P_g= 0.3973) and low indirect effects of days to accumulation of 40 flowers from emergence (P_p = 0.1429; P_g= -0.2567), days to accumulation of 50 flowers from emergence (P_p = 0.1500; P_g= 0.3162), percentage of ripe pods (P_p = 0.1790; P_g= 0.2115), harvest index (P_p = 0.0522; P_g= -0.0014) and shelling percentage (P_p = 0.0178; P_g= 0.0141). Thus, selecting for earliness will be more effective when selection is made for days to accumulation of 25 flowers and 40 flowers from emergence with careful consideration of percentage ripe pods.

4.6.2.5 Hundred kernel weight

Hundred kernel weight showed positive significant correlation (r_p = 0.6129**; r_g = 0.6582**) with high positive direct effect (P_p = 0.4237; P_g = 0.4228) on days to maturity at both phenotypic and genotypic levels. Other traits like days to initial flowering from emergence (P_p = 0.5973; P_g= 0.3289), days to accumulation of 25 flowers from emergence (P_p = 0.3317; P_g= 0.3698),

days to accumulation of 40 flowers from emergence (P_p = 0.1482; P_g= 0.3218), days to accumulation of 50 flowers from emergence (P_p = 0.1460; P_g= 0.3828) and percentage of ripe pods (P_p = 0.1966; P_g= 0.2323) through their indirect effects contributed for the positive association.

The residual effect (P_p = 0.6097; P_g = 0.5455) explains only about 40% of the variability in the character days to maturity. The reason could be very low and non-significant correlations of days to initial flowering from emergence, days from opening of 1st flower to opening of 25 number of flowers, days from opening of 1st flower to opening of 40 number of flowers, days to accumulation of 50 flowers from emergence, days from opening of 1st flower to opening of 50 number of flowers, shelling percentage and pod yield plant^{-1}. Inclusion of additional traits will account for understanding the variability for days to maturity.

Nigam and Aruna (2008) opined that for developing short duration cultures in groundnut, shorter plant stature, fewer days to initial flowering, accumulation of maximum number of early flowers, more flowers per node, absence of late flowers, lesser number of days for a peg to enter soil after fertilization, rapid pod and seed growth, effective seed partitioning and high shelling turnover are the characters to be considered. Ali *et al.* (1994) while studying the potential effectiveness of selection for early maturity reported that selection for larger fruit and heavier seed could result in high seed yield but may not favour early maturity. Hence, selection criteria for evolving early maturing genotypes could be days to accumulation of 25 and 40 flowers from emergence with optimal number of ripe pods at 90 days duration with a harvest index (< 50%), 100 pod weight (90-95 g) and 100 kernel weight (< 40 g) as observed in the present study.

Chapter - V

Summary & Conclusions

Chapter V

SUMMARY AND CONCLUSION

The present study entitled “Genetic studies for early maturity, yield and yield attributes in groundnut (*Arachis hypogaea L.)*” was carried out with the following objectives.

1. To quantify genetic variability and genetic parameters for traits contributing to early maturity, yield and yield components in groundnut.
2. To study genetic diversity among groundnut genotypes.
3. To elucidate information on trait associations among phenological traits contributing to earliness, yield and yield components.

Thirty six groundnut genotypes including released varieties and advanced breeding lines were evaluated at Regional Agricultural Research Station (RARS), Tirupati, during *Rabi* 2021-2022, in alpha lattice design with two replications. Observations were recorded on days to initial flowering from emergence, days from opening of 1st flower to opening of 25, 40 and 50 flowers, days to accumulation of 25, 40 and 50 flowers from emergence, days to 50 % flowering, days to maturity, percentage of ripe pods, plant height , number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of mature pods plant^{-1}, number of immature pods plant^{-1}, pod yield plant^{-1}, seed yield plant^{-1}, 100 pod weight, 100 kernel weight, shelling percentage, harvest index and number of sound mature kernels.

Analysis of variance carried out among twenty-two characters revealed significant differences among the genotypes for all the characters, indicating the presence of sufficient amount of variability among the experimental material. The genotypes, TCGS 2233, TCGS 2223, TCGS 2347, UBEK 21-67, UBEK 21-70, UBEK 21-68, Rohini and UBEK 21-76 were found promising based on mean performance and could be exploited for improvement of yield

and yield attributes in breeding programs as donors. On the other hand, UBEK 21-74, UBEK 21-40, UBEK 21-43, TAG 24, TCGS 2339 and TCGS 2326 were identified as early maturing genotypes which could be exploited as sources for earliness in further breeding programmes. Meanwhile, genotypes *viz.*, Rohini and UBEK 21-76 which are medium maturing genotypes can be utilized for improving yield and its contributing characters, along with maturity at the same time. All the early maturing genotypes were visualized with 100 pod weight below 90g, 100 kernel weight below 40g and harvest index below 50%. These characters are to be confirmed in future studies and in designing ideal plant type for early maturity.

High PCV and GCV were recorded for characters *viz.*, days from opening of 1st flower to 25 number of flowers, number of primary branches plant^{-1} and number of secondary branches plant^{-1} suggesting presence of sufficient amount of variation in the genotypes which can be harnessed for improvement of these characters through selection.

High heritability coupled with high genetic advance as per cent of mean were recorded for days from opening of 1st flower to opening of 25, 40 and 50 number of flowers, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of mature pods plant^{-1}, number of immature pods plant^{-1}, harvest index, 100 pod weight and 100 kernel weight indicating the preponderance of additive gene action in expression of these characters thereby, simple selection would be effective for improvement of these characters. High heritability coupled with moderate genetic advance as per cent of mean was observed for days to initial flowering, days to accumulation of 40 flowers from emergence, days to accumulation of 50 flowers from emergence, days to maturity and shelling percentage. Moderate heritability coupled with high genetic advance as per cent of mean was recorded for the pod yield plant^{-1} and seed yield plant^{-1} indicating that these characters were most likely to be controlled by additive gene action. High heritability coupled with low genetic advance as per cent of mean was exhibited by days to

50% flowering, days to accumulation of 25 flowers from emergence, percentage of ripe pods and number of sound mature kernels indicating the presence of non-fixable genetic variance in the expression of these characters and selection for these traits would be ineffective.

D^2 analysis revealed the presence of genetic diversity among the genotypes studied, by grouping them into 6 clusters. Days to maturity contributed maximum towards genetic diversity followed by days to initial flowering from emergence, plant height, number of secondary branches plant^{-1}, number of mature pods plant^{-1}, days to 50% flowering, days to accumulation of 40 flowers from emergence, days to opening of 1st flower to opening of 50 number of flowers and number of primary branches plant^{-1}.

Maximum intra cluster distance was observed in cluster II indicating the presence of high genetic diversity among the genotypes within that cluster. Maximum inter cluster distance was observed between cluster VI and III followed by cluster V and III, cluster II and III, cluster IV and VI and cluster I and VI. It indicates the presence of high genetic diversity between these clusters thereby selecting genotypes from these clusters as parents in a hybridizing programme could be fruitful. All the early maturing genotypes were found in the cluster III. Genotypes from cluster III (TAG 24, TCGS 2339, TCGS 2326, UBEK 21-40, UBEK 21-43, UBEK 21-74 and ISK-II-2020-12) and genotype (UBEK 21-67) from cluster IV for 100 pod weight and 100 kernel weight might be selected for developing genotypes with early maturity of 90 days. To develop genotypes with higher pod yields, genotypes from cluster II and V with high mean values for pod yield plant^{-1}(UBEK 21-68, UBEK 21-70), number of mature pods plant^{-1} (TCGS 2233, TCGS 2348, UBEK 21-68, ISK-II,2020-4), TCGS 2223 genotype from cluster V for high harvest index and TCGS 2347 genotype from cluster VI with high mean value for 100 pod weight and 100 kernel weight are to be involved in hybridization program.

Character association analysis revealed that pod yield plant^{-1} was positively correlated with seed yield plant^{-1} followed by 100 kernel weight, 100

pod weight, harvest index, days to maturity and number of mature pods plant^{-1} at both phenotypic and genotypic levels indicating selection for these characters will simultaneously improve pod yield plant^{-1}. From the path coefficient analysis, it becomes clear that the characters *viz.*, seed yield plant^{-1} and number of mature pods plant^{-1} should be given more weightage during selection programme for the improvement of pod yield in groundnut as they exhibited high positive direct effect on pod yield plant^{-1}. Days to maturity recorded phenotypic positive correlation with days to accumulation of 25 and 40 flowers from emergence. It also exhibited highly significant positive correlation with percentage ripe pods, harvest index, 100 pod weight, 100 kernel weight and pod yield plant^{-1} at both phenotypic and genotypic levels. Accumulation of 25 and 40 flowers from 1st flower could be an important phenology in groundnut which favours optimum 100 pod weight, 100 kernel weight and pod yield per plant^{-1} as it recorded positive association with these traits. Path analysis of early maturity and its contributing characters revealed that the direct selection based on days to accumulation of 25 and 40 flowers from emergence with optimal number of ripened pods at 90 days duration by effecting selection pressure for 100 pod weight up to 90 g, 100 kernel weight up to 40 g and harvest index up to 50% may serve the purpose of evolving high yielding early maturing lines.

Literature Cited

LITERATURE CITED

Agricultural Market Intelligence Centre, ANGRAU, 2021. *Groundnut outlook report, January to May*. https://angrau.ac.in.

Alam, M.K. 2014. Genetic correlation and path coefficient analysis in groundnut (*Arachis hypogaea* L.). *SAARC Journal of Agriculture*. *12*(1): 96-105.

Ali, N and Wynne, J.C. 1994. Heritability estimates and correlation studies of early maturity and other agronomic traits in two crosses of peanut (Arachis hypogaea L.). *Pakistan Journal of Botany*. *26*(1): 75-82.

Arunachalam, V. 1981. Genetic distance in plant breeding. *Indian Journal of Genetics and Plant Breeding*. *41*: 226-236.

Babariya, C.A and Dobariya, K.L. 2012. Correlation coefficient and path coefficient analysis for yield components in groundnut (*Arachis hypogaea* L.). *Electronic Journal of plant breeding*. *3*(3): 932-938.

Bailey, W.K and Bear, J.E. 1973. Components of earliness of maturity in peanuts (*Arachis hypogaea L). American Peanut Research and Education Society*. *5*(1): 32-39.

Bera, S.K., Pal, S., Dash, P and Dash, M.M. 2004. Variability estimates and search for earliness in a large heterogeneous population of groundnut (*Arachis hypogaea* L.) germplasm. *Indian Journal of Plant Genetic Resources*. *17*(1): 64-68.

Bhakal, M and Lal, G.M. 2015. Studies on genetic diversity in groundnut (*Arachis hypogaea* L.) germplasm. *Journal of Plant Science & Research*. *2*(2): 1-4.

Bhakal, M and Lal, G.M. 2017. Estimation of genetic variability, correlation and path Analysis in groundnut (*Arachis hypogaea* L.) germplasm. *Chemical Science Review and Letters*. *6*(22): 1107-1112.

Bhargavi, G., Rao, V.S and Babu, D.R. 2017a. Studies on variability, heritability and genetic advance as per cent of mean in Spanish bunch

groundnut genotypes (*Arachis hypogaea* L.). *Legume Research. 40*(4): 773-777.

Bhargavi, G., Rao, V.S., Babu, D.R and Rao, K.N. 2017b. Character association and path coefficient analysis of pod yield and yield components in Virginia bunch groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*. *8*(1): 262-268.

Burton, G.W. 1952. Qunatitative inheritance in grass. *Proceedings of Sixth International Grassland Congress*. *1*: 277-283.

Burton, G.W and Devane, E.M. (1953) Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal. 45*(10): 478-481.

Chavadhari, R.M., Kachhadia, V.H., Vachhani, J.H and Sharma, S. 2017a. Genetic divergence in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*. *8*(3): 1001-1005.

Chavadhari, R.M., Kachhadia, V.H., Vachhani, J.H and Virani, M.B. 2017b. Genetic variability studies in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*. *8*(4): 1288-1292.

Chiow, H.Y and Wynne, J.C. 1983. Heritabilities and genetic correlations for yield and quality traits of advanced generations in a cross of peanut. *Peanut Science*. *10*(1): 13-17.

Coffelt, T.A., Seaton, M.I and Van Scoyoc, S.W. 1989. Reproductive efficiency of 14 virginia type peanut cultivars. *Crop Science*. *29*: 1217-1220.

Coulibaly, M.A., Ntare, B.R., Gracen, V.E., Danquah, E.Y., Ofori, K and Mahamane, A.S. 2017. Phenotyping groundnut genotypes to identify sources of earliness in Niger. *International Journal of Innovations in Engineering Research and Technology (IJIERT)*. *4*(2): 238-242.

Dewey, D.R and Lu, K.H. 1959. Correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*. *51*(9): 515-518.

Directorate of Economics and Statistics, Department of Agriculture, cooperation and Farmers Welfare, GOI. 2021. *Agricultural Statistics at a glance.* 50-51.

Falconer, D.S and Mackay, T.F.C. 1996. Quantitative Genetics. *Harlow, Essex. Fourth edition, England Longman Group Ltd.*

FAOSTAT, 2020-2021. Food and Agriculture Organization of the United Nations. World Agricultural Production, Rome, Italy. http://faostat.fao.org/.

Fisher, R. A and Yates, F. 1967. *Statistical tables for Biological, Agricultural and Medical Research.* Oliver and Boyd, London. 44-63.

Gantait, S., Gunri, S.K., Kundu, R and Chatterjee, S. 2017. Evaluation of genetic divergence in Spanish bunch groundnut (*Arachis hypogaea L.*) genotypes. *Plant Breeding and Biotechnology*. *5*(3): 163-171.

Gupta, R.P., Vachhani, J.H., Kachhadia, V.H., Vaddoria, M.A and Reddy, P. 2015a. Genetic variability and heritability studies in Virginia groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*. *6*(1): 253-256.

Gupta, R.P., Vachhani, J.H., Kachhadia, V.H., Vaddoria, M.A and Bhatiya, V.J. 2015b. Genetic divergence in Virginia groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*. *6*(2): 566-569.

Hampannavar, M.R., Khan, H., Temburne, B.V., Janila, P and Amaregouda, A. 2018a. Genetic variability, correlation and path analysis studies for yield and yield attributes in groundnut (*Arachis hypogaea* L.). *Journal of Pharmacognosy and Phytochemistry*. *7*(1): 870-874.

Hampannavar, M.R and Khan, H. 2018b. Analysis of genetic diversity of groundnut (*Arachis hypogaea* L.) genotypes collected from various parts of India. *Journal of Pharmacognosy and Phytochemistry*. *7*(2): 1100-1103.

Islam, M.S. and Rasul, M.G., 1998. Genetic parameters, correlations and path coefficient analysis in groundnut. *Bangladesh Journal of Scientific and Industrial Research*. *33*: 250-254.

Jain, S., Singh, P.B and Sharma, P.P. 2016. Correlation and path analysis in groundnut (*Arachis hypogaea* L.). *International Journal of Current Research*. 8(8): 35811-35813.

Jogloy, C., Jaisil, P., Akkasaeng, C., Kesmala, T and Jogloy, S. 2011. Heritability and Correlation for Maturity and Pod Yield in Peanut. *Journal of Applied Sciences Research. 7*: 134-140.

John, K., Vasanthi, R.P and Venkateswarlu, O. 2008. Variability and correlation studies for pod yield and its attributes in F_2 generation of six Virginia × Spanish crosses of groundnut (*Arachis hypogaea* L.). *Legume Research. 31*(3): 210-213.

John, K., Vasanthi, R.P and Venkateswarlu, O. 2009. Studies on variability and character association in Spanish bunch grounndnut (Arachis hypogaeae L.). *Legume Research-An International Journal, 32*(1): 65-69.

John, K., Vasanthi, R. P., Sireesha, K and Giridhara Krishna, T. 2013. Genetic Variability Studies in Different Advanced Breeding Genotypes of Spanish Bunch Groundnut (Arachis hypogaea). *International Journal of Applied Biology and Pharmaceutical Technology. 4*(2): 185-187.

John, K and Reddy, P.R. 2015. Character association and path analysis studies for pod yield and its components in early segregating population of groundnut (*Arachis hypogaea* L.). *International Journal of Current Research in Biosciences and Plant Biology*. *2*(7): 149-157.

John, K., Madhavi Santhosi, M.V and Rajasekhar, P. 2019. Correlation and path analysis in groundnut (*Arachis hypogaea* L.). *Journal of Pharmacognosy and Phytochemistry*. *8*(12): 1521-1529.

Johnson, H.W., Robinson, H.F and Comstock, R.E. 1955a. Estimation of genetic and environmental variability in soybean. *Agronomy Journal. 47*(7): 314-318.

Johnson, H.W., Robinson, H.F and Comstock, R.E. 1955b. Genotypic and phenotypic correlation in soybean and their implications in selection. *Agronomy Journal*. *47*(10): 477-483.

Kadam, V.K., Chavan, B.H., Deshmukh, M.P and Mali, A.R. 2018. Study on character association and path analysis in summer groundnut (*Arachis hypogaea* L.). *Journal of Pharmacognosy and Photochemistry*. *7*(3): 3654-3657.

Khalfaoui, J.L. 1990a. Study of components of earliness in groundnut. *Oleagineux*. *45*(2): 81-87.

Khalfaoui, J.L. 1990b. Heredity of extreme precocity in the case of a cross between two Spanish cultivars. *Oleagineux. 45*(10): 419-436.

Kiranmai, M.S., Venkataravana, P and Push, H.D. 2016. Correlation and path analysis studies in groundnut under different environment. *Legume Research-An International Journal*, *39*(6): 1048-1050.

Korat, V.P., Pithia, M.S., Savaliya, J.J., Pansuriya, A.G and Sodavadiya, P.R. 2009. Studies on genetic variability in different genotypes of groundnut (*Arachis hypogaea* L.). *Legume Research. 32*(3): 224-226.

Korat, V.P., Pithia, M.S., Savaliya, J.J., Pansuriya, A.G and Sodavadiya, P.R. 2010. Studies on characters association and path analysis for seed yield and its components in groundnut (*Arachis hypogaea* L.). *Legume Research*. *33*(3): 211-216.

Kotzamanidis, S.T., Stavropoulos, N and Ipsilandis, C.G. 2006. Correlation studies of 21 traits in F2 generation of groundnut (*Arachis hypogaea L*). *Pakistan Journal of Biological Sciences. 9*(5): 929-934.

Krapovickas, A and Gregory, W.C. 1994. Taxonomia del genero *Arachis* (Leguminosae). *Bonplandia*. *8*:1-186.

Krishna Sastry, K.S., Chari, M., Prasad, T.G., Udayakumar, M and Sashidhar, V.R. 1985. Flowering pattern and pod development in bunch types of groundnut: is there a relationship between synchrony in flowering and pod development. *Indian Journal of Plant Physiology. 28*(1): 64-71.

Kumar, D.R., Sekhar, M.R., Reddy, R.K and Ismail, S. 2012. Character association and path analysis in groundnut (*Arachis hypogaea* L.*).*

International Journal of Applied Biology and Pharmaceutical Technology. 3(1): 385-389.

Kumar, I.S., Venkataravana, P and Marappa, N. 2010. Genetic divergence of new germplasm and advanced breeding lines of groundnut (*Arachis hypogaea* L.) studied under late *Kharif* situation. *Legume Research*. *33*(2): 124-127.

Kumar, N., Ajay, B.C., Rathanakumar, A.L., Radhakrishnan, T., Mahatma, M.K., Kona, P and Chikani, B.M. 2019. Assessment of genetic variability for yield and quality traits in groundnut genotypes. *Electronic Journal of Plant Breeding.* 10(1): 196-206.

Lenka, D and B. Mishra. 1973. Path coefficient analysis of yield in rice varieties. *Indian Journal of Agricultural Sciences. 43*: 376-379

Lush, J.L. 1940. Inter size correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proceedings of American Society of Animal Production*. 33: 293-301.

Mahalanobis, P.C. 1936. On the generalized distances in statistics. *National Institute of Sciences of India. 2*(1): 49-55.

Mahalakshmi, P., Manivannan, N. and Muralidharan, V., 2005. Variability and correlation studies in groundnut (*Arachis hypogaea* L.). *Legume Research*. *28*(3): 194-197.

Makinde, S.C.O and Ariyo, O.J. 2013. Genetic divergence, character correlations and heritability study in 22 (*Arachis hypogaea* L.) accessions of groundnut. *Journal of Plant Studies. 2*(1): 60-66.

Meta, H.R and Monpara, B.A. 2010. Genetic variation and trait relationships in summer groundnut (*Arachis hypogaea* L.). *Journal of Oilseeds Res*earch. *27*(1): 8-11.

Mitra, M., Gantait, S and Kundu, R. 2021. Genetic variability, character association and genetic divergence in groundnut (*Arachis hypogaea* L.) accessions. *Legume Research. 44*: 164-169.

Nageswara, R.R.C. and Nigam, S.N. 2003. Genetic options for drought management in groundnut in groundnut. *Oxford & IBH Publishing Co. Pvt. Ltd.* 123-141.

Narasimhulu, R., Kenchanagoudar, P.V and Gowda, M.V.C. 2012. Study of genetic variability and correlations in selected groundnut genotypes. *International Journal of Applied Biology and Pharmaceutical Technology*. *3*(1): 355-358.

N'Doye, O and Smith, O.D. 1993. A note on the earliness of offspring from crosses among five short growth-duration peanut lines. *Peanut Science*. *20*(2): 132-137.

Nigam, S.N and Aruna, R. 2008. Improving breeding efficiency for early maturity in peanut. *Plant breeding reviews*. *30*: 295-322.

Oppong-Sekyere, D., Akromah, R., Ozias-Akins, P and Kena, A.W. 2018. Screening and selection of groundnuts (*Arachis hypogaea* L.) for earliness. *The International Journal of Science and Technoledge.* *6*(10): 20-33.

Panse, V.G and Sukhatme, P.V. 1961. *Statistical methods for agricultural workers*, 2nd edition, ICAR, New Delhi.

Passioura, J.B. 1986. Resistance to drought and salinity: Avenues for improvement. *Australian Journal of Plant Physiology*. *13*: 191-201.

Pattee, H.E., Wynne, J.C., Young, J.H and Cox, F.R. 1977. The seed-hull weight ratio as an index of peanut maturity. *Peanut Science*. *4*(2): 47-50.

Patterson, H.D and Williams, E. 1976. A new class of resolvable incomplete block designs. *Biometrika*, *63*(1): 83-92.

Patil, A.S., Punewar, A.A., Nandanwar, H.R and Shah, K.P. 2014. Estimation of variability parameters for yield and its component traits in groundnut (*Arachis hypogaea* L.). *The Bioscan*. *9*(2): 749-754.

Patil, S., Shivanna, S., Irappa, B.M and Shweta. 2015. Genetic variability and character association studies for yield and yield attributing components in groundnut (*Arachis hypogaea* L.). *Trends in Biosciences*. *8*(18): 4906-4909.

Pavan, C.K., Rekha, R., Venkateswarulu, O and Vasanthi, R.P. 2013. Correlation and path coefficient analysis in groundnut (*Arachis*

hypogaea L.*). International Journal of Applied Biology and Pharmaceutical Technology*. *5*(1): 8-11.

Pilbeam C.J. (1996). Variation in harvest index of maize (*Zea mays*) and common bean (*Phaseolus vulgaris*) grown in a marginal rainfall area of Kenya. *Journal of Agricultural Science*. *126*(1): 1-6.

Prabhu, R., Manivannan, N., Mothilal, A and Ibrahim, S.M. 2015. Correlation coefficient analysis for yield and yield attributes in groundnut (*Arachis hypogaea* L.). *Plant Archives*. *15*(2): 685-689.

Rao, C. R. 1952. *Advanced statistical methods in biometrical research*. John Wiley and Sons. New York. 236-272.

Rao, M.V., Nigam, S.N and Huda, A.K.S. 1992. The thermal time concept as a selection criterion for earliness in peanut. *Peanut Science*. *19*(1): 7-10.

Rao, V.T., Venkanna, V., Bhadru, D and Bharathi, D. 2014. Studies on variability, character association and path analysis on groundnut (*Arachis hypogaea* L.). *International Journal of Pure and Applied Biosciences. 2*(2): 194-197.

Rathod, S.S and Toprope, V.N. 2018. Studies on variability, character association and path analysis in Groundnut (*Arachis hypogaea* L.). *International Journal of Pure Applied Biosciences. 6*(2): 1381-1388.

Raza, M., Sekhar, M.R., Priya, M.S., Prasad, T.N.V.K.V and Rajarajeswari, V. 2018. Genetic variability studies for pod yield and component traits in groundnut. *Electronic Journal of Plant Breeding*. *9*(4): 1436-1442.

Reddy, A.T., Sekhar, M.R., Vijayabharathi, A., Pathy, T.L., Reddy, G.L and Jayalakshmi, V. 2017. Correlation and path analysis of kernel yield and its components in groundnut (*Arachis hypogaea* L.). *International Journal of Current Microbiology and Applied Sciences*. *6*(12): 10-16.

Saini, H., Sharma, M.M., Saini, L.K., Solanki, K.L and Singh, A.G. 2020. Genetic divergence analysis in groundnut (*Arachis hypogaea* L.). *International Journal of Chemical Studies*. *8*(1): 1781-1784.

Shoba, D., Manivannan, N and Vindhiyavarman, P., 2009. Studies on variability, heritability and genetic advance in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*. *1*(1): 74-77.

Shoba, D., Manivannan, N and Vindhiyavarman, P. 2012. Correlation and path coefficient analysis in groundnut (*Arachis hypogaea* L.). *Madras Agricultural Journal. 99*(1-3): 18-20.

Shrotri, S.M., Dhuppe, M.V., Sargar, P.R., Gavade, S.S and Ralebhat, B.N. 2021. Assessment of genetic variability, heritability and genetic advance for yield and yield contributing traits in groundnut (*Arachis hypogaea* L.). *The Pharma Innovation Journal*. *10*(11): 1008-1012.

Singh, P. B., Bharti, B., Kumar, A., Singh, R., Kumar, N and Rathnakumar, A. L. 2017. Genetic characterization, character association for yield and yield component traits in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding. 8*: 1229-1235.

Singh, R.K and Chaudhary, B.D. 1977. Biometrical methods in quantitative genetic analysis. *Kalyani Publishers.* New Delhi. 215-218.

Sivasubramanian, S and Madhavamenon, P. 1973. Path analysis for yield and yield components of rice. *Madras Agricultural Journal*. *60*: 1217-1221.

Suneetha, N., Vasanthi, R.P., Sudhakar, P and Reddy, K.R. 2013. Genetic diversity analysis among released and pre-release cultures in groundnut. *Legume Research. 36*(3): 208-213.

Upadhyaya, H.D and Nigam, S.N. 1994. Inheritance of two components of early maturity in groundnut (*Arachis hypogaea L.*). *Euphytica. 78*(1): 59–67.

Upadhyaya, H.D., Reddy, L.J., Gowda, C.L.L and Singh, S. 2006. Identification of diverse groundnut germplasm: Sources of early maturity in a core collection. *Field Crops Research. 97*(2-3): 261-267.

Vasanthi, R.P., Suneetha, N and Sudhakar, P. 2015. Genetic variability and correlation studies for morphological, yield and yield attributes in groundnut (Arachis hypogaea L.). *Legume Research*, *38*(1): 9-15.

Venkateswarlu, O., Sudhakar, B.V.G., Sekhar, M.R and Sukhakar, P. 2011. Genetic divergence in confectionary types of groundnut (*Arachis hypogaea* L.). *Legume Research. 34*(1): 1-7.

Virmani, S.M and Singh, P. 1986. Agroclimatological characteristics of the groundnut-growing regions in the semi-arid tropics. *International Symposium: Agrometeorology of Groundnut.* 35-45.

Wilks, S.S. 1932. Certain generalizations in the analysis of variance. *Biometrika*. *24*(3): 471-494.

Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research*. *20*: 557-587.

Yadav, S.R., Rathod, A.H., Shinde, A.S., Patade, S.S., Patil, C.N and Vaghela, P.O. 2014. Genetic variability and divergence studies in groundnut (*Arachis hypogaea* L.). *International Journal of Agricultural Sciences*. *10*(2): 691-694.

Yusuf, Z., Zeleke, H., Mohammed, W., Hussein, S and Hugo, A. 2017a. Estimate of genetic variability parameters among groundnut (*Arachis hypogaea* L.) genotypes in Ethiopia. *International Journal of Plant Breeding and Crop Science. 4*(2): 225-230.

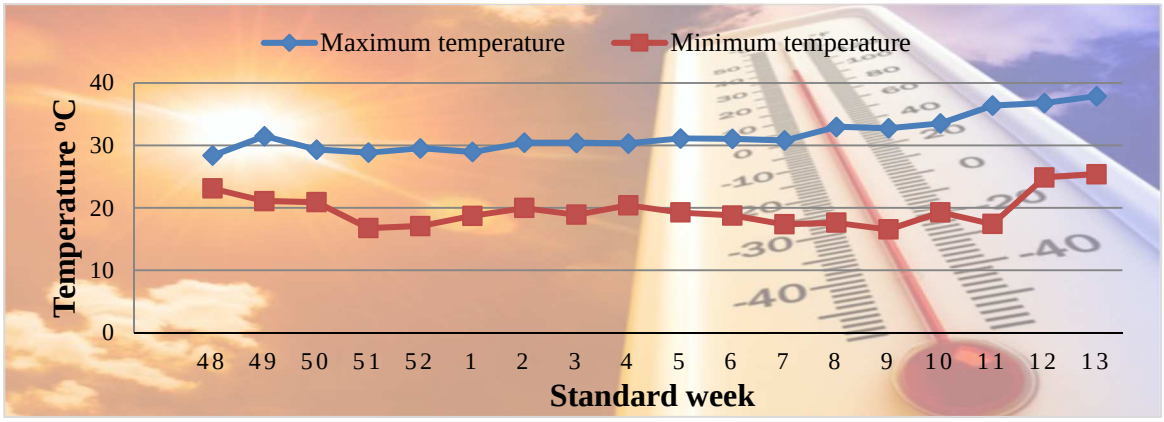
Zaman, M.A., Tuhina-Khatun, M., Moniruzzaman, M and Yousuf, M.N., 2010. Genetic divergence in groundnut (*Arachis hypogaea* L.). *Bangladesh Journal of Plant Breeding and Genetics*, *23*(1): 45-49.

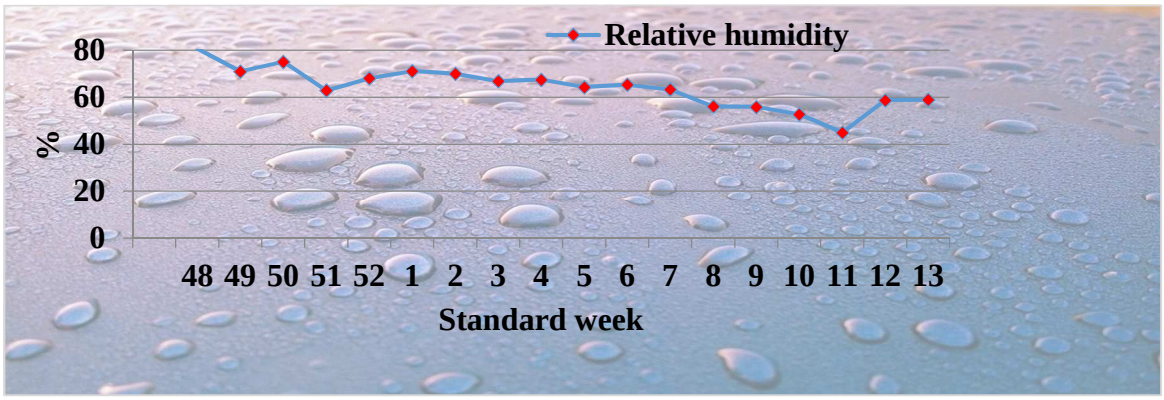
Zaman, M.A., Tuhina-Khatun, M., Ullah, M.Z., Moniruzzamn, M and Alam, K.H. 2011. Genetic variability and path analysis of groundnut (*Arachis hypogaea* L.). *The Agriculturists*. *9*(1-2): 29-36.

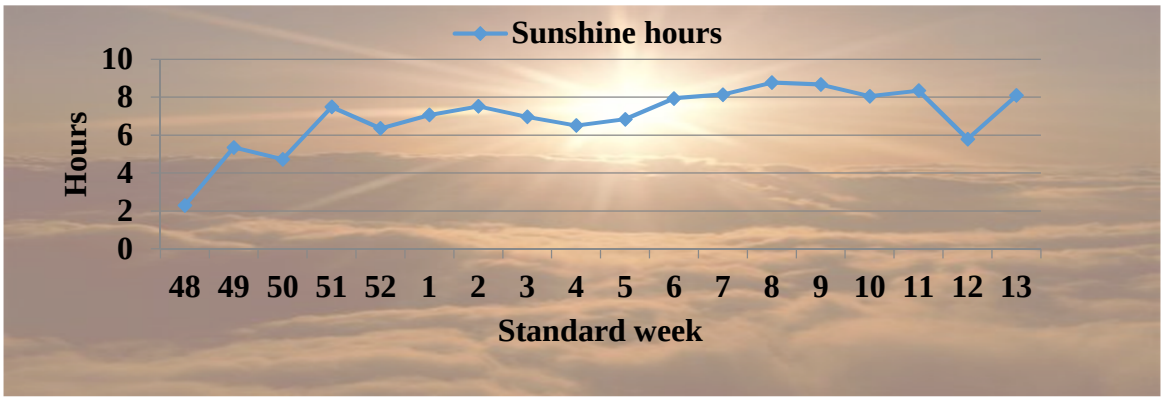
Appendices

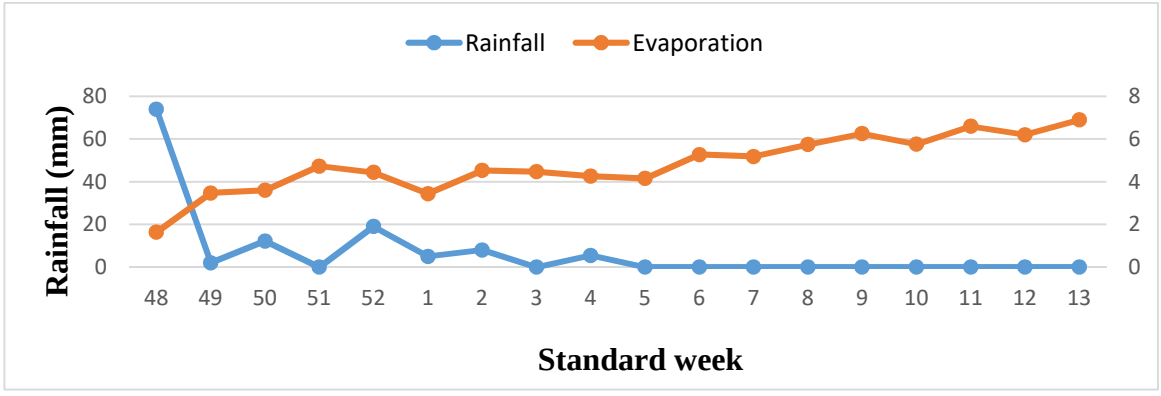
APPENDIX

Meteorological data









GENETIC STUDIES FOR EARLY MATURITY, YIELD AND YIELD ATTRIBUTES IN GROUNDNUT (*Arachis hypogaea* L.)

Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati

Name of the Student: Gumma Vineela Neeharika **I.D. No. :** TAM/2020-016

Major Advisor : Dr. C. Kiran Kumar Reddy

ABSTRACT

Breeding for earliness in groundnut is always a significant part of the objectives in many crop improvement programs across the globe. However, limited studies were available on sources of earliness and its contributing traits coupled with yield and yield components. No coherent character association studies were available for early maturity and its contributing traits. Therefore, the present study was conducted to estimate the extent of genetic variability, genetic divergence and trait associations for high yield, earliness and their contributing traits in groundnut where thirty six groundnut genotypes were evaluated in alpha lattice design with two replications at Regional Agricultural Research Station, Tirupati, during *Rabi*, 2021-22. Variability among all the 36 genotypes is highly significant for all the traits studied. Of all the thirty six entries tested, TAG 24, TCGS 2339, TCGS 2326, UBEK 21-40, UBEK 21-43 and UBEK 21-74 were noteworthy early maturing entries (90 days) with superior agronomic characters. All these genotypes were visualized with 100 pod weight below 90g, 100 kernel weight below 40g and harvest index below 50%. These characters are to be confirmed in future studies and in designing ideal plant type for early maturity. Study of genetic variability revealed high PCV and GCV for characters *viz.,* days from opening of 1st flower to opening of 25 number of flowers and number of primary and secondary branches per plant. High heritability coupled with high genetic advance as per cent of mean were recorded for days from opening of 1st flower to opening of 25, 40, 50 number of flowers, plant height, number of primary and secondary branches per plant, number of mature pods per plant, harvest index, 100 pod weight and 100 kernel weight. Genetic divergence studies revealed the diversity among 36 genotypes by grouping them into 6 clusters. Maximum inter cluster distance was observed between cluster VI and III followed by cluster V and III, cluster II and III, cluster IV and VI and cluster I and VI. Genotypes from cluster III and genotype (UBEK 21-67) from cluster IV can be selected for developing early maturing genotypes. To develop genotypes with higher pod yields, genotypes from cluster II and V are to be utilized in hybridization programs. Character association studies revealed two phenological traits *viz.,* days to accumulation of 25 and 40 flowers from emergence contributed significantly to days to maturity. Even though other traits exhibited significant inter-se correlations among them, their association with days to maturity was negligible. Therefore, for developing early maturing genotypes, selection for early accumulation of 25 and 40 flowers from emergence would be advantageous. For pod yield plant^{-1}, significant positive correlations were observed with days to maturity, seed yield plant^{-1}, number of mature pods plant^{-1}, 100 pod weight, 100 kernel weight and harvest index but number of immature pods plant^{-1} was observed to be negatively correlated. Thus, for developing high yielders, selection should be focused on number of mature pods plant^{-1}, days to maturity, harvest index, 100 pod weight, 100 kernel weight and seed yield plant^{-1}. For developing early maturing genotypes with optimum yield levels, selection criteria could be days to accumulation of 25 flowers and 40 flowers from emergence with optimal number of ripened pods at 90 days duration with a harvest index (<50%), 100 pod weight (90g) and 100 kernel weight (<40g).