GENETIC ANALYSIS OF MORPHOLOGICAL, PHYSIOLOGICAL AND BIOCHEMICAL CHARACTERS IN RELATION TO YIELD AND QUALITY IN GROUNDNUT (*Arachis hypogaea* L.)

By

M. HEMANTH KUMAR
M.Sc., (Ag.)

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

DOCTOR OF PHILOSOPHY
IN THE FACULTY OF AGRICULTURE

DEPARTMENT OF GENETICS AND PLANT BREEDING
SRI VENKATESWARA AGRICULTURAL COLLEGE
ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY
TIRUPATI - 517 502, (A.P.) INDIA

2004

CERTIFICATE

This is to certify that the thesis entitled, **"GENETIC ANALYSIS OF MORPHOLOGICAL, PHYSIOLOGICAL AND BIOCHEMICAL CHARACTERS IN RELATION TO YIELD AND QUALITY IN GROUNDNUT** (*Arachis hypogaea* **L.)"** submitted in partial fulfilment of the requirements for the degree of **DOCTOR OF PHILOSOPHY IN AGRICULTURE** of the Acharya N. G. Ranga Agricultural University, Hyderabad is a record of the bonafide research work carried out by Mr. M. Hemanth Kumar under our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee.

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

(Dr. G. LAKSHMI KANTHA REDDY)
Chairman of the Advisory Committee

Thesis approved by the Student's Advisory Committee

Chairman : (Dr. G. LAKSHMI KANTHA REDDY)
Associate Dean
Agricultural College
Bapatla

Member : (Dr. P. VENKATRAMA REDDY)
Professor
Plant Physiology
Regional Agricultural Research Station
Tirupati

Member : (Dr. M. REDDI SEKHAR)
Assistant Professor
Department of Genetics & Plant Breeding
S. V. Agricultural College
Tirupati

Member : (Dr. N. P. ESWAR REDDY)
Associate Professor
Department of Plant Pathology
S. V. Agricultural College
Tirupati

Member : (Dr. S. ISMAIL)
Associate Professor
Department of Statistics and Mathematics
S. V. Agricultural College
Tirupati

CERTIFICATE

Mr. M. Hemanth Kumar has satisfactorily prosecuted the course of research and that the thesis entitled, **"GENETIC ANALYSIS OF MORPHOLOGICAL, PHYSIOLOGICAL AND BIOCHEMICAL CHARACTERS IN RELATION TO YIELD AND QUALITY 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 the thesis or part there of has not been previously submitted by him for a degree of any University.

Date: 8.12.04

Place: TIRUPATI

(Dr. G. LAKSHMI KANTHA REDDY)

Major Advisor

LIST OF CONTENTS

LIST OF FIGURES

LIST OF TABLES

LIST OF PLATES

APPENDICES

ACKNOWLEDGEMENT

With great respect and deep sense of gratitude I extend my inexpressible indebtedness to my 'guru' and chairman of the Advisory Committee, Dr. G. Lakshmi Kantha Reddy, Associate Dean, Agricultural College, Bapatla, for his erudite counsel, dexterous guidance, adroit suggestions, unremitting encouragement, assiduous support and concern throughout the period of my investigation which helped me to carry out this earnest task successfully.

I take this opportunity to express my esteemed thanks to Dr. K. Chandrasekhar Rao, Associate Dean, S.V. Agricultural College, Tirupati and Dr. K. Raja Reddy, Professor and Head, Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati, in providing space and funds to establish a quality analysis lab in which I executed my experiments. Special thanks are due to my professor who gave me optimum workload and more time to complete this dissertation.

I record my profound thanks to Dr. P.V. Reddy, Professor, Department of Plant Physiology, Regional Agricultural Research Station, Tirupati who encouraged me to work on groundnut quality aspects. The facility provided in his lab under ACIR / ICRISAT / ANGRAU – Collaborative Project on "Selection for peanut varieties with low aflatoxin risk" translated my dream into a reality. His valuable suggestions and critical review of the manuscript has brought out the final shape of this thesis.

I am ineffable to express my deep sense of reverence to members of my Advisory Committee; Dr. N. P. Eswar Reddy, Associate Professor, Department of Plant Pathology, Dr. M. Reddi Sekhar, Assistant Professor, Department of Genetics and Plant Breeding and to Dr. S. Ismail, Associate Professor, Statistics and Mathematics, S.V. Agricultural College, Tirupati for timely corrections and candid criticism during the preparation of the thesis.

I am happy to gratify the help rendered by Dr. N. Ramavataram, Professor and Head, Department of Soil Science, S.V. Agricultural College, Tirupati, Dr. P. Harinath Naidu, Associate Professor, Department of Plant Pathology, RARS, Tirupati and my friend, Dr. P. Sudhakar, Assistant Professor, Department of Plant Physiology, RARS, Tirupati in carrying out the lab studies. I may fail in duty if I do not thank my friend, Dr. S. Kaleemullah, Assistant Professor, Department of Agricultural Engineering, S.V. Agricultural College, Tirupati who had taught me to type this manuscript.

My special thanks are due to Dr. S. N. Nigam, Principal Scientist (Groundnut), ICRSAT, Dr. V. Muralidharan, Director, Department of Oil Seeds, TNAU, Coimbatore, Dr. G. Nagaraj, Professor, DOR, Rajendranagar, Dr. J. Tyagarajan, Associate Professor, Department of Biochemistry, S.V. University, Tirupati, Sri M. R. L. Prabhu, Dr. Eswar Prasad, Dr. Padmaja of the Department of Biochemistry, Veterinary College, Titupati, and Dr. R.P. Vasanthi, Associate Professor, R.A.R.S, Tirupati for their apposite suggestions and timely help during the course of work.

My heartfelt thanks are due to my colleagues, Dr. K. Hariprasad Reddy, Associate Professor, Sri K. Murali Krishna, Assistant Professor and Smt M. Shanti Priya, Assistant Professor for their help rendered in sharing the extra teaching hours and giving me more time to work on the project.

My sprits were kept high during my Ph.D course with the affectionate association of my friends, Dr. Y. Rama Reddy, Madhavi Latha, Nagarjuna Sagar, Ramana, Tagore, Venkateswarlu, my student friends, Sri Lakshmi, Radha, Srividya, Jayaprada, Kiran, Kalyan, Seethala, Sumathi, Gnanesh, Ravi, Subbarayudu, Sambasivudu, Chari, Anjaneyulu, Sireesha and lot more.

I can never forget the assistance provided by the record assistants, Sri Munikrishna, Krishnaiah, Munaswamy, Vidyasagar, Neelakantam and Meena of the Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati.

I am beyond words in offering prayers to my parents, Sri Narasimhulu and Smt Narayanamma for their interminable blessings to persecute higher studies. Inexplicable is my fervent gratitude to my wife, Dr. Uma and my sons, Varun and Anuj for their perpetual love, benign care, fanatical encouragement and moreover their sweet bothering, which gave me, the moral support and relaxation through out this endeavour.

Date : 8.12.04

DECLARATION

I, **M. HEMANTH KUMAR**, hereby declare that the thesis entitled, **"GENETIC ANALYSIS OF MORPHOLOGICAL, PHYSIOLOGICAL AND BIOCHEMICAL CHARACTERS IN RELATION TO YIELD AND QUALITY IN GROUNDNUT (*Arachis hypogaea* L.)"** submitted to Acharya N.G. Ranga Agricultural University for the degree of **Doctor of Philosophy** in Agriculture is the result of original work done by me. I also declare that the materials contained in this thesis has not been published earlier.

Date: 8.12.04

(M. HEMANTH KUMAR)

LIST OF ABBREVIATIONS AND ACRONYMS

%	:	Per cent
@	:	At the rate of
^{0}C	:	Degree Celsius
µg	:	Microgram
µl	:	Microlitre
AFB_1	:	Aflatoxin B_1
AFPA	:	*Aspergillus flavus/parasiticus* agar medium
APEDA	:	Agricultural and Processed Food Products Export Development Authority
ARS	:	Agricultural Research Station
BARC	:	Baba Atomic Research Center
BSA	:	Bovine Serum Albumin
c.f.u	:	Colony forming units
cc	:	Cubic centimeter
CCFAC	:	Codex Committee on Food Additives and Contaminants
CD	:	Critical Difference
CGR	:	Crop Growth Rate
cm	:	Centimeter
CV	:	Coefficient of Variation
DAE	:	Days After Emergence
DAI	:	Days After Inoculation
DAS	:	Days After Sowing
df	:	Degrees of freedom
di	:	Relative heterosis
dii	:	Heterobeltiosis
diii	:	Standard heterosis
ELISA	:	Enzyme Linked Immunosorbent Assay
et al.	:	And others
F_1	:	Filial generation one
Fig.	:	Figure
g	:	Grams
GA	:	Genetic Advance
GAM	:	*Genetic Advance as per cent of Mean*
gca	:	General combining ability
GCV	:	Genotypic Coefficient of Variation
GDP	:	Grand Domestic Product
GOI	:	Government Of India
h	:	Hours
$h^2_{(b)}$	:	Heritability in broad sense
ha	:	Hectare
HPLC	:	High Pressure (performance) Liquid Chromatography
HPS	:	Hand Picked and Selected
i.e.,	:	Which is to say in other words

ICAR	:	Indian Council of Agricultural Research
ICRISAT	:	International Crop Research Institute for Semi arid Tropics
kg	:	Kilogram
LAI	:	Leaf Area Index
LAR	:	Leaf Area Ratio
lt	:	Liter
m	:	Meter
mg	:	Milligram
min.	:	Minutes
ml	:	Milliliter
mm	:	Millimeter
MSL	:	Mean Sea Level
ng	:	Nanogram
NMR	:	Nuclear Magnetic Resonance analyzer
No.	:	Number
NRCG	:	National Research Center for Groundnut
OD	:	Optical Density
oz	:	Ounce
PCV	:	Phenotypic Coefficient of Variance
Per se	:	As such with mean
ppb	:	Parts per billion
psi	:	Per square inch
RARS	:	Regional Agricultural Research Station
RBD	:	Randomised Block Design
RH	:	Relative Humidity
rpm	:	Revolutions per minute
Rs	:	Rupees
sca	:	Specific combining ability
SCMR	:	SPAD (Soil Plant Analytical Development) Chlorophyll Meter Reading
SE	:	Standard error
Sec.	:	Seconds
SEm	:	Standard error of mean
SLA	:	Specific Leaf Area
SLW	:	Specific Leaf Weight
SMK	:	Sound Mature Kernel
Spp.	:	Species
t	:	Tones
USDA	:	United States Department of Agriculture
viz.,	:	Namely

Title of the thesis : **GENETIC ANALYSIS OF MORPHOLOGICAL, PHYSIOLOGICAL AND BIOCHEMICAL CHARACTERS IN RELATION TO YIELD AND QUALITY IN GROUNDNUT (*Arachis hypogaea* L.).**

Author : **M. HEMANTH KUMAR**

Major Advisor : Dr. G. Lakshmi Kantha Reddy

Submission for the award of the degree : Doctor of Philosophy

Faculty : Agriculture

Department : Genetics and Plant Breeding

University : Acharya N. G. Ranga Agricultural University

Year of submission : 2004

ABSTRACT

A total of 54 groundnut genotypes were evaluated for 31 morphological, physiological and biochemical characters at the College Farm, S.V. Agricultural College, Tirupati from *kharif*, 2002 to *kharif* 2003. Nine parents from 54 genotypes were selected based on association, variability and divergence analyses. The 20 F_1 crosses obtained through L X T mating of nine parents were evaluated for combining ability effects, gene action and heterosis to suggest a breeding strategy for developing high yielding aflatoxin resistant groundnut cultivars.

Evaluation through ranks and scores given for mean values of morphological and biochemical characters related to quality revealed that TPT 4, M 13 and ICGV 86564 were the best genotypes suitable for cultivation and trading as HPS varieties. Whereas, ICGV 86552 was identified as the most physiologically efficient genotype for end-of-season drought.

Based on the association analysis, pod volume, shelling percentage, mature pods per plant, immature pods per plant, 100 seed weight, protein content, non-reducing sugar content, SLA at 60 DAS, SLW at 60 DAS, CGR at 60 and at 90 DAS, LAR at 90 DAS, harvest index and pod weight per plant might be selected for their improvement in the positive direction and shell volume, free space in pod, oil percentage and carbohydrate content in negative direction.

When variability, heritability and GAM were considered together, shell volume, pod volume, free space in pod, immature pods per plant, mature pods per plant and 100 seed weight among morphological characters; reducing sugar content and non-reducing sugar content among biochemical characters and CGR at 60 and at 90 DAS among physiological characters were found to be a better choice of characters.

D^2 values for the characters suggested that there was considerable diversity in the material studied. This range of variation allowed for grouping of 54 genotypes into 11 clusters for morphological and biochemical characters and in to 17 clusters for physiological characters.

Combining ability studies revealed that non-additive genetic variance was higher in magnitude for majority of the characters indicating the preponderance of dominance gene action in controlling the expression of these characters. GCA variance was greater in proportion than SCA variance for the characters; pod volume and aflatoxin content. As such, these characters can be improved by employing breeding methods, which exploit additive gene action.

Results on the combination of both *per se* performance and gca effects revealed that identification of superior segregants in the crosses involving ICG 3245, M 13 and TPT 4 might be possible for most of the characters studied. The cross, ICG 7633 X M 13 showed promise for recombination breeding with its non-significant sca and significant gca of its parents for kernel weight per plant.

The classification of crosses based on mean, sca and heterosis for all the characters identified ICG 1326 X ICGV 86564, and ICG 7633 X TPT 4 as superior crosses for increasing kernel weight and aflatoxin resistance. As their parental gca effects were highly significant for more than 50 % of the characters they can be persuaded in developing recombinant genotypes with high yield coupled with aflatoxin resistance by adopting simple breeding methods like pedigree method and selecting both in early as well as advanced stages of segregation to exploit both additive and non-additive gene effects.

The efforts made in identifying the characters (low shell volume, low free space in pod, low carbohydrates, high shelling percentage, high 100 seed weight, high protein content and high crop growth rates during end-of season moisture stress), the genotypes (ICGV 86564, ICG 3245, M 13, and TPT 4) and the crosses (ICG 1326 X ICGV 86564 and ICG 7633 X TPT 4) related to aflatoxin resistance were successful to initiate a breeding program that could produce high yielding varieties with aflatoxin resistance.

CHAPTER I

INTRODUCTION

CHAPTER – I

INTRODUCTION

Agriculture has always been a core sector of Indian economy contributing 30% to the country's GDP. In addition, agricultural commodities also account for about 20% of total exports earning of the country. The country has enjoyed the fruits of "green revolution" and was able to cross 200 million tons mark in food grain production from a meager 50 million tons prior to independence. On oil seeds front, the country also experienced "yellow revolution" with a quantum jump in the production from 11 to 25 million tons just in last one decade (Paroda, 2002). India on an average accounted for 9.9% of the global oilseeds production, 8.7% of protein meal and 9.2% of oil meal exports. In India groundnut ranks first in terms of production, contributing 36% of the total oilseeds production. And its share in global production is 27.31% and is second largest producer next to China (Rai mangala, 2002).

"Yellow revolution" has ushered a quantum leap in oil seeds production due to successful outcome of a National Technology Mission on Oil seeds. However there are problems of sustainability of the national gains and growth achieved by way of the yellow revolution, which we need to look into for appropriate mid-course correction for further strategy and action. This is evident by the fact that in 1998-99, about 45 lakh tons of edible oil valued at Rs 9000 crores was imported. On the contrary, huge quantities of export have been witnessed in the years 1999-2000 and 2000-01, particularly in groundnut extractions, sesame seed and castor oil. A quantity of 1,87,000 tons valued at Rs 14 crores of groundnut extractions were exported but the quantity of HPS groundnut exceeded the exports of groundnut extractions and it was 13,67,000 tons valued at

Rs 316.78 lakh during 2000-01 (Damodaram and Hegde, 2000 and Rai mangala, 2002). However exports of peanuts constitutes only 1-3% of total domestic production. Most of the groundnuts produced are locally consumed. About 80% of the production is used for oil extraction and a small proportion is consumed as roasted, salted or fried nuts or as meal in various recipes (Kadam and Chavan, 1991). In the USA and in some other countries such as those of Western Europe it is utilized primarily as whole seeds (Desai *et al.*, 1999). As many as 400 products from groundnut are available today for direct consumption (Chandrasekhar, 1991 and Sulochana *et al.*, 2000). There is no denying the fact that demand for confectionery grade oilseeds used for direct human consumption is steadily increasing (Tushar Tanna, 2002).

Oil seed as an export item has caught our attention only recently. Value added groundnut food products could earn large amounts of foreign exchange. Value addition through quality enhancement and processing of oil and by-products has assumed importance both from domestic and international perspective (Dayanatha Jha, 2002). Confectionery grade oilseeds are premium oilseeds highly priced in the international market. As Indian oilseeds markets are globally integrated and domestic demand becomes more sophisticated, it will be essential to pay greater attention to quality standards, value-addition and processing. This potential scope in world market for HPS groundnut requires to be targeted. The country does have the potential to supply medium and small seeded groundnut varieties. There is now a rekindled awareness among policy makers and oil seed researches about the advantage of developing confectionary grade oilseeds. We have to develop large seeded varieties for international market. The one important aspect of such varieties we have to concentrate on is quality as the international standards have become very stringent over the years. Various physical, sensory and biochemical factors determine the quality of groundnut seed. Physical factors include intact testa, size and shape of the seed, ease of blanching and resistance to seed splitting. Sensory factors include seed colour, texture and flavor. Biochemical factors are mainly concerned with low oil, more protein and more sugars.

The quality requirements for groundnut in the world food market are rather rigid and exacting. Natural Resources Institute of the U.K. Ministry for overseas development listed many quality requirements for groundnut pods and kernel and the over-riding consideration with regard to quality is without doubt freedom from aflatoxin. Aflatoxin, a toxic metabolite, contamination is of major concern in confectionary groundnuts. Aflatoxins are now known to be hepatotoxic, carcinogenic and teratogenic (Mehan *et al.*, 1991). AFB_1 is the most common and also the most toxic aflatoxin produced by *Aspergillus flavus* and *Aspergillus parasiticum* (Dube, 1990). Semi-arid tropics, of the developing countries from which most of groundnut produce is coming, are considered to be high-risk areas for aflatoxin contamination. India has no exception. At present some 50 countries impose aflatoxin regulations and most countries have a separate maximum acceptable level for food and feed (Van Egmond, 1989). The ministry of commerce, GOI vide public notice No. 68 (RE) 1997-2002 dated 3.2.99 announced that exports to European Union will be allowed subject to compulsory registration of contracts with Agricultural and Processed Food Products Export Development Authority (APEDA) along with controlled aflatoxin level certificate as a part of export development given by agencies/laboratories nominated by APEDA before shipment. In some countries the problem was predominantly post-harvest and in others it was largely preharvest. Adoption of recommended cultural and produce handling procedures (Mehan *et al.*, 1991) had been reasonably effective in reducing levels of aflatoxin in groundnut products in developed countries, there was little evidence of small-holding farmers in tropical developing countries adopting the improved practices. Therefore the effective solution to the problem would be to grow groundnut cultivars that were immune to infection or those cultivars, if colonized by the fungus did not support production of aflatoxins.

Resistance to *Aspergillus flavus* in groundnut operates at three sites in the plant, namely pod, seed coat and cotyledons (Nigam *et al.*, 1991). Three different genes controlled the three mechanisms (Utomo *et al.*, 1990). However, with exception for seed testa resistance, genetic mechanism of no other resistant trait was worked out (Murthy and Ghewande, 1996). Resistance to preharvest seed infection, *in vitro* seed colonization and aflatoxin production *per se* was also identified (Knauft and Wynne, 1995). All these types of resistance are not necessarily correlated, nor do laboratory, green house, and field studies show consistent findings. Therefore prevention of *A. flavus* initial infection into the groundnut plant may be an important strategy for developing genetic resistance to the organism because of two reasons; one reason is that *A. flavus* is a weak pathogen and the other reason is that it finds its entry in to the pods when the plant is experiencing drought stress and when the soil temperatures in the pod zone are high (Cole, 1989). Hence, on one hand, development of pre-harvest resistance against a weak pathogen and on the other hand, the development of drought tolerant lines may be useful in reducing the infection of the fungus as well as the effect of drought. The components of proximate analysis of groundnut cotyledons like lipids (Holbrook *et al.*, 1994) and proteins (Ghewande *et al.*, 1987) have some association with reduced aflatoxin contamination. Deleterious effects of mycotoxins produced by the fungus on these component characters were also established (Mehan *et al.*, 1991). But studies related to quality attributes that are related to low or high levels of aflatoxin are not many. Furthermore, to what extent a compromise can be made on quality aspects with permissible levels of aflatoxin has to be investigated.

Assessment of variability, diversity, heritability, genetic advance and association analyses form the basis for crop improvement programme by way of formulating selection criteria. The success of hybridization in self pollinating crops like groundnut mainly depends upon the genetic divergence of the parents involved, the nature of gene action and combining ability which gains an insight into inheritance of the traits and helps in identifying parents with good GCA and crosses with high SCA effects. Variability and diversity in edible groundnuts for carbohydrates, oil and protein in total were worked out but not for their components. Genetic analyses of quality parameters also are limited. Furthermore, we need to understand the relevance of physiological characters to suggest a holistic approach for the development of high yielding, aflatoxin tolerant groundnut varieties. Hence, present investigation was taken up with the following objectives.

- To estimate genetic variability and divergence of morphological, physiological and biochemical characters in groundnut.
- To screen edible groundnut varieties for aflatoxin content in post harvested seeds.
- To workout relationship of morphological and biochemical characters with aflatoxin content in seeds as well as with yield.
- To understand the relationship of physiological characters with yield.
- To study nature and magnitude of gene action in inheritance of morphological, physiological and biochemical characters.
- To estimate heterosis and combining ability of selected characters.
- To suggest a suitable breeding strategy for the development of aflatoxin tolerant edible groundnuts.

CHAPTER II

REVIEW
OF
LITERATURE

CHAPTER – II

REVIEW OF LITERATURE

A brief resume of relevant literature is presented under the following sub headings:

2.1 Quality and aflatoxin content

2.2 Association analysis

2.3 Variability and genetic parameters

2.4 Genetic divergence

2.5 Combining ability and

2.6 Heterosis

2.1 QUALITY AND AFLATOXIN CONTENT

2.1.1 Quality

Quality in groundnut is a broad term, which encompasses physical, chemical, and functional properties. The quality attributes that are important for end uses of groundnut vary among the developed and developing countries. In developed countries, groundnut is mainly used for making peanut butter and consumed as roasted groundnut or in confections, while in several developing countries including India, it is mainly processed for its oil. It was pointed that by exporting 1 t of premium priced HPS groundnut, India could earn a foreign exchange that could be used to import 2 t of cheaper substitutes like palm oil (Chandrasekhar, 1991). In this context quality in groundnut should be referred to those characters that are required by the developed nations.

Misra *et al.* (2000) evaluated groundnut cultivars for their worthiness for export. Among physical attributes high SMK, high 100 kernel mass, light pink colour testa, elongated kernels with tapering ends and seed size uniformity were considered to be desirable while among the chemical attributes, low-oil, high stability index, high protein, high sucrose, low reducing sugar and low free amino acids were considered desirable.

Ahmed and Young (1982) reported that the high stability index of oil gives longer shelf life in groundnut products. They also indicated that low calorie (low oil) groundnuts are preferred from confectionery point of view due to increasing figure and health awareness among the consumers.

Nigam *et al.* (1989) considered higher values for SMK, 100 seed mass, kernels with elongated shape, tapering ends which facilitate easy blanching and pink to light brown testa colours as desirable quality traits.

Newell *et al.* (1967) reported that higher the protein content, the more was the nutritional value. Among carbohydrates, sucrose was considered desirable from organoleptic point of view. Sugars, especially monosaccharide (reducing sugars) and the free amino acids reacted during roasting to impart characteristic colour of roasted groundnut and also nutty flavour (characteristic feature of Indian groundnuts which is desirable). However if reducing sugars and free amino acids are present in higher quantities, the discoloration of the cooked product occured due to excessive browning (Misra *et al.*, 2000).

Natural Resources Institute of the UK Ministry for Overseas Development listed quality requirements for groundnut pods and kernels (Chandrasekhar, 1991). Pod quality included, pod colour and type; size (12-14 pods oz^{-1}); pod texture; cleanliness; freedom from aflatoxin and damage; absence of blind nuts; and ease of dehulling. Kernel quality included, kernel size (>1 g $kernel^{-1}$); uniformity in size and shape, resistance to splitting, ease of testa removal (tapering ends), flavour (nutty), colour (pink or light brown testa), sugar content and freedom from aflatoxin (< 5 ppb). The over-riding consideration with regard to quality was without doubt freedom from aflatoxins.

2.1.2 AFLATOXIN CONTENT

Aflatoxins are toxic metabolites produced by certain fungi belonging to the group of *Aspergillus* growing in groundnut foods and feeds. A concise presentation of the relevant scientific literature on various aspects of aflatoxin problem in groundnut is made under appropriate sub-headings as under.

2.1.2.1 What is aflatoxin?

Aflatoxins are highly oxygenated heterocyclic compounds. Among eight forms (AFB_1, AFB_2, AFG_1, AFG_2, AFM_1, AFM_2, AFB_2a, and AFG_2a), aflatoxins, AFB_1, AFB_2, AFG_1 and AFG_2 are more commonly encountered and AFB_1 ($C_{17}H_{12}O_6$) is the most common and also the most toxic aflatoxin produced by *Aspergillus flavus* and *Aspergillus parasiticum* (Dube, 1990). Aflatoxins are now known to be hepatotoxic, carcinogenic and teratogenic (Mehan *et al.*, 1991). Childhood cirrhosis in Indian children is one among the many abnormalities caused by aflatoxin (Bhat, 1989).

2.1.2.2 Fungi

Among the four most economically important species *Aspergillus flavus* and *A. parasiticus* produce aflatoxins. *A flavus* belonging to the family Eurotiaeae is ubiquitous saprophyte and successful facultative plant pathogen. Not all wild-type strains of *A. flavus* produce aflatoxins. In a literature survey of published studies encompassing 3343 isolates, a total of 1847 or 56 % were aflatoxigenic. It invades and contaminates groundnuts before harvest, during post harvest field drying and during storage. Many modes of pre-harvest infection were observed and late-season drought stress, particularly in the semi-arid tropics, observed by Mehan (1987) was a major factor associated with aflatoxin contamination. Fluctuating soil moisture conditions are prone to pod splitting and subsequent invasion and contamination (Graham, 1982). Pods on a developing plant seem predisposed to *A. flavus* infection when plants are undergoing drought stress and soil temperatures in the pod zone are high (Cole, 1989). Therefore, the development of drought-tolerant peanut lines may be useful in reducing the effects of *A. flavus* as well as of drought. Isleib *et al.* (1994) opined that as *A. flavus* was a weak pathogen, prevention of its initial infection in to the plant might be an important strategy for developing genetic resistance to the organism.

2.1.2.3 *Regulations*

Aflatoxins cause economic and trade problems at almost every stage of marketing of groundnut especially during export. At present some 50 countries impose aflatoxin regulations and most countries have a separate maximum acceptable level for food and feed (van Egmond, 1989). For domestic use, the U.S. Department of Agriculture (USDA) requires three 22 kg laboratory samples to average less than 15 total ng g^{-1} of aflatoxin for acceptance. Where as the European Union requires one 30 kg laboratory sample to test less than 15 total ng g^{-1} for raw groundnuts and three 10 kg laboratory samples to all tests less than 4 total ng g^{-1} for consumer-ready groundnuts sold for direct human consumption (Adams *et al.*, 2004). Australia set maximum permissible limit for groundnut at 15 ppb kg^{-1} seed. In India permissible level for aflatoxin in groundnut is 30 ppb kg^{-1} seed (ICAR, 1987). Pitt (2004) recommended 15 μg kg^{-1} aflatoxins in groundnuts as maximum permitted level in international trade. Various surveys conducted in different parts of the country (Sahay and Rajan, 1990 and Verma *et al.*, 1997) had shown a range of aflatoxin levels in groundnut food products; raw kernels (0.8 to 2200 μg kg^{-1}), edible flour (0 to 200 μg kg^{-1}), unrefined oil (up to 786μg kg^{-1}), and cake (27 to 1122μg kg^{-1}) depending upon the agro-climatic location and storage conditions (Ghewande, 1997). In Andhra Pradesh groundnut samples contain 15-19 per cent excess aflatoxin than the permissible level. In order to protect the international trade, in 29th meeting of codex committee on food additives and contaminants (CCFAC) a draft level of 15 micrograms per kilo for total aflatoxin in groundnuts intended for further processing was proposed as the maximum level.

2.1.2.4 Screening and estimation of aflatoxin content

Mixon and Rogers (1973) developed a laboratory inoculation method for screening groundnut genotypes for resistance to *Aspergillus flavus* invasion and colonization of seeds. Naguib *et al.* (1989) observed that sporulation and growth of *A. flavus* was dense on the seeds of susceptible cultivars but was sparse on resistant lines. They regarded that genotypes with 15 % or fewer seeds colonized as resistant. Likewise a range of 3-16 % of seed colonization was considered as resistance to screen groundnut cultivars by Li Sinlin *et al.* (1996).

Field screening techniques involving imposing late season drought or creating a water-deficit gradient or adding artificial inoculum have been perfected to screen material for *A. flavus* infection and aflatoxin contamination (Mehan, 1989).

Dowell *et al.* (1992) recommended ELISA for identification of contaminated loads of farmers' stock groundnuts. Ramakrishna and Mehan (1993) made a comparison between direct and indirect methods and concluded that both were useful for routine analysis of AFB_1 in groundnuts. The precision of ELISA was comparable with HPLC (Azer and Cooper, 1991).

Reddy *et al.* (2003) applied inoculum @ 2.5 g per meter row length at 25 and 40 days after sowing and screened the genotypes for pre harvest aflatoxin resistance.

2.1.2.5 Management

In some countries the problem was predominantly post-harvest and in others it was largely pre-harvest. Adoption of recommended cultural and produce handling procedures (Mehan *et al.*, 1991) had been reasonably effective in reducing levels of aflatoxin in groundnut products in developed countries, there was little evidence of small-holding farmers in tropical developing countries adopting the improved practices. It was suggested that effective solution to the problem would be to grow groundnut cultivars that were immune to infection or that cultivars, if colonized by the fungus did not support production of aflatoxins (Ghewande *et al.*, 1993).

Palanisami *et al.* (1990) observed that incidence of storage fungi ranged from 4-34 % depending on the moisture content of fresh pods (22 36 %) and drying conditions. They also reported that immature and shriveled pods were 2-3 times more heavily contaminated than mature pods.

Harvesting the crop beyond optimum maturity was correlated with increased pod damage by many soil borne insects, which in turn enhance the invasion by *A. flavus* (Eeden *et al.*, 1994).

Krishnappa *et al.* (2003) observed that the percentage and number of storage mycoflora increased with increasing storage period in all packaging materials. They further observed that the most common storage fungi, *A. flavus* and *A. niger* infection was less when stored in moisture impervious containers rather than moisture pervious containers.

2.1.2.6 Genetic Resistance to *A. flavus* infection

Nigam *et al.* (1991) summarised that resistance to *A. flavus* in groundnut operated at three sites in the plant, namely pod, seed coat and cotyledons. Seed-coat resistance had been attributed to the presence of chemicals such as tannin and dimethoxyioflavone, and to the contents of soluble amino compounds and arabinose. Seed-coat resistance was only operative in seeds with an intact testa. Varietal differences had been reported in seed ability to support aflatoxin production. However, very little was known about its mechanism. Differences in pod shell structure, presence of antagonistic mycoflora in the shell and the presence of thick-walled parenchyma cells had been cited as responsible for varietal differences in pod resistance.

The three mechanisms of resistance; pre-harvest infection resistance (PIR), dry seed resistance (DRS) and aflatoxin production resistance (APR) as described by Reddy and Murthy (1994) had different genetic controls and had heritability ranging from 0.2 to 0.7 (Utomo *et al.*, 1990).

Seed testa characters of the host such as thickness, cell structure, cell arrangement, permeability, waxy surface, tannin content were found to be associated with seed/pod colonization and aflatoxin development (Murthy and Ghewande, 1996).

Intact testae, coloured testae confer greater resistance to invasion than damaged testae, white or variegated testae (Carter, 1973). In all reported cases of resistance to seed colonization, the protective role of the seed testa has been emphasized. Resistance has been correlated with thickness, density of palisade cell layers, absence of fissures and cavities, presence of wax layers on the testa, fungistatic phenolic compounds in testa, low levels of certain amino acids and carbohydrate compounds in testa *etc.* (Mehan *et al*, 1991). The groundnut shell has logically been considered a barrier to penetration by fungi

(Nahdi, 1989). The genetic mechanism of any of the host traits described above, except seed testa resistance, has not been worked out so far (Murthy and Ghewande, 1996). Resistance could result from combinations of physical, chemical and biological factors operating in the testa rather than being due to a specific mechanism.

Waliyar and Bockeiee-mor Van (1989) reported significant varietal differences in levels of seed invasion by *A. flavus* at harvest. They also showed that under field conditions, resistance was positively correlated with *in vitro* seed colonization. Mehan *et al.* (1991) indicated that none of the 13 confectionary groundnut genotypes showed stable resistance to *A. flavus* although there was certain degree of resistance to seed colonization in the genotypes studied. Ghewande *et al.* (1993) observed that the correlation between *A. flavus* infection in bold-seeded groundnut and colonization was high and that in between colonization and aflatoxin production was low. They also reported high regression coefficient for infection and colonization. Davidson *et al.* (1982) opined that the levels of *A. flavus* seed infection cannot be directly correlated to the aflatoxin production because levels of *A. flavus* infection and aflatoxin contamination were related primarily to environmental conditions especially to drought stress during pod maturation, soil insect pod damage, leaf drop due to foliar diseases and antagonistic mycoflora present in the soil. The relationships between different resistant mechanisms, and their interactions have not been clearly established and there is a need to elucidate the mechanisms of resistance to pod/seed infection and aflatoxin production (Waliar, 1997).

The heritability estimates for resistance to seed infection had been reported to be low in USA (Utomo *et al.*, 1990) but moderate to high in India (Upadhyaya *et al.*, 1997).

In a diallel study, significant reciprocal effects were noticed in some crosses indicating maternal influence on testa structure (Rao *et al.*, 1989). The allelic relationship among various sources for each resistance trait needs to be elucidated to enable breeders to pyramid the non-allelic genes for each resistance mechanism.

At ICRISAT, a mass-pedigree method of selection and its modifications have been practiced to develop eight stable derivatives (ICGVs 86168 to 86171 and 86173 to 86177) having seed coat resistance levels equal to those of the donors J 11 and UF 71513 (Rao *et al.*, 1989). Recently ICRISAT has identified ICGVs 91278, 91283, and 91284 as improved lines for pre harvest seed infection (Upadhyaya *et al.*, 2001).

2.1.2.7 Genetic resistance to aflatoxin production

Breeding for resistance was relied on information obtained in the assessment of *A. flavus* infection in harvested, mature, dried seeds, as the laboratory screening test can readily be used to compare progenies for resistance (Rao *et al.*, 1989). However, when dealing specifically with resistance to natural seed infection in the field, resistance mechanism may operate at the pod surface, within the shell at the seed surface and within the testa/cotyledons. This makes it difficult for breeders to specify particular resistance traits to aim for. There appear to be different genes in conferring resistance to seed colonization, pre-harvest seed infection and alfatoxin production. Reddy *et al.* (2003) also reported that seed colonization and aflatoxin content had no consistent relationship.

Although several factors of seed testa have been reported to contribute towards *A. flavus* resistance, no efforts have been made to breed for these traits (Rao *et al.*, 1989). This may be due to their susceptibility to environmental factors (Mehan *et al.*, 1991). Nahdi (1996) reported that late drought stress increased aflatoxin contamination in seeds of testa resistant genotypes like J 11 and PI 337394. Waliyar *et al.* (1994) also reported environmental influence on aflatoxin resistance. Anderson *et al.* (1996) reported low broad sense heritability for aflatoxin resistance. For resistance to aflatoxin production, the heritability estimates were reported to be low to moderate (Utomo *et al.*, 1990).

Ghewande *et al.* (1993) observed that the correlation between *A. flavus* infection and colonization in bold-seeded groundnut was high and that in between colonization and aflatoxin production was low.

Cultivars resistant to fungus invasion in the soil would be particularly desirable for semi-arid regions where pre-harvest aflatoxin contamination is a serious problem. It also reduces plant stand due to aflaroot disease. Significant correlation between *A. flavus* contamination in groundnut seeds and low germination percentage in field was observed by Kanniyan and Sithanatham (1991).

The importance of lipids reported in groundnut to support infection by *A. parasiticus* and production of AFB_1 by Reddy *et al.* (1992) indicates a possible resistance of low lipid genotypes. Ghewande *et al.* (1989) observed that low protein content in seed showed less aflatoxin contamination. The aflatoxin content of inoculated seeds of nuts like almond, walnut and groundnut was observed to be positively related to moisture content and was not significantly related to protein, fat and total carbohydrate contents (Zafar Iqbal *et al.*, 2004).

Many sources of resistance have been reported; PI 337409, PI 337394 F, UF 71513, J 11, Ah 7223, U-4-47-7, 55-437 and 73-30 for pre-harvest field infection and *in vitro* seed invasion, colonization and aflatoxin production (IVSCAF); U-4-7-5 and VRR 245 for aflatoxin production. Two wild sps., *Arachis chardenassi* and *A. duranenesis* were also resistant to IVSCAF. The resistant lines to pre-harvest seed infection did not show resistance when tested for IVSCAF and vice-versa was also true (Nigam *et al.*, 1991). Murthy and Ghewande (1996) compiled 33 aflaroot resistant sources in groundnut. Harish babu *et al.* (2003) recorded lower infection on TG 49 (1.69) than the resistant genotype, J 11 (2.87).

2.1.2.8 *Alternate strategies*

Holbrook *et al.* (2000) evaluated 20 genotypes of groundnut having drought tolerance and susceptibility. These results indicated that susceptible genotypes had greater pre harvest aflatoxin contamination and drought tolerant genotypes had less pre harvest aflatoxin contamination. The susceptibility of peanuts to aflatoxin contamination was observed to be related to kernel moisture content and temperatures during pre-harvest and post-harvest conditions (Cole *et al.*, 1995). Under prolonged drought conditions, groundnut genotypes, which maintain high kernel moisture, showed enhanced resistance and produced low aflatoxin (Cole *et al.*, 1993). Venkataramanamma *et al.* (2004) reported similar results by indicating that the genotypes, which maintained high pod and kernel moisture, had low aflatoxin contamination. End season drought stress had significantly increased the seed infection with *A. flavus* in all the tested genotypes (Nahdi, 1996). Drought and temperature stress on peanut as observed by Musingo *et al.* (1989) increased accumulation and/or synthesis of carbohydrates and certain polypeptides and might be thus enhaced *Aspergillus* invasion and aflatoxin production. Nageswara Rao *et al.* (2001) suggested that management of drought, by escape, tolerance or avoidance mechanisms may therefore have a significant impact on genotype's ability to resist aflatoxin production. Reddy *et al.* (2003) indicated that aflatoxin production in groundnut was negatively related to pod wall moisture during terminal drought and genotypes tolerant to moisture stress by maintaining high water content, had reduced levels of aflatoxin.

Scientists have focused on understanding the aflatoxin biosynthesis pathway. They have identified o-methyl-sterigmatiocystin as the last known precursor, and the enzyme oxido-reductase, that catalyses the conversion of this precursor to aflatoxin B_1. When the gene responsible for the enzyme is located, it could be removed or altered to stop production of aflatoxin (Nigam *et al.*, 1991).

2.2 ASSOCIATION ANALYSIS

Among the quantitative characters, pod yield is the most complex and was reported to be associated with over 40 other characters. Among these, number of mature pods, 100-seed weight had been reported to affect pod yield directly, as revealed from path analysis studies (Reddy and Murthy, 1994). With respect to mature pods per plant, irrespective of group, habit and duration, many research workers had observed positive significant estimates of correlation. A phenotypic correlation less than its genetic counterpart, together with a small positive environmental correlation will occur where the genes governing two traits are similar but where the environments pertaining to expression of these traits have low correlation (Searle, 1961).

2.2.1 Morphological characters

Varisai Muhammad *et al.* (1973) concluded that bold-seeded nature was associated with low shelling outturn. Rama Reddy (1991) in his correlation studies stated that shelling percentage and number of mature pods had high positive correlation with pod yield per plant. Suresh Kumar (1993) in his studies revealed that in both parents and crosses, number of mature pods, shelling percentage and harvest index had significant positive association with pod and kernel yields. In parents, all the characters had positive indirect effect on pod yield through kernel yield and pod yield showed highest positive effect on kernel yield.

Positive association of seed size with 100 seed weight was reported by Borate *et al.* (1993). Ursal *et al.* (1995) reported significant and positive direct effect of 100 kernel weight, number of developed pods, kernel weight and shelling% on pod yield. According to Mishra (1995) pod yield was found to be positively and significantly correlated with harvest index and number of pods per plant, whereas number of pods per plant had significant positive correlation with harvest index. Anuradha (1995) indicated through correlation analysis that number of mature pods per plant, 100 kernel weight and kernel yield were the major components contributing to pod yield. She also showed high direct effects on pod yield. Uddin *et al.* (1995) reported that at genotypic level, seed yield per plant was negatively associated with shelling percentage and 100 seed weight. They also observed large direct effects of pods per plant on seed yield per plant.

Vindhiya Varman and Raveendran (1996a) observed positive and significant association of pod yield with number of mature pods per plant and kernel weight per plant with shelling outturn. They have also observed significant negative association of mature pods with kernel weight per plant. Salara and Gowda (1998) recorded high correlation of pod number and test weight with pod yield in the F_2 progenies of groundnut.

Genotypic correlation of pod yield per plant as observed by Cherian Mathews *et al.* (2000) was positive and significant with kernel yield per plant and 100-kernel yield. Maximum direct effect was also observed by them to be exhibited by kernel yield on pod yield per plant. Sah *et al.* (2000) studied 24 genotypes of mutant cultures of groundnut and reported that pod yield per plant was positively and significantly correlated with number of pods per plant, 100 seed weight and oil yield per plant and it had negative association with shelling percentage. The direct effects of seed yield on oil and plant yield were also reported to be high. The characters, number of pods per plant, 100 seed weight indirectly through seed yield per plant effected pod yield.

Singh *et al.* (2000) observed highly significant positive association of pod yield with 100-kernel weight and number of mature kernels. Venkataravana *et al.* (2000a) revealed that the genotypic correlation coefficients were observed to be relatively of higher magnitude than the corresponding phenotype correlation coefficients, which indicated the strong inherent association between the characters, existed in the study. Pod yield had significant positive association with number of mature pods, shelling percent, 100 kernel weight and kernel yield. Furthermore, mature pods, shelling percent, 100 kernel weight, kernel yield and oil per cent were reported to be positively associated with one another. They also reported high and positive direct effects of kernel yield and number of mature pods on pod yield. Mathews *et al.* (2000) revealed maximum direct effect of kernel yield per plant on pod yield per plant.

Singh and Singh (2001) studied 15 genotypes of Spanish bunch groundnut for seven characters and observed that number of pods had the highest phenotypic correlation with pod yield per plant followed by harvest index. They also observed high positive direct effect of 100-kernel weight, harvest index on pod yield. Maximum direct effect on pod yield was also observed for 100 kernel weight and harvest index and most of the characters were observed to influence pod yield via 100 kernel weight.

Kernel yield was found to be correlated with pod yield and expressed positive direct effect on pod yield (Dhaliwal *et al.*, 2003). Jayalakshmi (2003) reported highly significant and positive phenotypic correlation between kernel yield and mature pod number per plant.

2.2.2 Physiological characters

In groundnut conventional breeding methods to improve drought adaptation have been based on selection for pod yield in a given drought environment. While direct selection for yield can be effective (Wright *et al.*, 1994), the limitations of this approach are high resource investment and poor repeatability of the results due to the large G X E interaction for yield (Cooper and Hammer, 1996). Study on physiological processes contributing to yield, which are relatively stable, needs to be investigated. Simple analytical crop models should be devised for understanding of genotypic variation for these characters and their relationship to drought and yield. A brief review on the physiological characters related to yield and the influence of drought on their expression is cited in this chapter.

Pallas and Samish (1974) reported no correlation between SLW and net photosynthesis in peanut. Williams *et al.* (1975) reported that kernel growth rate early in the reproductive phase of groundnut was influenced by CGR.

Natarajaratnam (1979) found that the harvest index was highly correlated with economic yield and concluded that a high harvest index indicated a favorable partitioning of dry matter towards pods. A positive correlation between SLW and dry weight, and SLW and yield was observed in black gram (Subramanyam and Pandey, 1981).

Madhavi (1988) on correlation studies indicated that LAI in the initial stages was positively correlated with pod yield, kernel yield, number of pods, and SLW at maturity. She has also observed strong correlation of LAI from 60 days with pod yield, kernel yield and total dry matter. She concluded that initial LAI together with initial dry matter could be employed profitably as selection criteria to select productive genotypes in groundnut breeding.

Correlation studies carried out by Madhavi (1988) revealed that SLW at maturity was associated with LAI at 45 and 60 DAE. SLW at 45 and 60 DAE was also positive with LAI in the initial stages. She reported non-significant, positive correlations for SLW at 30 DAE with pod yield, kernel yield and number of pods, while at rest of the stages SLW was negatively correlated with the these characters. Pod weight in the her study was found to be correlated positively and significantly with kernel weight, LAI from 60 DAE, while a non-significant but positive correlation was observed with SLW at 30 DAE. Its correlation with harvest index was negative but non-significant. The correlation of kernel yield with LAI form 60 DAE was positive and significant but with LAI at 30 and 45 DAE, SLW at 30 DAE was non-significant though positive. Harvest index on the other hand exhibited negative correlation with SLW and LAI.

Wright *et al.* (1991) identified harvest index, as a major factor in improving pod yield in response to drought stress and it was associated with a more synchronous development. Venkateswarlu *et al.* (1991) in their correlation studies revealed that pod yield was closely associated with harvest index.

Suresh Kumar (1993) in his correlation studies revealed that harvest index showed significant positive association with number of pods, and shelling percent. He further stated that harvest index showed high positive direct effect on pod yield both in parents and crosses. Positive significant correlations were found for pod yield with harvest index and for harvest index with oil percent from the studies of Arunachalam (1993).

The importance of physiological traits such as harvest index, crop growth rate and total dry matter accumulation as yield contributing traits had also been established by character association studies (Reddy and Murthy, 1994). Similar positive association between harvest index and yield was reported by Mishra (1995).

Sharma and Varshney (1995) indicated the possibility of improving harvest index in groundnut by increasing pod yield, pod number and shelling percentage because of their positive significant correlations. The direct effects of pods per plant, kernels per plant, pod yield per plant and shelling percentage on harvest index were high and positive. The residual effect of factors was high suggesting thereby that considerable amount of variation manifested in harvest index remained unaccounted by other characters not measured in the study.

Ursal *et al.* (1995) reported significant and positive direct effect of harvest index and dry matter production on pod yield. Among physiological characters studied by Anuradha (1995) crop growth rate between 30-60 DAS and harvest index expressed significant positive association on pod yield.

Patra *et al.* (1995) found that LAI at 50 and 70 DAS had positive and significant influence on number of pods per plant, shelling percentage, 100 kernel weight, pod yield, oil content and oil yield per plant. Yield components such as number of pods per plant, number of kernels per pod, shelling percentage, 100 kernel weight and oil content were positively and significantly correlated with each other and also influenced pod and oil yields. It was concluded that LAI at 70 DAS along with dry matter accumulation at 70 DAS were key growth variables positively influencing pod and oil yields in groundnut.

Harvest index and mature pods per plant were positively associated with kernel yield per plant in the segregating generations studied by Jayalakshmi (1997) implying the usefulness of these attributes in selecting for high kernel yields. Harvest index was associated positively with SLA in parents and F_1s, but exhibited non-significant association in F_3 generation suggesting that concurrent improvement in both the characters might be possible in the advanced generations.

Arjunan *et al.* (1997) observed that LAI had the highest significant positive correlation with pod weight and harvest index had the negative correlation before stress (at 40 DAS), after imposing stress (at 75 DAS) and at final harvest. Plant growth and leaf expansion were much affected due to limited water supply and hence total dry matter production and LAI had significance in pod filling. They indicated that correlations between physiological traits were much easily affected during the developmental stages with the imposition of stress. It was opined that this was to adjust the altered physiology of the plant due to stressed environment. Further SLA showed positive correlation with harvest index and carbon isotope discrimination. They concluded that leaf was the photosynthetic apparatus wherein the more leaf area in turn higher total dry matter production resulting in accumulation of photosynthates for high pod yield. They indicated that SLA might be employed in selection for carbon isotope discrimination since SLA was simple and inexpensive one as compared to the more expensive carbon isotope measurement.

Arjunan *et al.* (1999) reported that leaf area and harvest index were positively associated with pod yield. SLW exhibited negative correlation with transpiration rate. They indicated that the increased leaf thickness (SLW) resulted in reduced transpiration. The direct effect of SLW and harvest index on pod yield was negative and high. The indirect effect of SLW on leaf area was positive and high. They suggested that use of total dry matter production and number of functional leaves at harvest can be used as selection indices for development of drought resistance.

In a growth analysis study Sanjeeva Kumar *et al.* (2000) reported that GCR increased as crop growth progressed and was highest between 60 and 90 DAS in all the cultivars belonging to Virginia and Spanish groups. LAI, LAR and CGR significantly affected pod yields in Virginia group but had no definite trend in cultivars of the Spanish group.

Nigam *et al.* (2001) opined that in groundnut, water use efficiency was correlated with specific leaf area and suggested that the latter could be used as a surrogate trait for selecting for water use efficiency. They also reported that partitioning of assimilates as measured by the harvest index had the greatest effect on pod yield.

Some studies showed that SLA was influenced by factors such as time of sampling, leaf age (Wright and Hammer, 1994; Nageswara Rao *et al.*, 1995; and Rao *et al.*, 2001) and accuracy of the measurement. In another study Nageswara Rao *et al.* (2001a) highlighted the importance of a standardized sampling method to select for SLA in large-scale peanut breeding programs. This study has also shown significant correlations between SLA with SPAD Chlorophyll Meter Readings (SCMR) and suggested that SCMR could be used as a rapid, low-cost, non-destructive technique to screen large breeding populations for SLA. Similarly Rao *et al.* (2001) showed that a hand-held portable SPAD chlorophyll meter could be used effectively following necessary protocols for rapid assessment of SLA and specific leaf nitrogen, as surrogate measures of water use efficiency in groundnut.

Nautiyal *et al.* (2002) observed that water deficit imposed at various stages of crop growth in four groundnut cultivars influenced LAI, harvest index and pod yield. LAI increased rapidly from 40-100 DAS. Plants experiencing stress at vegetative phase had higher LAI during reproducing phase (80-120 DAS). Irrespective of cultivars LAI decreased during stress and increased after the relief producing more new leaves in their studies.

The hypothesis that, since transpiration efficiency in groundnut was controlled mainly by mesophyll rather than stomatal factors (Udayakumar *et al.*, 1998), parameters such as SCMR which was strongly linked with mesophyll efficiencies was also proved to be linked with transpiration efficiency in correlation studies of Bindu Madhava *et al.* (2002). Jayalakshmi (2003) observed highly significant and positive phenotypic correlation between kernel yield and SLA.

An inverse relationship was observed by Reddy *et al.* (2004) between SLA and SCMR in groundnut. A positive correlation between SCMR and seed yield, and a negative correlation between SCMR and SLA observed in this study further substantiated the conclusion that SCMR was a potential physiological trait to employ as a surrogate for transpiration efficiency.

John *et al.* (2004) reported positive and significant regression coefficients of SCMR with pod yield per plant and kernel yield per plant. Clavel *et al.* (2004) opined that as water deficit affected leaf area index and transpiration at approximately two weeks after the occurrence of water deficit at the soil level and as genotypic differences seemed to be greatest at this time, measuring physiological traits during this period might provide useful information for breeding early groundnut cultivars under end-of season water deficit conditions.

2.2.3 Biochemical characters

Penning de Vries *et al.* (1974) have estimated that 1 g of glucose produced by photosynthesis can be used by the crop to produce 0.83 g of carbohydrates or 0.4 g of protein when nitrate is the nitrogen source and opined that an increase in protein content requires more photosynthate, thus decreasing available photosynthate for starch synthesis and thus grain yield.

During seed development, sucrose translocated to the seed is metabolized to precursors of protein and oil. Enzymes of protein and oil (PEP carboxylase and pyruvate kinase) activities appeared to contribute significantly to protein and oil biosynthesis during seed development in maize (Smith *et al.*, 1990).

The negative correlation observed between seed weight and percentage protein in the seeds of bread wheat is a function of the fact that increase in seed size is commonly associated with a disproportionately larger deposition of starch relative to protein (Diehl *et al.*, 1978). The difficulty in simultaneous selection for both high-protein and high yield was implicated to negative correlation between them (Simmonds, 1995). He further opined that nitrate reductase activity (NRA) was a physiological criterion for selection of high protein and high yield. Singhal *et al.* (1977) working with wheat linked the negative correlation between grain protein content and grain yield to the negative correlation between grain protein content and 1000 grain weight. Kitbite (1990) suggested that the inverse phenotypic correlation between grain yield and grain protein concentration are not caused by genetic factors such as linkage or pleiotropy, but arise from the intrinsic physiological and mathematical relationships, the two characters have in common.

In groundnut bold seeds had more protein content than the small seeds (Deodhar *et al.*, 1973). The negative relationship between oil and protein, pod and kernel yield with oil and protein and positive relationship between protein and sugar content was observed by Layrisse *et al.* (1980). Seed size has also been reported to have correlation with lipids (Raheja *et al.*, 1986).

Oil and protein contents were reported to be positively correlated though not significantly even though yield of groundnut pods was negatively correlated with oil and protein contents (Makne and Bhale, 1987).

Protein content was considered to influence aflatoxin contamination levels (Ghewande *et al.*, 1987).

Kale *et al.* (1988) recorded a positive and significant correlation between oil content per seed and 100 seed weight and concluded that medium-sized seeds should be used to assess oil content as maximum percentage of oil was in medium sized seeds. Bold seeds were observed to possess more oil content than the small seeds (Sahoo *et al.*, 1988).

Inverse correlation between protein and oil contents was reported by Dwivedi *et al.* (1990). Their study with 64 groundnut genotypes revealed that seed weight had no relationship with oil or protein content. However when 64 genotypes were graded on seed weight basis, oil content within a genotype showed a significant linear increase as seed weight increased in the graded samples, but no such relationship was observed for protein content. Misra *et al.* (1992) also reported negative correlation between oil and protein contents.

Reddy *et al.* (1992) in a study with different crops including groundnut observed that groundnut cotyledons, with most lipids, supported the greatest production of AFB_1 and suggested that lipids were more important in determining growth and AFB_1 production by *A. parasiticus*. Ghewande *et al.* (1993) screened bold seeded groundnut genotypes for dry seed resistance to *A. flavus* and for the production of aflatoxin under artificially inoculated conditions. They did not observe any correlation between sugar content and infection, colonization or aflatoxin content. Holbrook *et al.* (1994) reported some association of fatty acids with reduced aflatoxin contamination.

Ursal *et al.* (1995) reported significant and positive direct effect of oil percent and protein percent on pod yield. Positive association of kernel weight per plant with oil content was evident in the studies of Vindhiya Varman and Raveendran (1996a). Further more, they have observed the kernel weight had high positive direct effect on oil content. The highest direct effect of pod yield on oil content was nullified by indirect effect via shelling out turn. Oil content and yield were observed to be positively associated from the studies of Ali *et al* (1996).

Amino acid components (Murthy and Ghewande, 1996) of seeds also were considered to influence aflatoxin contamination levels.

Kale *et al.* (1988) observed that medium size seeds contain more oil percentage and more protein percentage compared to large and small seeds.

Bera and Das (1998) recorded correlation between seed yield and oil content and no significant association between 100 seed weight and oil content. They observed that PI 314817, a Valencia type not only had a very high seed oil content, its seed yield per plant and 100 seed weight were also very high and indicated that the genotype combined effectively high seed yield potential with high oil yielding capacity.

A significant negative correlation between protein and oil contents was noticed by Sadhana Kumari and Snehalatha Reddy (1998) in groundnut. Venkataravana *et al.* (2000a) revealed that pod yield had positive and significant association with oil yield per plant. Path analysis also revealed direct effect of oil yield on pod yield. Oil yield per plant was observed to be associated positively with number of pods per plant, 100 seed weight and seed yield per plant (Sah *et al.*, 2000).

Vindhiya Varman (2000) reported maternal effect of oil content in seven out of fifteen reciprocal crosses of groundnut.

Singh and Singh (2001) observed negative correlation of 100-kernel weight with protein content. They concluded that as oil content had no correlation with any other characters independent improvement for oil content was suggested. A strong inverse relationship between oil and protein (0.69) was also recorded in F_1 crosses of groundnut (Parmar *et al.*, 2001). Parmar *et al.* (2002) indicated positive and significant relationship between pod yield and protein content and negative association between oil and protein.

Dobaria *et al.* (2004) encouraged the direct selection for high protein content that may eventually result in high sugar but low oil content based on the correlations they observed in their studies. They had also observed positive correlation of protein content with sugar and negative correlation with oil contents.

2.3 VARIABILITY AND GENETIC PARAMETERS

Successful plant breeding rests on the availability of information on variation, either continuous or discontinuous present in crop plants. Variation in groundnut was conveniently categorized as morphological, physiological and biochemical variation and discussed in this chapter. Genetic variability in groundnut is extensive (Singh and Simpson, 1994) and much of this variability had been described by Murthy and Reddy (1996). Many pod and seed characteristics including seed composition were generally observed to be quantitatively inherited (Knauft and Wynne, 1995). Bandyopadhyay *et al.* (1985) suggested two selection indices for the evaluation of F_1s and further generations. First method was the use of yield components, and the second was the use of both physiological traits and yield. They concluded that the second method was the best one.

2.3.1 Morphological characters

Arunachalam and Bandyopadhyay (1986) reported variation in kernel yield and explained that this variation was due to pod yield, shelling percentage and 100-kernel weight.

Velu and Gopalakrishnan (1985) reported wide variations in yield and harvest index among the varieties and habit types. They concluded that quality characters were associated with habit types. The values of shelling percentage and 100-seed weight increased from bunch to semi-spreading to spreading types; bunch being particularly heterogenous for those two characters.

Chauhan and Shukla (1985) studied 20 strains each of bunch and spreading groundnuts and reported that the GCV, heritability in broad sense and genetic advance were high for pod yield per plant in both groups.

Reddy and Gupta (1992) reported high estimates of GCV, heritability and GAM for kernel weight in groundnut. On the other hand they recorded higher estimates for all the genetic parameters viz., GCV, heritability and GAM for mature pods per plant.

Mishra and Yadav (1992) reported a high GCV, PCV, heritability and GAM for 100 seed weight. Chaudhary (1993) studied a collection of 404 genotypes of all types of groundnut and reported high GCV, heritability and GAM for immature pods per plant.

Ali and Wynne (1994) observed fairly high estimates of narrow and broad sense heritabilty in F_2 progenies for seed weight (g/100g seed) and suggested that selection for the character could be practiced in early segregating generations. Heritability estimates for pod yield in various studies ranged from 0.13 to 0.98 (Reddy and Murthy, 1994).

shelling out-turn in most of the studies recorded low to medium heritability (0.1 to 0.42) estimates in populations (Reddy and Murthy, 1994). Therefore they opined that early generation selection might not be fully rewarding. They also indicated that shelling out-turn could also be increased beyond 70 % by genetically manipulating shell thickness which was a qualitative trait.

Moderate GAM was reported for pod weight by Chavan and Dhoble (1994). Medium heritability was reported for pod weight (Sumathi and Ramanathan, 1995). Kernel weight per plant was found to possess low GCV and GAM in the studies of Nisar Ahmed (1995). Ganesan and Sudhakar (1995) recorded medium values for GCV, heritability in broad sense and GAM for mature pods per plant.

Uddin *et al.* (1995) obtained high GCV, heritability and genetic advance for seed yield per plant and 100 seed weight. They reported moderate to high genetic advance for shelling percentage. Low GCV estimates for shelling outturn as observed by Vindhiya Varman and Raveendran (1996a) indicated limited scope for improvement due to low magnitude of variability. They also reported low heritability and GAM for shelling outturn.

Ali *et al.* (1996) reported high GCV and heritability for pod weight. Sufficient variability existed in the crosses made by Salara and Gowda (1998) between Spanish and Virginia cultivars for pod yield and/pod number. They reported that the GCV and genetic advance was high for test weight and shelling percentage.

Naik *et al.* (2000) revealed high GCV and GAM for pod weight per plant and 100-kernel weight and low GCV for shelling percentage. Heritability in broad sense for 100 seed weight alone was observed to be high.

Vijayasekhar (2002) reported high GCV, PCV, high heritability coupled with genetic advance as per cent of mean for harvest index, 100-seed weight and shelling percentage indicating that these traits could be improved by simple selection methods.

Higher GCV, heritability and genetic advance for pod yield were observed by Dhaliwal *et al.* (2003). Makhan Lal *et al.* (2003) reported high PCV than GCV for number of mature pods per plant.

Amit Vikram *et al.* (2003) constructed selection index for 33 lines of groundnut based on the relative magnitude of variation (harvest index and yield per plot), correlation analysis (harvest index and yield per plant), regression analysis (yield per plant), and importance from breeder's point of view (number of mature pods per plant, yield per plant, harvest index, shelling percentage and yield per plot). They also reported maximum genetic gain for 12 traits, which included mature pods per plant, harvest index, shelling percentage and yield per plant.

Moderate values of heritability, GCV, PCV and genetic advance were reported by Vasanthi *et al.* (2004) for mature pods per plant, immature pods per plant and pod weight per plant.

John *et al.* (2004) observed high to moderate estimates of PCV and GCV for number of mature pods per plant and kernel yield per plant; high PCV for pod yield per plant; high GAM for mature pods per plant, pod yield per plant and kernel yield per plant, and suggested selection for improvement of these characters as they were under the control of additive gene action. They also reported the presence of additive gene action for mature pods per plant, pod yield per plant and kernel yield per plant as they exhibited high heritability coupled with high GAM.

2.3.2 Physiological characters

Breeders too often rely on the two most unstable morphological characters; pod number and weight for formulating selection indices and as such could not make much progress over the already existing varieties in terms of yield. The significance of physiological traits though envisaged (Duncan *et al.*, 1978; Obraztsov, 1983; Prasad *et al.*, 1984 and Nageswara Rao, 1992) could not be framed in the breeding programmes due to the lack information on genetic variability, heritability and genetic control of these traits. Therefore a very little progress has been made in terms of exploitation of genetic traits for physiological factors influencing yield components. Furthermore, there is a need to develop simple screening techniques for such desirable traits.

A review of groundnut varietal improvement work in India indicates that more emphasis was laid on improvement on pod size (Reddy, 1988) and number of pods per plant (Prasad et al., 1984) as selection criteria. However, very little progress has been made in terms of identification and exploitation of variability present in physiological characters.

The slow early growth of groundnut was found to be due to the slow development of LAI (Kasam *et al.*, 1975). They also reported that LAI reached large values up to 5.5 to 7 and a large leaf area was normally maintained until just before maturity.

The leaf canopy of the peanut crop though not very well defined, the density of canopy measured as LAI increased from very low levels early in the season to maximum values which ranged between 4 to 7 (Enyi, 1977). He further reported that maximum LAI occurred during early to mid-pod filling stage.

Duncan *et al.* (1978) showed that for a canopy of groundnuts, light interception reached a maximum at a LAI of 3. They reported that selection for higher yields in groundnut through traditional breeding methods did not show corresponding increases in crop growth rates.

According to Sivakumar and Shaw (1978), the marked increase in CGR at later part of the growing season could be due to a combination of decreased leaf area and increased dry weights. Duncan *et al.* (1978) reported non-significant differences for mean CGR values among the varieties.

Sudhakar Rao (1980) reported that the cultivars of groundnut differed in total chlorophyll content of leaves and opined that the dark green colour and leaf thickness might be due to higher chlorophyll content.

Santos and Sutton (1982) showed that in Virginia bunch varieties of groundnut, LAI before pod filling was much larger than needed. Maximum LAI was observed at 75 DAS by Murthy *et al.* (1983).

Hari Singh *et al.* (1982) from studies on genetic variability and heritability for morpho-physiological attributes in groundnut revealed significant differences among genotypes and high range of variability for number of undeveloped pods, harvest index, number of pods per plant and pod yield. The differences between phenotypic and genotypic variations were reported to be high for harvest index, pod yield and a low heritability values, while shelling percent and number of undeveloped pods had high heritability values.

Heritability was reported to be high for harvest index in the studies of Nagabhushanam *et al.* (1982) in their investigation on Spanish and Valencia groups. High genotypic variation and high broad sense heritability for harvest index was reported by Qadri and Khunti (1982).

Murthy *et al.* (1983) reported the highest CGR at 50 DAS and again at 75 DAS. Specific leaf weight is one of the many characters considered useful to the selection of varieties. SLW was reported to be an indicator of the photosynthetic efficiency of a genotype (Hiremath *et al.* 1984).

Low heritability values were reported for harvest index by Chauhan and Shukla (1985).

Differences among five bunch varieties of groundnut in respect of LAI, CGR were reported by Patil *et al.* (1986). A higher LAI in the initial stages was observed by Madhavi (1988) and she opined that it would result in higher dry matter production in groundnut. In some strains despite a relatively higher LAI in the initial stages, a decline in the leaf area at 60 days was observed and it was implicated that LAI before pod filling begins, might be larger than the needed. CGR of most of the varieties showed an increase in the initial stages from 45 to 60 DAE. She recorded increased SLW in groundnut varieties up to 60 to 75 DAE and thereafter it remained constant. Significant differences in the overall mean values of SLW observed by her reflected variability for photosynthetic efficiency.

Wells *et al.* (1991) found that the newer, higher yielding cultivars in United States allocated a greater proportion of dry matter to reproductive tissue than older cultivars.

Reddy and Gupta (1992) recorded high GCV for harvest index. Similarly high GAM values for harvest index were also reported.

Genotypes with lower SLA (thicker leaves) are known to have more of photosynthetic machinery i.e., more chlorophyll content (Rao and Wright, 1994).

Anuradha (1995) studied advanced generation pure line cultures of 28 genotypes of groundnut for variability and genetic diversity in physiological attributes and reported low values of GCV, heritability and genetic advance for SLA at 90 DAS. LAI at 30 DAS was observed to exhibit moderate heritability.

Vindhiya Varman *et al.* (1990) reported that the CGR increased up to pod formation (50-70 DAS) and then decreased. LAI was maximum during pod formation (50-70 DAS) then decreased while LAR decreased markedly after flowering (50 DAS).

In a study with different habit groups of groundnut, Sharma and Varshney (1995) found that the extent of variability observed for pod yield per plant, biological yield per plant and harvest index was high with high heritability in broad sense, and genetic advance indicating thereby that variability in these traits was largely accounted by fixable components and considerable improvement in these traits could be achieved through selection.

High heritability estimates for harvest index (Vaddoria and Patel, 1990) were reported. Narrow sense heritability values were recorded by Jayalakshmi (1997) for SLA, SLW despite low genetic variance. She also recorded high GCV and high heritability for harvest index.

Desai *et al.* (1999) reported that leaf area in groundnut ranged from 4 cm^2 in young seedling up to 80 cm^2 in the fully developed plants, with the specific leaf weight of 4.1 to 6.7 mg cm^{-2}. Several authors have reported that groundnut plant canopy in terms of leaf area index increases from very low levels early in the season to maximum values, ranging from about 4 to 7 and the maximum LAI occurs during the early-to-mid pod filling stage. The crop growth rate estimates increase from a very low value early in the season to a maximum at about 60 to 90 days after planting. The maximum values of crop growth rate estimates reported in different experiments averaged 19.6±4.2 g m^{-2} day^{-1}.

Moderate to high genetic advance were reported in F_2 generation in a study of five crosses by Vasanthi and Raja Reddy (2002) for harvest index and pod yield per plant.

The study of Nautiyal and Joshi (2003) indicated that groundnut genotypes with lower SLA (thicker leaf) might perform better under water deficit environment. Vasanthi *et al.* (2004) in their studies on heritability observed moderate values of heritability, GCV, PCV and genetic advance for SPAD chlorophyll metre reading. They also reported that the traits that conferred water use efficiency, high SPAD and low SLA showed moderate to high heritability and moderate to low GAM. They inferred that there was more scope for bringing improvement in SPAD through phenotypic selection than in SLA.

2.3.3 Biochemical characters

Oil content expressed low estimates of GCV, heritability and GAM (Nadaf and Habib, 1987). High heritability was recorded by Basu *et al.* (1988) for oil content.

A wide range of variability for protein content has been reported in groundnuts, from 16.2 to 36 % (Dwivedi *et al.*, 1990).

Nagaraj (1996) compared different botanical groups and observed that Virginia bunch group was rich in oil followed by Spanish bunch while, Valencia's had higher protein content and Virginias were rich in soluble sugars.

Misra *et al.* (1992) analyzed protein and oil contents in 38 groundnut genotypes and reported that oil content ranged from 42.5 to 54.5 % and protein content ranged from 15.4 to 26.5 %.

Variability for oil content in groundnut genotypes in the study of Jambunathan *et al.* (1993) ranged from 31-55 %. In a review, Reddy and Murthy (1994), observed that low to medium heritability of oil content and absence of high variability within cultivated groundnut have so far hampered the programmes aimed at improving oil content in groundnut seeds.

The comparative studies of seed size on seed quality as observed by Prathiba and Reddy (1994) revealed that protein content of small seeded varieties was high compared with bold seeded varieties, whereas sugar content of bold seeded varieties was higher.

Rajgopal *et al.* (1994) evaluated 15 Virginia bunch and 25 Virginia runner accessions for the preferred quality traits of low oil, high sugar and protein contents, and tolerance of *Aspergillus flavus* çolonization and identified that two each Virginia bunch (NRCG 2863 and NRCG 5505) and Virginia runner (NRCG 1005 and NRCG 2746) genotypes had the best overall combination of desirable quality traits with high pod yield and seed weight.

Inheritance of oil content was reported to be paternal and segregation followed a monogenic 3 : 1 normal : low-oil ratio (Knauft and Wynne, 1995).

Carbohydrate contents between 22 and 33 % have been reported for groundnuts but few studies have examined genetic differences. Carbohydrates in the seed include disaccharides (primarily sucrose), oligosaccharides (primarily starch), and insoluble compounds (Knauft and Wynne, 1995).

Vindhiya Varman and Raveendran (1996a) observed low GCV for oil content and opined that high heritability coupled with low genetic advance for this trait indicated the contribution of non-additive genetic effect.

Nagaraj (1996) reported that the variability in groundnut ranged from 40-50 % for oil, 35-55 % for protein, 7.4-14.2 % for total sugars and 2.86-6.35 % for sucrose.

Moderate heritability values for oil content were reported by Jayalakshmi (1997). Wide variation was noticed by Sadhana Kumari and Snehalatha Reddy (1998) for oil and fatty acid composition in groundnut varieties.

Pattee *et al.* (2000) observed high broad sense heritability for 18 carbohydrate components in groundnut. The observed high genotypic variation in carbohydrate components was similar to the high genotypic variation observed for the sweetness attribute in roasted peanuts indicating possible interrelationships. The establishment of such interrelationships was felt to be most beneficial to peanut breeding programs to ensure the maintenance of flavour quality in future peanut varieties.

Misra *et al.* (2000) reported high variability for reducing sugar content, moderate for protein content and the least in oil content. Moderate to high heritability for protein content was recorded and low environmental influence on this trait by Parmar *et al.* (2001 a) suggesting its usefulness in selection. Parmar *et al.* (2002) reported low heritability estimates in narrow sense for oil and high estimates for protein content in F_1 and F_2 generations of groundnut crosses.

2.4 GENETIC DIVERGENCE

Genetic divergence studies conducted on groundnut could not be categorized under morphological, physiological and biochemical characters as the available literature contained reports that analyzed all these characters collectively but not separately. Hence a brief resume of work reported for these characters is presented.

Bhagat *et al.* (1984) reported wide diversity in most of the characters studied among Virginia, Spanish and Valencia types. They suggested a classification based on 100-seed weight.

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

Reddy and Murthy (1994) reviewed genetic divergence studies conducted with parents of different habit groups and summarized that an optimum level of genetic divergence, irrespective of habit forms, was enough between the parents to realise heterosis in F_1 generation.

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

Vindhiya Varman and Raveendran (1996) observed that 60 cross combinations were grouped into five clusters. The clustering pattern revealed that the crosses, which had common pistillate parent ICGS 44, clustered mostly in clusters, I and II.

Nayak and Patra (1997) studied 128 genotypes of groundnut belonging to Spanish, Valencia, Virginia bunch and Virginia runner types on 18 characters using D^2 statistic and grouped them into 15 clusters. D^2 clustering pattern revealed lack of relationship between geographic origin and genetic diversity of genotypes.

The observations of John Joel and Mylsamy (1998) revealed that the analysis of dispersion using Wilk's criterion showed highly significant differences among the genotypes for the aggregate of nine characters. D^2 analysis established the presence of moderate genetic diversity among these types by forming of three clusters. The minimum intra and inter cluster distances observed were implicated to the common origin of the genotypes.

Venkataravana *et al.* (2000) studied genetic divergence in 144 groundnut genotypes by using Mahalanobis D^2 analysis for 15 characters and grouped them into seven clusters. They found that the distribution of genotypes in different clusters was not according to their geographical origin. They also observed that Cluster VII with only one genotype, ICGV 86564 recorded the highest mean values for most of the traits viz., pod yield per plant, shelling percentage, 100-kernel weight, SMK weight, kernel yield per plant, harvest index, oil percentage and oil yield per plant.

The studies of Vijayasekhar (2002) revealed that the Mahalanobis D^2 analysis formed ten clusters for 64 genotypes. The mode of distribution of genotypes to various clusters was at random suggesting that there was no correlation between geographical distribution and genetic diversity. The characters harvest index, 100-seed weight and shelling percentage contributed maximum towards genetic divergence in both D^2 analysis and canonical root analysis.

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

Olorunju *et al.* (2003) evaluated 25 early maturing cultivars of groundnut by considering the parameter shelling percentage over five locations. Their results showed differences between the genotypes and between the locations with respect to the pattern of clustering. They have indicated that the use of clustering method provided a suitable tool for the farmer or plant breeder to make a choice of alternative genotype from a given group of lines that formed a cluster for any given trait or parameter studied. The procedure was more useful where genotype x environment interaction is high for a specific crop.

2.5 COMBINING ABILITY

Most of the pod and seed traits were largely controlled by additive genetic effects. Maternal and maternal interaction effects were also significant in many cases (Dwivedi *et al.*, 1989). In general, additive gene effects are likely to play more important role in the inheritance of quantitative traits in groundnut, if the selected parents were less divergent (Isleib and Wynne, 1983). Both additive and non-additive components of genetic variances were important for yield and related traits, although in most of the studies conducted so far, additive gene action has been reported to be preponderant for pod yield *per se* (Reddy and Murthy, 1994).

2.5.1 Morphological characters

Manoharan *et al.* (1985) reported predominance of additive gene action for shelling percentage and yield of groundnuts form line X tester analysis and suggested that improvement of these characters could be achieved through pedigree breeding. They also reported non-additive gene action for pod number.

According to Basu *et al.* (1987) both gca and sca effects were significant for number of mature pods. Shelling percentage expressed maximum additive gene effects. They also reported additive gene effects for pod yield per plant.

For kernel yield per plant both additive and non-additive gene effects were reported (Reddy and Reddy, 1988) to be important. As kernel weight was an important criterion deciding the premium price of the export groundnuts Basu *et al.* (1988) advocated early generation selection for the improvement of kernel weight in the crosses involving small seeded genotypes.

Non-additive gene effects were reported for pod yield in groundnut by Dwivedi *et al.* (1989). Both additive and dominance genetic effects were reported for mature pod number by Vindhiya Varman *et al.* (1990). For kernel yield per plant, additive gene effects were reported by Hariprasad, (1990). Predominance of additive genetic effects for number of mature pods per plant was reported by Upadhyaya *et al.* (1992).

The genetic studies by Chaudhary (1993) on 100-kernel weight indicated that the variation was due to additive gene action. Where as, Anderson *et al.* (1993) indicated that the variation for 100 seed weight was due to non-additive gene action.

Suresh Kumar (1993) in his combining ability analysis revealed that predominance of non-additive gene action for number of mature pods, kernel and pod yield per plant. For shelling percentage both additive and non-additive gene actions were observed to be equally important.

Vindhiya Varman and Raveendran (1994) observed the role of both additive and non-additive gene action for shelling out turn in their line x tester analysis and non-additive gene action for mature pods. Studies by Reddy and Murthy (1994) on inheritance of shelling percentage revealed that both additive and non-additive genetic effects were important for shelling percent. For kernel yield per plant non-additive gene effects were reported by Nisar Ahmed, (1995).

eed size was reported to be dominant to small size and monogenic control Murthy and Reddy, 1996).

Jayalakshmi (1997) reported non-additive gene effects for kernel yield per plant nd pod yield per plant. She also reported both additive and dominance genetic effects for ature pod number.

Vindhiya Varman and Senthil (1998) studied combining ability studies in inter-sub specific crosses in groundnut. They observed that the variance due to sca was higher than gca for number of mature pods, pod yield, shelling out-turn and hundred kernel weight and indicated predominance of non additive gene action in Virginia x Spanish crosses. The worthiness of M 13 for more traits was revealed. Out of 30 crosses 11 combinations for shelling out turn and ten combinations for hundred kernel weight recorded significant sca effects.

Predominance of non-additive gene action was evident in semi-spreading x bunch crosses made by Senthil and Vindhiya Varman (1998) for mature pods, 100 kernel weight and pod yield. Importance of additive gene effects for shelling percentage was reported by Kumar and Patel (1999).

Vindhiya Varman (2000) reported greater sca variance than gca variance for the number of mature pods, pod yield, shelling outturn and oil content where as, the reverse was true for kernel weight in 30 F_1 groundnut hybrids studied. He has observed additive gene action for pod yield in two crosses involving JL 24 as male parent due to greater sca for these crosses which could be used for further selection to obtain high yielding progenies. Seven out of the fifteen crosses observed to have significant reciprocal effect for the traits, pod yield and oil content indicating maternal effect on these economic traits.

Non-additive gene action for number of mature pods was found to be predominant in the studies of Mathur *et al.* (2000). Dobaria *et al.* (2004) observed non-significance of genetic components and indicated that additive-dominance variance was inadequate to explain the observed variation and the role of complex genetic systems governing pod yield and 100-kernel weight. They cautioned early generation selection and advocated postponing of selection to later filial generations to isolate superior large seeded genotypes.

Shelling out-turn is an important quality trait that determines the market value of bold seeded groundnut genotypes either for local consumption or for export purpose. Predominance of dominance genetic effects for shelling out-turn was observed by Dobaria *et al.* (2004) for all the crossed studied.

2.5.2 Physiological characters

There are conflicting reports concerning information on genetic control of harvest index in groundnut. Harvest index was reported to be governed by additive genes (Suresh Kumar, 1993, Nisar Ahmed, 1995; Jayalakshmi, 1997; Dwivedi *et al.*, 1998 and Nigam *et al.*, 2001), both additive and non-additive genes (Makne, 1992 and Vindhyavarman and Raveendran, 1994) and non-additive (Makne, 1992).

Devi (1997) during a genetic study on F_2 generation observed that most of the physiological characters (leaf area index, leaf area ratio, specific leaf area, and specific leaf weight) were under the control of non-additive gene action with an exception to crop growth rate, which was observed to be under the control of both additive and non-additive genes.

SLA in groundnut in a diallel study involving seven parents, Jayalakshmi *et al.* (1999) reported predominance of additive gene effects and identified breeding lines TMV 2, NLM and ICGV 86031 as good general combiners for SLA.

The significance of additive effects as observed by Nigam *et al.* (2001) contributing to SLA and harvest index in three crosses suggested that effective selection for SLA and harvest could be practiced even in the early generations in all the crosses.

2.5.3 Biochemical characters

Oil content showed additive gene action (Skyes and Michaels, 1986) as well as non-additive gene action (Basu *et al.*, 1987). Bansal *et al.* (1992) reported predominance of additive gene effects both for oil content and protein content in groundnut inter and intra growth habit crosses.

In most of the studies as observed by Reddy and Murthy (1994) both additive and non-additive genes action were important for inheritance of oil content in groundnut. Similarly they have observed the importance of both additive and non-additive gene action for inheritance of seed protein content.

Makne *et al.* (1994) reported that the analysis of variance for combining ability (gca) and sca mean squares were highly significant in F_1 and suggested that additive as well as non-additive gene effects were important for protein content. Highly significant differences observed among parents, F_1 crosses and parents vs F_1 crosses indicated that sufficient variation in protein content among genotypes. In F_1 generation 13 crosses had positive and highly significant sca effects and suggested that non-additive interallelic gene interactions were quite important in determining protein content.

Jayalakshmi (1997) reported that oil content showed both additive and non-additive gene action. Parmar *et al.* (2001a) reported preponderance of non-additive gene effects in the inheritance of oil content while additive and non-additive gene effects for protein content. They suggested that breeding procedures like pedigree and or biparental mating and exercising selection at later generations might be followed to mop up additive and non- additive gene effects of respective traits.

Parmar *et.al.* (2002) performed genetic analysis of oil and protein contents on 28 non-reciprocal diallel set of crosses involving eight bold seeded Virginia groundnut genotypes. The estimates of genetic components of variance indicated that dominance genetic effects were significant for oil content while additive and dominance components were significant for protein content in F_1 and F_2 generations. However dominance components were greater in magnitude than additive components suggesting the predominance of dominance in governing these two important quality attributes. They suggested that to breed for high protein and low oil content, breeding procedures, which effectively mop up non-additive variance like biparental mating or reciprocal recurrent selection scheme for simultaneous improvement of yield and protein may be adopted.

Findings of Dobaria *et al.* (2004) indicated that the confectionery qualities like sugar and protein contents are predominantly under additive gene action while pod yield and oil content are controlled by dominance. They suggested breeding procedures aiming to improve confectionery qualities and pod yield in a population should accumulate favourable additive genes while simultaneously maintaining the heterozygosity. Population improvement procedures as followed in other self-pollinated crops may be difficult to apply in groundnut owing to the difficulties associated with cleistogamous inflorescence of groundnut. However use of recurrent selection scheme as followed in other self-pollinated crops (Hanson *et al.*, 1967) was suggested to improve the protein and sugar content.

Isleib *et al.* (2004) observed that GCA for oil content was closely followed values of the parental lines and reciprocal cross differences for starch and sugar contents suggesting influences of cytoplasmic genes on these traits.

2.6 HETEROSIS

Heterosis is a complex biological phenomenon often manifested in the superiority of a hybrid over parental forms according to the rate of development of one or complex characters (Konarev, 1974). With the realization of the possibility of producing F_1 hybrids on a large scale, increasing attention has been given to heterosis in self-pollinated crops (Hays and Foster, 1974).

2.6.1 Morphological characters

Wynne *et al.* (1970) reported higher levels of heterosis for vegetative characters in the crosses involving Valencia x Virginia and greater degree of heterosis for yield and fruit characters in the crosses involving Valencia x Spanish types.

Heterosis over mid parent in certain crosses for pod and seed size, pod and seed number and shelling percentage was reported by Garet (1976). High hererosis over mid and better parent was observed in groundnut by Sridharan and Marappan (1980) for number of mature and immature pods per plant, 100 kernel weight and pod yield.

Arunachalam *et al.* (1982) identified heterosis in majority of the crosses involving parents with high and low general combining abilities. Heterosis was recorded over the mean parental value for pod yield, pod size and seed yield.

Isleib and Wynne (1983) measured heterosis as a deviation of the F_1 performance from the mean parental value, and also observed heterosis for all traits studied. Heterosis up to 19 per cent above the better parent occurred for pod size. They opined that for pod and seed yield dominance was the more important source of non-additive genetic variation, while epistasis was more important for pod and seed number. They also found a linear and increasing relationship of heterosis to divergence between parents, for the traits, which exhibited more dominance while, for the others a curvilinear relationship was observed.

Negative heterosis in most of the crosses for the characters for 100 kernel weight and pod yield per plant and positive heterosis was found for shelling outturn (Sivakumar, 1984).

Arunachalam *et al.* (1984) studied heterosis in relation to genetic divergence. They concluded that the frequency of heterotic crosses and the magnitude of heterosis for yield and its components were high in crosses between parents in intermediate divergence classes than the extreme ones. Deshmukh *et al.* (1986) also suggested that genetic divergence of parents was most important for greater magnitude of heterosis. Arunachalam and Bandyopadhyay (1986) postulated that the chances of high frequency and magnitude of heterosis were greater in crosses between parents with high genetic divergence.

The significant positive heterotic effects for fruits per plant in several crosses as suggested by Dwivedi *et al.* (1989) was due to predominance of non-additive genetic effects.

Reddi et al. (1989) in a 6 x 6 diallel analysis reported that heterosis was positive for mature pods per plant, pod yield and kernel yield. For most of the yield components they observed that Spanish X Virginia combination resulted in positive heterosis and heterosis was comparatively higher in magnitude when Spanish lines were used as ovule parents.

For kernel weight per plant Vanisree (1992) recorded high positive heterosis. Bansal *et al.* (1993) recorded positive and significant heterosis for mature pods per plant. Positive and significant heterosis was reported by Dwivedi *et al.* (1994) for pod weight per plant.

Prasad (1996) indicated that greater heterosis than that of the best parent was expressed for pod size in intrasubspecific crosses and heterosis in pod and seed yield was primarily due to dominance, but epistasis was more important in heterosis for pod and seed number and protein content.

Jayalakshmi (1997) reported high average heterosis for kernel yield followed by mature pods per plant. High heterobeltiosis for mature pods, 100-kernel weight and yield were observed by Senthil and Vindhiya Varman (1998a) in inter sub-specific crosses of groundnut. They opined that although there was no feasibility of exploiting hybrid vigour in groundnut owing for constraints in the production of large scale F_1 seeds if heterosis is due to epistatic gene action, particularly additive x additive type or due to linked loci exhibiting partial or complete dominance, it should be possible to fix allele at the interacting loci to preserve the heterotic effect in the pure lines isolated from such populations. The allopolyploidy of this crop will also favour preservation of such fixed hybrid vigour for a considerable number of generations.

2.6.2 Physiological characters

Swe and Branch (1986) reported that crosses of Spanish x runner type parents showed negative heterosis for harvest index. Positive and significant heterosis for harvest index was reported by Nisar Ahmed (1995).

Madhavi (1988) reported positive heterosis for LAI in most of the crosses over the better parents and negative heterosis for LAI in the F_1 s involving Valencia or Spanish variety as female parent. Almost all the F_1s were observed to be heterotic as compared with their better parents for SLW. None of the crosses were positively heterotic for harvest index. SLA was the least heterotic character among various physiological characters studied by Jayalakshmi (1997).

2.6.3 Biochemical characters

Positive and significant heterosis was reported for oil content by Makne and Bhale (1991). Low average heterosis was reported for oil by Jayalakshmi (1997). Parmar *et al.* (2001) observed very low mid-parental heterosis (0.72 –6 %) for oil compared to the protein content in majority of the crosses.

CHAPTER III

MATERIAL
AND
METHODS

CHAPTER – III

MATERIALS AND METHODS

The experimental materials used and the methods followed during the course of present investigation are briefly described here under.

3.1 LOCATION OF THE EXPERIMENTAL SITE

The present investigation entitled "Genetic analysis of some morphological, physiological and biochemical characters in relation to yield and quality in groundnut (*Arachis hypogaea* L.)" comprised of two experiments. In the experiment-I, character association, variability and divergence were worked out on data obtained during the rainy season (*kharif*) of 2002. The experiment-II was executed during rainy season (*kharif*) of 2003 to estimate the heterosis and combining ability effects of crosses generated during post rainy season (*rabi*) of 2002. Both the experiments were conducted at wetland block of S. V. Agricultural College farm, Tirupati, Acharya N. G. Ranga Agricultural University, which is located at an altitude of 182.9 m above mean sea level on 79^0 E longitude and 13^0 N latitude and situated in the Southern Agroclimatic Zone of Andhra Pradesh. According to the Troll's climatic classification, the experimental site falls under Semi Arid Tropics (SAT).

3.2 WEATHER DURING THE CROP PERIOD

Data on two crucial weather parameters in the present investigation; rainfall and soil temperature were observed during *kharif*, 2002 and 2003. The rainfall data pertaining to the crop period recorded at S.V. Agricultural College Meteorological Observatory are presented year wise separately (Appendix B and Fig. 1a and 1b). A total rainfall of 382.6

Fig. 1a: RAINFALL AND SOIL TEMPERATURE DURING *KHARIF*, 2002 (30.08.02-28.12.02)

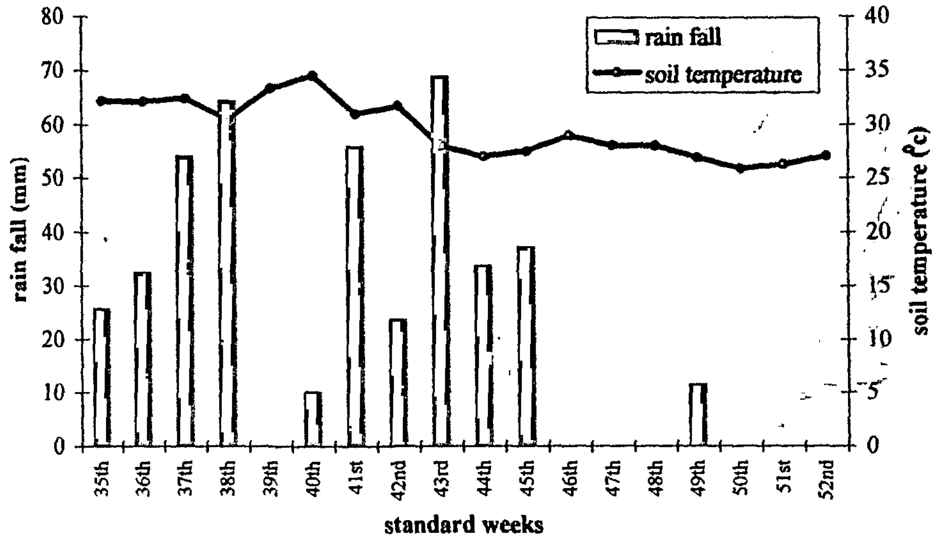
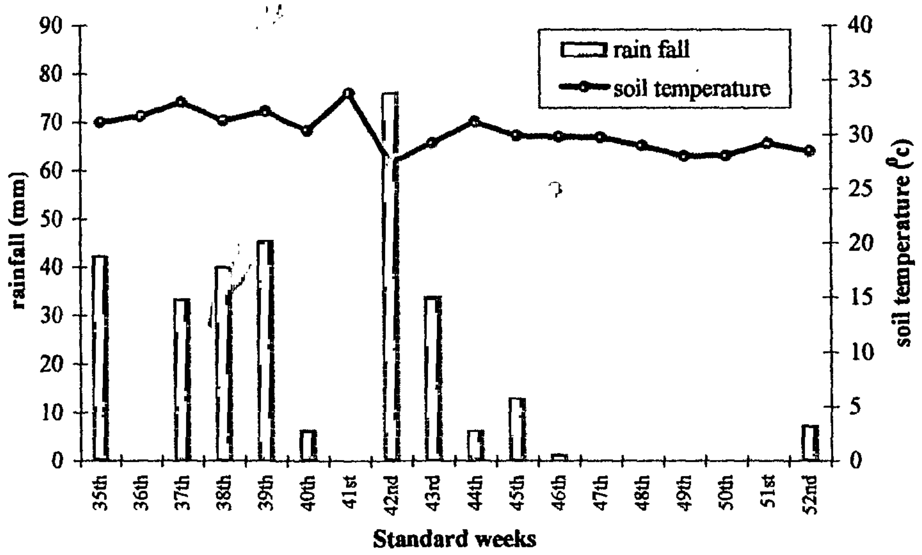


Fig. 1b: RAINFALL AND SOIL TEMPERATURE DURING *KHARIF*, 2003 (27.08.03-25.12.03)



mm was received in 27 rainy days during the crop period (*kharif*, 2002) against the decennial average of 598.17 mm in 31 rainy days. During the crop period of *kharif*, 2003 a total rainfall of 303.8 mm was received in 17 rainy days as against the decennial average of 583.42 mm in 31 rainy days. There were dry spells in between 10.11.02 to 7.12.02 for 27 days and between 14.11.03 and 25.12.03 for 41 days during crop growth periods in the two seasons respectively.

Soil temperatures at 10 – 15 cm depth were recorded at 7.12 LMT (7.00 IST) in the morning and at 2.12 LMT (2.00 IST) in the afternoon. The average soil temperature during the crop period of *kharif* 2002 was 29.5 ^{0}c. Where as during the crop period of *kharif* 2003 it was 28.67 ^{0}c.

3.3 SOILS

Soil samples were drawn from 0–30 cm depths of the experimental field at 10 random spots. They were analysed for different physico-chemical properties. The results of the analysis revealed that the soils were sandy loam in texture, slightly alkaline in reaction (p^H = 8.1) with normal EC (0.16 dS m^{-1} at 25^0 C). They were low in organic carbon (< 0.5 %), low in P_2O_5 (6.4 kg ha^{-1}) and medium in K_2O (112 kg ha^{-1}). The previous crop grown was groundnut during *kharif*, 2001.

3.4 MATERIALS

3.4.1 Plant material

The experimental material consisting 54 genotypes provided by ICRISAT, Patancheru; NRCG, Junagadh; BARC, Trombay; RARS, Tirupati and ARS, Kadiri are furnished in table 1 along with their salient features.

3.4.2 Pathogen

The virulent strain of the pathogen (*Aspergillus flavus)* was made available by the Department of Plant Pathology, RARS, Tirupati. It was considered to be aggressive and, toxigenic strain (plate 2).

3.5 METHODS

3.5.1 Field trials

Meticulous care was taken to provide common crop management methods during the two seasons of experimentation. The experimental plots during the two seasons were supplied with fertilizers at the rate of 30 kg N, 60 kg P_2O_5 and 45 kg K_20 per hectare. The crop was provided with irrigation at suitable intervals but was withheld between 80 and 100 days after sowing when the crops during two seasons were experiencing moisture stress. However, a life saving irrigation was given during the stress period in *kharif*, 2003. Necessary plant protection measures were taken during crop growth period on the plant but not as soil application. The mass multiplied inoculum of *A. flavus* was applied at 45 days after sowing by opening a furrow on a side of the plant row. As a matter of fact the fungus was mass multiplied by organic-matrix method as per the modified procedure given by Will *et al.*,(1994). Cracked pearl millet seeds were soaked in water overnight and sterilized in an autoclave at 121^{0}C for 15 min. A 5 mm disc of *A. flavus* from actively growing ten days old culture was transferred to the sterilized seeds and incubated at 25-30^{0}C for seven days. The cracked pearl millet seeds treated in this manner were applied at the rate of 2.5 g per one-meter length of the crop to facilitate the infection of the pathogen to the crop. Care was taken to keep the soil wet at the time of application of the fungus. After harvest, the pods were shade dried for seven days and stored in a galvanized iron container.

Table 1: Salient features of 54 groundnut genotypes during *kharif*, 2002

S. No.	Genotype	Botanical group	Pedigree	Source	Salient features
1	ICG 50 (RS 148)	Valencia	---	India	Low protein
2	ICG 1326 (J11)	Spanish	Ah 4218 x Ah 4354	India	Aflatoxin and collar rot resistant
3	ICG 1416 (A 27)	Spanish	---	Sudan	High protein
4	ICG 2184 (AH 3524)	Spanish	---	India	Low protein
5	ICG 2411 (Guthikdadal)	Spanish	---	India	High oil and low protein
6	ICG 3245 (TS 38)	Spanish	---	Zaire	High oil
7	ICG 3509 (US 9)	Valencia	---	Argentina	High protein
8	ICG 3542 (2-2)	Spanish	---	India	Low oil
9	ICG 3643 (Ndalo)	Spanish	---	Tanzania	---
10	ICG 4749 (PI 337394 F)	Spanish	---	Argentina	Aflatoxin resistant
11	ICG 4893 (AH 7763)	Spanish	---	Argentina	Low oil
12	ICG 5502 (AH 7763)	Valencia	---	Argentina	Low oil
13	ICG 6690 (Manyema)	Valencia	---	Zimbabwe	High protein
14	ICG 7332 (Cavalo)	Virginia	---	Brazil	Low oil
15	ICG 7633 (UF 71513)	Valencia	---	USA	Aflatoxin resistant
16	ICG 7637 (M 107-74 K)	Virginia	---	Nigeria	High oil
17	ICG 7749 (M 380-72)	Virginia	---	Nigeria	High protein
18	ICG 8325 (NC 10243 B)	Virginia	---	USA	Bold seeded
19	ICG 8666 (Schwartz 21)	Spanish	---	Indonesia	Aflatoxin resistant
20	ICG 10352 (N12)	Spanish	---	Zimbabwe	Low protein
21	ICG 11386 (CS 1110)	Spanish	---	India	High oil
22	ICG 13938 (ICGS 5)	Spanish	---	ICRISAT	High oil
23	ICGV 86031	Spanish	(F334 A-B-14 X NC Ac 2214)	ICRISAT	Multiple resistance to spodoptera, lear miner, jassids and thrips
24	ICGV 86552	Virginia	[Robut 33-1 x NC Ac 2821) x NC 3033]	ICRISAT	Bold seeded
25	ICGV 86564	Virginia	(Ah 114 x NC Ac 1107)	ICRISAT	Bold seeded
26	ICGV 86584	Virginia	(Shulamit x AG 114)	ICRISAT	Bold seeded
27	ICGV 88448	Virginia	(*A. hypogaea* x *A. cardenasii*)	ICRISAT	Bold seeded

Table 1 (cont.)

S. No.	Genotype	Botanical group	Pedigree	Source	Salient features
28	ICGV 89214	Virginia	(ICGV 87123 x ICG 6150)	ICRISAT	Bold seeded
29	ICGV 96234	Virginia	ICGV 88448 (EMS)	ICRISAT	Bold seeded
30	ICGV 96235	Spanish	ICGV 88448 (EMS)	ICRISAT	Bold seeded
31	ICGS 11	Spanish	(Robut-33-1) selection	ICRISAT	Medium duration, high yielding
32	ICGS 21	Spanish	(Robut-33-1 x NC Ac 2698)	ICRISAT	Medium duration, high yielding
33	BAU 13 (Birsa Bold)	Spanish	---	Ranchi	Bold seeded
34	TG 39	Virginia	TAG 24 X TG 19	Trombay.	Early, large seeded, high harvest index
35	TG 40	Spanish	TAG 24 X TG 19	Trombay	Early, large seeded, high harvest index
36	TG 41	Spanish	TG 28 X TG 22	Trombay	Early, large seeded, high harvest index
37	TG 42	Spanish	TG 19 X TG 26	Trombay	Early, large seeded, high harvest index
38	TG 45	Spanish	---	Trombay	Early, large seeded, high harvest index
39	TG 49	Spanish	TG 28A X TG 26	Trombay	Early, large seeded, high harvest index
40	M 13	Virginia	Selection from NC 13	Junagadh	Bold seeded, tolerant to leaf spot,dark green and wax coated leaves
41	JL 24	Spanish	Selection from EC 94943	Jalagoan	Smooth pod, compact bearing, large green leaves, early duration
42	K 134 (Vemana)	Spanish	Kadiri 3 X JL 24	Kadiri	Tolerant to drought, collar rot and bud necrosis
43	TPT 1	Spanish	EC 106983/3A	Tirupati	Tolerant to drought, wax on leaves, high shelling
44	TPT 2	Spanish	GAUG 1 x NC Fla 14	Tirupati	Higher yields in rabi, strong peg strength
45	TPT 4	Spanish	JL 24/Ah 316/S	Tirupati	Medium bold seeds, tolerant to mid season drought
46	TCGS 29 (Narayani)	Spanish	JL 24/Ah 316/S	Tirupati	Early, medium bold seeds, drought tolerant
47	TCGS 61	Spanish	JL 24 X M 7	Tirupati	Bold seeded
48	TCGS 91	Spanish	JL 24 X EC 76446(292)	Tirupati	High sugar content
49	TCGS 320 (Kalahasti)	Spanish	TCG 1709/TCG 1518	Tirupati	Medium bold seeded, high oil, nematode resistant
50	TCGS 407	Spanish	Kadiri 3 X PI 350680	Tirupati	High oil
51	TCGS 584	Spanish	Selection from TCGS 153-1	Tirupati	Low aflatoxin
52	TCGS 596	Spanish	TCG 273/TCG 1518	Tirupati	High oil
53	TCGS 617	Spanish	TCG 273/TCG 1518	Tirupati	Bold seeded, high yielding
54	TCGS 634	Spanish	TPT 1 X ICGV 86398	Tirupati	High oil

Plate 1: Hybridization plot

3.5.1.1 *Experiment I (kharif, 2002).* Fifty four genotypes were grown in a randomized block design (RBD), replicated thrice during rainy season (*kharif*) of 2002. The crop was sown on 30.08.02. Each genotype was grown in two rows, each 4.5 m length with spacing of 45 cm X 15 cm. Five random plants per replication were uprooted at 30, 60 and 90 DAS for estimating physiological characters. Another five random plants per replication were used to record data on morphological and biochemical characters. Thus in all data were recorded for 31 plant characters.

3.5.1.2 *Hybridization (rabi, 2002).* Nine genotypes out of 54 were selected as parents (selection criteria explained under 3.5.5.6) for the crossing programme in Line X Tester mating design to generate 20 F_1s. Four lines and five testers were grown on raised bunds for convenience (plate 1). The length of the row was 5 m with an intra-row spacing of 20 cm. Three staggered sowings of the male parents were taken up at ten days interval to have synchrony in flowering between lines and testers. Crosses were effected on 25 plants for each line by hand emasculation and pollination to generate sufficient F_1 seed for various analyses.

3.5.1.3 *Experiment II (kharif, 2003).* Twenty F_1s (generated during *rabi*, 2002) alongwith their parents were raised in a randomized block design, replicated thrice during *kharif*, 2003. The crop was sown on 27.08.03. Each entry was raised in two rows of 4.5 m length. A spacing of 45 cm X 15 cm was adopted. Data were recorded on five random plants per replication on morphological and biochemical characters. Five random plants were picked up to record data on physiological characters at 30, 60 and 90 DAS. Based on the analyses carried out during *kharif*, 2002 observations were recorded on only the most important 14 plant characters (selection criteria is described under 3.5.5.6 in this chapter).

3.5.2 Data recording

Data for the following characters were recorded on sampled plants:

3.5.2.1 *Morphological characters*

3.5.2.1.1 *Shell volume per pod (cc):*

Ten random pods were shelled and their volume was estimated by water displacement method. It was expressed as cc per pod.

3.5.2.1.2 *Pod volume per pod (cc):*

The volume of ten random pods was estimated by water displacement method and expressed as cc per pod.

3.5.2.1.3 *Seed volume per pod (cc):*

Seeds from ten random pods were used to estimate seed volume by water displacement method and expressed as cc per pod.

3.5.2.1.4 *Free space in pod (cc):*

Seeds obtained from ten random pods were used to estimate seed volume per pod by water displacement method. The seed volume per pod and shell volume per pod were subtracted from pod volume per pod to estimate free space in pod and expressed in cc.

Free space in pod = pod volume - shell volume - seed volume

3.5.2.1.5 *Shelling percentage (%):*

Shelling percentage was calculated using the following formula:

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

3.5.2.1.6 *Mature pods per plant:*

The mean value of total number of mature pods stripped from five random plants gave the number of mature pods per plant.

3.5.2.1.7 *Immature pods per plant:*

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

3.5.2.1.8 *100 seed weight (g):*

Hundred random seeds were counted and weighed on an electronic balance (0.01 g graduation) for each genotype in each replication.

3.5.2.1.9 *Pod weight per plant (g):*

Weight of mature pods from five random plants was recorded and the mean was worked out for estimating pod weight per plant.

3.5.2.1.10 *Kernel weight per plant (g):*

Kernel weight per plant was derived from the mean value of kernel weight from five random plants.

3.5.2.1.11 *Shape of kernel*:

Shape of kernels, an important quality parameter was recorded as per the scale (1-5) suggested by Misra *et al.* (2000). An elongated shape was considered the best and was accordingly given a rating of 1 while round (spherical shape) was assigned the lowest rating.

3.5.2.1.12 *Seed size uniformity*:

Seed size uniformity is a quality character and was measured as per the scale (1-10) provided by Misra *et al.* (2000). A rating of 1 was assigned to the genotype, which gave the maximum uniformity in size of kernels and a rating of 10 to that which, showed maximum variation in size, i.e., a mixture of small-medium-large kernels.

3.5.2.1.13 *Testa colour*:

The colour code for testa was assigned to the genotypes by visually comparing the colour of testa with those given by Nigam *et al.* (2004). Pink to light brown testa colours were considered desirable (Nigam *et al.*, 1989) and were given a rating of 1, where as dark red to purple as undesirable and were assigned a rating of 10.

3.5.2.2 *Physiological characters*

The basic data on leaf area, leaf weight and total dry matter weight (without roots) were used to calculate the following growth parameters.

3.5.2.2.1 *Specific leaf area (cm^2 g^{-1}):*

Specific leaf area (SLA) was recorded at 30, 60, and 90 days after sowing. Eight leaves (3rd fully expanded leaf from the top on the primary branch) were collected from each treatment in each replication for calculating SLA. These leaves were cleaned and their leaf area was estimated using a leaf area meter (LI-COR Model – 3100). They were dried in a hot air oven at 80 °c and dry weight recorded. The formula used was:

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

3.5.2.2.2 *Specific leaf weight (g cm^{-2}):*

Specific leaf weight (SLW) was recorded at 30, 60 and 90 days after sowing as follows:

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

3.5.2.2.3 *Crop growth rate (g m^{-2} day^{-1}):*

Crop growth rate (CGR) was recorded at 60 and 90 days after sowing using the formula:

$$\text{CGR} = \frac{w_2 - w_1}{t_2 - t_1} \text{ X } \frac{1}{p}$$

Where, w_1 and w_2 are the plant dry weights per square meter at times t_1 and t_2 respectively and p is the land area.

3.5.2.2.4 *Leaf area ratio (cm^2 g^{-1}):*

Leaf area ratio (LAR) was estimated at 90 days after sowing as follows:

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

3.5.2.2.5 *Leaf area index:*

Leaf area index (LAI) was estimated at 90 days after sowing as follows:

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

3.5.2.2.6 *Harvest index:*

Harvest index (HI) was estimated after harvest using the formula:

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

3.5.2.2.7 *SPAD Chlorophyll Meter Reading (SCMR):*

SPAD Chlorophyll Meter Reading (SCMR) was recorded at 30 days after sowing with SPAD (Soil Plant Analytical Development) chlorophyll meter (SPAD-502, Minolta Corp., Ramsey, NJ). The instrument is a simple hand held and portable instrument which provides information on the relative amount of leaf chlorophyll. Measurements were made on the 3rd leaf on main axis of five randomly selected plants.

3.5.2.3 Biochemical characters:

Two days after drying, 20 grams of seeds of each genotype, replication-wise, were powdered in a blender and were used for recording the data on biochemical characters like protein, carbohydrate, reducing sugar and non-reducing contents. For estimating seed moisture percentage and oil percentage the seeds were not powdered. But for estimating aflatoxin content seeds were powdered after one month of storage and used.

3.5.2.3.1 *Seed moisture percentage:*

Seed moisture percentage was estimated from shade dried seeds using the formula:

$$\text{Seed moisture percentage} = \frac{\text{Shade dried seed weight - Oven dried seed weight}}{\text{Shade dried seed weight}} \times 100$$

3.5.2.3.2 *Oil percentage:*

Oil in the seed was estimated with the help of NMR (Nuclear Magnetic Resonance, Model New Port Analyser, Oxford Analytical Instruments, England) analyzer. About 12 – 15 g of oven dried seed samples (130^{0}C for one hour) were taken in a test tube and feeded into the analyzer and the oil content was recorded directly as percentage of oil. Precision of the NMR analyzer was 2 min; integration period was ± 2 units, which is equivalent to oil content of ± 0.1 %. A value of 48.4 % obtained with a groundnut variety, CoGN-4 was used as standard.

3.5.2.3.3 *Protein content (mg g^{-1}):*

Protein content in this study refers to the total protein content in the seed. The method of Lowry *et al.* (1951) was adopted for estimating protein content with Folin-Ciacalteu reagent. 500 mg of defatted (with hexane) seed sample was homogenized with 10 ml of cold 10 % TCA (Trichloro Acetic Acid). Seed sample in TCA was collected in a test tube and kept in ice for 15 min. The contents were centrifuged at 6,000 x g for 15 min. The pellet was washed thrice with 5 ml of TCA, 3 ml of hexane and 1 ml of acetone. It was suspended in 4 ml of 2 N NaOH, thoroughly mixed, and incubated at room temperature overnight. The contents were centrifuged at 3,500 x g for 15 min. Two ml of the supernatant was collected and the volume was made up to 10 ml with distilled water. Then 0.1 ml of the sample extract was used to estimate the protein content by adding 5 ml of alkaline copper sulphate solution. After 10 min., 0.5 ml of freshly prepared Folin-Ciacalteu reagent was added, thoroughly mixed and allowed to stand for 30 min. for colour development. The optical density was measured at 660 nm in a spectrophotometer against a reagent blank. 0.1 ml of distilled water was used in place of the sample in preparation of a blank. Standard curve was prepared with a range of 0 to 300μg ml^{-1} of bovine serum albumin and it was linear within the range (R^2 = 0.9793). The protein content (mg g^{-1}) of the sample was calculated substituting sample OD values in the formula derived from the graph (y = 0.0023 x). Where, y = OD value of the sample and x = concentration (μg ml^{-1}) of the protein.

3.5.2.3.4 *Carbohydrate content (mg g^{-1}):*

The supernatant obtained with TCA while extracting total proteins was directly used for the estimation of total carbohydrates using anthrone reagent as per the procedure described by Sadasivam and Manickam (1996). Anthrone reagent was prepared with 200 mg anthrone dissolved in 100 ml cold concentrated H_2SO_4 (95%). The total anthrone positive substances referred here include free sugars and polysaccharides. Anthrone reagent (4 ml) was added to 0.1 ml (made up to 1 ml with distilled water) of the sample solution, mixed well and the test tubes covered with aluminium foil were placed in a boiling water bath for 8 min. They were then cooled and the extinction was read at 630 nm against a reagent blank (1ml of distilled water). A set of standard glucose solutions (0 to 200μg ml^{-1}) was taken for standard curve preparation. From the linear graph (R^2 = 0.9783) a formula was derived (y = 0.0057 x). The sample OD values were substituted to arrive at carbohydrate concentrations (μg ml^{-1}). Total carbohydrate content was expressed in mg g^{-1} seed.

3.5.2.3.5 *Reducing sugar content (mg g^{-1}):*

Reducing sugar content includes some of the reducing sugars like, glucose, galactose, lactose and maltose. The method described by Nelson (1944) and modified by Somogyi (1952) was employed for estimating reducing sugars. Reagent A was prepared by mixing 4 ml of copper sulphate solution (15 g of $CuSO_4$ dissolved in a small volume of distilled water and one drop of H_2SO_4 was added then the volume was made up to 100 ml) and 96 ml of alkaline copper tartrate reagent (2.5 g anhydrous Na_2CO_3, 2 g of Na_2HCO_3, 2.5 g of potassium sodium tartrate and 20 g of anhydrous sodium sulphate were dissolved in 80 ml water and made up to 100 ml in a volumetric flask). Reagent B was prepared by dissolving 2.5 g of ammonium molybdate in 45 ml of distilled water adding 2.5 ml H_2SO_4. Separately 0.3 g of disodium hydrogen arsenate (Na_2HSO_4. $7H_2O$) was dissolved in 25 ml distilled water, and both solutions were mixed and placed in an incubator at 37^{0}C for 24 h.

500 mg of seed was grinded with mortar and pestle. Sugars were extracted with 5 ml of hot 80 % ethanol twice. The extract was centrifuged at 3,500 x g for 10 min. Supernatant was collected and the ethanol was evaporated by keeping the test tubes in a water bath at 80^{0}C for 3-4 h. Sugars collected at the base of the test tube were dissolved with 5 ml distilled water and thoroughly mixed. Aliquots of 0.5 ml of sample were pipetted out in separate test tubes and the volume was made up to 1 ml with distilled water. One ml of reagent A was added to the sample and placed in boiling water bath for 10 min. After cooling the test tubes, 1 ml of reagent B was added and the volume was made up to 8 ml with distilled water. The absorbance of the solution was measured in a spectrophotometer at 620 nm. The amount of reducing sugars was estimated using a standard graph (R^2 = 0.9921 and y = 0.011 x) prepared with glucose.

3.5.2.3.6 *Non-reducing sugar content (mg g^{-1}):*

Non-reducing sugars, which include sucrose, were extracted from alcohol and estimated by the method of Nelson (1944). The alcoholic extracts obtained during reducing sugars extraction were directly used for estimating non-reducing sugar content in groundnut seed. 3 ml of 3N HCl was added to the extract and kept in boiling water bath for 3 min. It was then cooled and neutralized with 30 % NaOH. 0.1 ml of the sample was drawn and made up to 1 ml with distilled water. The same method of estimation of reducing sugars was employed to estimate non-reducing sugar content.

3.5.2.3.7 *Aflatoxin content (ppb kg^{-1} seed):*

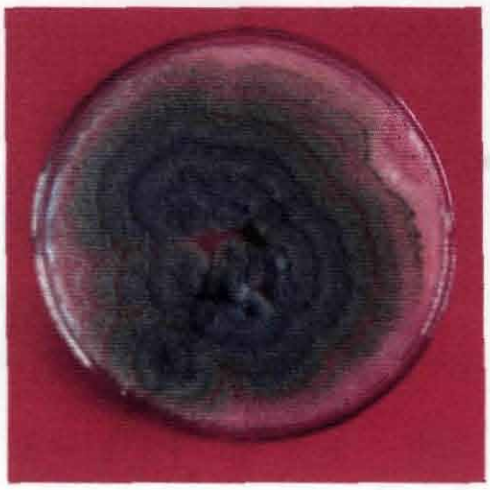
The pods after harvesting and shade drying were stored in a galvanized iron container under normal storage conditions. Aflatoxin content in groundnut kernels was estimated after one month of storage by indirect competitive Enzyme Linked immunosorbent Assay (ELISA) as per the procedure given by Reddy *et al.* (1988).

a) Sample extraction:

Fifty grams of seeds were collected at random and powdered. Twenty grams of this powder was grinded in a blender with 70 per cent methanol containing 0.5 g KCl. This extract was transferred to a conical flask and kept in a shaker for 30 min at 300 rpm. The extract was filtered through Whatman No.41 filter paper and the filtrate was collected in glass test tubes for estimating aflatoxin.

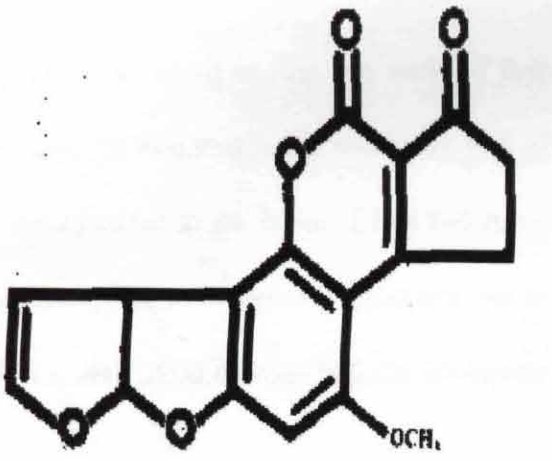
Health groundnut (HGN) extract was also prepared with the same extraction procedure and this is free from aflatoxin.

Infected groundnut pod



Pure culture of *Aspergillus flavus*

Mass multiplication



Aflatoxin, AFB$_1$ ($C_{17}H_{12}O_6$)

Plate 2: *Aspergillus flavus* and Aflatoxin

b) Aflatoxin estimation:

Coating:

ELISA plates were coated with 150 µl of AFB_1-BSA conjugate (1 µl AFB_1-BSA in 10 ml of 0.2 per cent carbonate buffer). They were incubated in an incubator at 37^0C for one hour. The plates were washed thrice with PBS-T 20 (phosphate buffer saline-tween) for three min.

Blocking:

To these plates, 160 µl of 0.2 per cent BSA (bovine serum albumin) was added and incubated at 37^0C for one hour. The plates were washed thrice with PBS-T 20.

Competition:

100 µl of pure toxin of AFB_1 (50 ng ml^{-1}) was added to first two wells of first column of ELISA plate. It was serially diluted from 50 to 0.9 µl in the remaining well of first row. Then 100 µl of diluted HGN extract was added to the wells of first two rows. The rest of the wells were loaded with 90 µl of BSA + 10 µl of sample extract that had to be analysed. Then 50 µl of pre incubated antiserum (1 : 2000 dilution in 0.2% BSA) was loaded to all wells of ELISA plate and kept in shaker for 10 min. The plate was incubated for one hour at 37^0C to facilitate reaction between toxin and antibody. It was then washed thrice with PBS-T20.

Conjugation:

150 µl of goat anti-rabbit IgG with labeled enzyme (alkaline phophatase) was loaded to all wells. Plates were incubated for one hour at 37^0C and then washed thrice with PBS-T20.

Substrate:

150 µl of substrate buffer [PNPP (P-Nitro Phenyl Phosphate) in 10 percent diethanolamine] was added to each well. Substrate alone was added to top left corner well of ELISA plate as blank. The plates were incubated at normal temperature in dark for colour development for 15 min. Absorbance was measured at 405 nm in ELISA reader. AFB_1 content was estimated by the following formula:

$$AFB_1 \text{ content} = \frac{AFB_1 \text{ conc. (mg ml}^{-1}\text{) in sample extract X (times dilution with buffer) X extract solvent volume used (ml)}}{\text{sample weight (g)}}$$

and expressed as ppb kg^{-1} seed.

3.5.2.3.8 *Seed colonization percentage.*

After one month of storage in a galvanized iron container, groundnut seeds were studied for seed colonization. Forty sound mature seeds with intact seed coat and free from any damage were selected from each genotype for *in vitro* inoculation by *A. flavus* according to the procedure given by Mixon and Rogers (1973). They were placed in a 250 ml beaker, soaked for 15 to 20 min. in sterile distilled water using two changes of approximately 100 ml each in the soaking process. After the second change, the water was drained from the seed and the sample was inoculated with one ml of spore suspension (4 X 10^6 spores ml^{-1}) obtained from 10 days old culture of *Aspergillus flavus* multiplied on AFPA medium. Seeds were plated on three layers of sterile blotting papers and kept in a petridish @ 10 seeds per plate. Sterile water was added to adjust the seed moisture to about 30 per cent. They were incubated in a humid chamber (98 % relative humidity) for seven days at 25^0C. The fungus infected seeds produced green coloured conidia on their rface. Seeds with infection were counted and the percentage of seed colonization was lculated with the following formula:

$$\text{Seed colonization percentage} = \frac{\text{Number of seeds infected}}{\text{Total number of seeds}} \text{ X } 100$$

3.5.3 Media used

A) Potato Dextrose Agar (PDA) medium was used for maintaining *Aspergillus flavus* culture throughout the experimental period.

Composition of PDA

Peeled potato slices	: 200 g
Dextrose	: 20 g
Agar	: 20 g
Distilled water	: 1000 ml

The medium was sterilized in an autoclave at 15 psi for 15 min.

B) The *Aspergillus flavus / parasiticus* Agar (AFPA) medium was used for estimation of *Aspergillus flavus* population in soil.

Composition of AFPA medium (Pitt, 1982)

Bacteriological peptone	: 10 g
Yeast extract	: 20 g
Ferric ammonium citrate	: 0.5 g
Chloramphenical	: 0.2 g
Agar	: 15 g
Dichloran	: 2 mg
Distilled water	: 1 l

3.5.4 Estimation of the fungal population in soil

Population of the fungus, *Aspergillus flavus* was estimated at three-times; once before sowing, second 10 days after soil inoculation and third after harvest to observe sufficient load of the pathogen in the soil to cause pre-harvest infection to the pods during both the seasons of experimentation by the method suggested by Johnson and Curl (1972).

3.5.4.1 *Soil sample collection.* The experimental plot in two seasons was divided into convenient number of blocks forming bunds for ease in irrigation. Each block comprised five genotypes of two rows each. About half a kilogram of soil was collected from each corner and center of all the blocks at 5 – 10 cm depth in pod zone. All the soil samples were composited and mixed thoroughly. A representative sample of ½ kg was drawn from the composite sample for use in estimating fungal population.

3.5.4.2 *Serial dilution method.* The representative soil sample was shade dried for three days. The dried sample was sieved through 1 mm sieve. 10 g of this soil was added to 90 ml of sterile distilled water and shaken thoroughly. One ml of this soil solution was taken and added to nine ml of sterile distilled water. This dilution was continued up to 10^{-4} dilutions. One ml of final diluted soil solution was added to sterile petriplates containing AFPA medium and incubated at 25± 1^0C for four days. Brilliant orange yellow colonies of *A. flavus* were observed and were counted. The number of colonies per plate was counted and multiplied with the dilution of the soil sample used and represented as number of colony forming units per gram of soil as follows:

Number of c.f.u. per gram of soil = Number of colony forming units per plate X 10^4

3.5.5 Statistical analyses

The data obtained on various quantitative characters were subjected for estimation of character association, variability, diversity and combining ability analyses.

3.5.5.1 *Analysis of variance.* Analysis of variance for each character was carried out by the method suggested by Panse and Sukhatme (1979). The significance was tested by referring to "F" table values of Fisher and Yates (1963).

3.5.5.2 *Estimation of genetic parameters.* GCV and PCV were calculated using the formulae suggested by Burton (1952). Heritability in broad sense was worked out according to the formula given by Allard (1960). Genetic advance and Genetic advance as percentage of mean were estimated as per the methods provided by Johnson *et al.* (1955).

- Genotypic coefficient of variation (GCV %) = $(\sigma_g / \overline{X}) \times 100$
- Phenotypic coefficient of variation (PCV %) = $(\sigma_p / \overline{X}) \times 100$

Where,

σp = Phenotypic standard deviation

σg = Genotypic standard deviation

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

Categorization of the range of variation was effected as proposed by Sivasubramanian and Menon (1973).

< 10%	-	Low
10-20%	-	Moderate
>20%	-	High

- Heritability in broad sense ($h^2_{(b)}$) = $\frac{\sigma^2_g}{\sigma^2_p} \times 100$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The heritability classification as high, moderate and low was followed as suggested by Stansfield (1969).

More than 50%	High
20-50%	Medium
Below 20%	Low

- Expected Genetic Advance (GA) = $(K) \cdot (\sigma p) \cdot (h^2_{(b)})$

Where,

GA = Expected genetic advance under selection

K = Selection differential in standard units which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

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

- Expected Genetic Advance as percentage of mean (GAM) = $(GA / \overline{X})$ X 100

Where,

GA = Expected genetic advance under selection

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

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

Less than 10%	Low
10-20%	Moderate
More than 20%	High

3.5.5.3 *Simple correlation coefficients.* Simple genotypic and phenotypic correlation coefficients of morphological and biochemical characters with kernel yield and aflatoxin content and that of physiological characters with kernel yield were calculated by using covariance technique (Falconer, 1964).

$$r(xi\,xj) = \frac{Cov(xi.xj)}{\sqrt{V(xi) \times V(xj)}}$$

Where,

$r(x_i\,x_j)$ = Correlation between ith and jth characters

Cov $(x_i\,x_j)$ = Covariance between ith and jth characters

$V(x_i), V(x_j)$ = Variance for the ith and jth characters

Significance of correlation was tested by referring to 'r' table values (Fisher and Yates, 1963).

3.5.5.4 *Path analysis.* Path coefficients were worked out for morphological and biochemical characters on kernel yield and on aflatoxin and that for physiological characters on kernel yield by solving the following simultaneous equations as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

$$r_{1y} = P_{1y} + P_{2y}r_{12} + P3yr13 + \ldots\ldots\ldots P_{ky}\,r_{1k}$$

Where,

r_{1y} = Simple correlation coefficient between x_1 and y

p_{1y} = Direct effect of x_1 on y

$p_{2y}r_{12}$ = Indirect effect of x_1 on y through x_2

$p_{3y}r_{13}$ = Indirect effect of x_1 on y through x_3

r_{12} = Correlation coefficient between x_1 and x_2

r_{13} = Correlation coefficient between x_1 and x_3

$p_{ky}r_{1k}$ = Indirect effect of x_1 on y through k variables

Similarly, equations for r_{2y}, r_{3y}, r_{4y} up to r_{ky} were written and path coefficients viz., direct and indirect effects were calculated.

The residual effect was calculated by using the formula,

$$R = \sqrt{1-\left(p_{1y}.r_{1y}+p_{2y}.r_{2y}+p_{3y}.r_{3y}+\ldots\ldots\ldots\ldots\right)^2}$$

Where,

R = Residual effect

P_{1y} = Direct effect of x_1 on y

R_{1y} = Correlation coefficient of x_1 and y

The direct and indirect effects were classified based on the scale given Lenka and Misra (1973).

More than 1.0 - very high

0.30 to 0.99 - high

0.20 to 0.29 - moderate

0.10 to 0.19 - low

0.00 to 0.09 - negligible

3.5.5.5 *Genetic divergence.* The genetic diversity among 54 genotypes for 15 morphological and biochemical characters and 13 physiological characters were estimated separately by using Mahalanobis D^2 Statistic (1936).

Multivariate analysis using D^2 statistic:

A measure of group distance based on multiple characters was given by Mahalanobis D^2 – technique (1936) with the help of which, genetic diversity between genotypes can be estimated. The D^2 value between i^{th} and j^{th} genotypes for 'P' characters was calculated as:

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

Where,

$\bar{Y}_{it}$ = Uncorrelated mean value of i_{th} genotype for (t) character

$\bar{Y}_{jt}$ = Uncorrelated mean value of j_{th} genotype for (t) character and

D^2_{ij} = D^2 between i_{th} and j_{th} genotype

The steps involved were,

<u>1. Test of significance</u>. was calculated from all the characters studied. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1977). From the estimates, a dispersion table was prepared. After testing the differences between genotypes for each of the characters, a simultaneous test of significance of differences between the mean values of a number of correlated variables was done (Rao, 1952) by using 'V' statistic, which in turn utilizes Wilks' 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 estimates of 'λ' (Wilks' criterion) were done using the following relation,

Where,

λ = Wilks' criterion

W = determinant of error matrix

S = determinant of error + variety matrix

$$\text{'V'}_{stat} = -m\log_e \lambda = -\left[n - \frac{p+q+1}{2}\right]\log_e \lambda$$

Where,

$$m = \frac{n-(p+q+1)}{2}$$

p = number of variables or characters

q = number of genotypes – 1

n = degrees of freedom of error + varieties

$\log_e \lambda$ = $2.3026 \log 10 \lambda$

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

2. Transformation of correlated variables. In the present model, computation of D^2 values was reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e., $\sum d^2 i$, therefore, transformation of correlated variables into standardized uncorrelated ones was done before working out D^2 values. Transformation was done using pivotal condensation method.

3. Computation of D^2 values. For a given combination of 'i' and 'j' genotypes the mean deviation, $\bar{Y}_{it} - \bar{Y}$ for t = 1, 2, ... P variables were computed and the D^2 values were calculated as sum of squares for the deviation i.e.,

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

4. Testing of significance of D^2 values. The D^2 values obtained for a pair of genotypes was taken as the calculated value of χ^2 and tested against tabulated χ^2 at 'P' degrees of freedom where 'P' is the number of variables or characters considered.

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

The first step in grouping the genotypes into different clusters was to arrange the genotypes in order based on their relative distances from each other. For this purpose, D^2

h, the two genotypes having the smallest distance from each other are considered to hich a third genotype having the smallest D^2 from the first two genotypes were added. milarly, the fourth one was chosen to have the smallest average D^2 from the first three d this procedure was continued. At certain stage when it was felt that after adding a rticular variety, there was an abrupt increase in the average D^2, then that variety was not nsidered for inclusion in that cluster. This process was continued till all the genotypes ere included into one or the other cluster. After the formation of the clusters, the average intra and inter cluster divergences were calculated by taking into consideration all the omponent D^2 values possible between the members of two clusters. The square root of the average D^2 value obtained from the above represent the distance 'D' between and within clusters.

3.5.5.6 *Selection criteria*

a) Selection of important characters

Not all the plant characters under all circumstances are helpful to a plant breeder in ormulating selection criteria for crop improvement. Also, selection criteria vary with lant material studied. Only a few of the humpty number of plant characters defined have elevance in solving specific crop problems. The problem identified in the present vestigation was improvement of aflatoxin resistance and yield in groundnut. As both the haracters are quantitatively inherited, indirect negative selection for aflatoxin content and ositive selection for kernel yield should be applied. Hence, data on 28 morphological, ysiological and biochemical characters contemplated to have some relevance in the present context were subjected to six biometrical techniques viz., correlations, path analysis, coefficients of variation, heritability, genetic advance and diversity to frame a selection criteria. Greater emphasis was given for characters association studies and the plant characters that had strong negative association with aflatoxin content and strong positive association with kernel weight per plant were selected (table 34). Then their importance was adjudged based on the extent of variability available, their heritability and genetic advance. Due importance was given to their contribution towards genetic divergence. Accordingly, 14 important characters were identified to formulate a selection criterion.

b) Selection of genotypes.

The nine genotypes identified for crossing programme were selected on the basis of significant mean values recorded for fourteen selected characters. The fourteen selected characters based on the association, variability and divergence analyses were assigned with arbitrary scores. Priority was given to low aflatoxin and a score of three was assigned to this character. A compromise was made on kernel weight per plant to avoid selection of aflatoxin susceptible genotypes and a score of two was given to it. The remaining 12 characters were assigned with a score of one. Thus the overall score was worked out to be 17. The genotypes with a total scoring more than 45 % ($\geq$ 7.65 score) of the overall score were considered superior than the rest and they were selected.

3.5.5.7. *Combining ability studies.*

Combining ability analysis in a line x Tester design was carried out following Kempthorne (1957). The mathematical model for combining ability analysis is given below.

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where,

y_{ijk} = Any measurable character of the cross i x j

g_i = gca effect of the 'ith' female parent

g_j = gca effect of the 'jth' male parent

s_{ij} = sca effect of the 'ixjth' cross

r_k = 'k^{th}' replication effect

e_{ijk} = Environmental effect particular to (ijk) individual

μ = Population mean effect

ANOVA for Line x Tester analysis

Source of variation	d.f.	SS	MSS	Expectations
Replications (*r*)	*r*-1	*r*SS	*r*MS	...
Entries (*en*)	*en*-1	*en*SS	*en*MS	...
Parents (*p*)	*p*-1	*p*SS	*p*MS	...
Females (*f*)	*f*-1	*f*SS	*f*MS	...
Males (*m*)	*m*-1	*m*SS	*m*MS	...
f vs. *m*	1	*fm*SS	*fm*MS	...
Hybrids (*c*)	*c*-1	*c*SS	*c*MS	...
Females in hybrids (*fh*)	*f*-1	*fh*SS	*fh*MS (M_l)	$\sigma^2 e + r\, Cov\,(FS) - 2\, Cov\,(HS) + mr\, Cov\,(HS)$
Males in hybrids (*mh*)	*m*-1	*mh*SS	*mh*MS (M_t)	$\sigma^2 e + r\, Cov\,(FS) - 2\, Cov\,(HS) + fr\, Cov\,(HS)$
fh x *mh* (L X T)	(*f*-1) (*m*-1)	*fmh*SS	*fmh*MS (M_{lxt})	$\sigma^2 e + r\, Cov\,(FS) - 2\, Cov\,(HS)$
p vs. *c*	1	*pc*SS	*pc*MS	...
Error (*e*)	(*e*-1) (*r*-1)	*e*SS	*e*MS (M_e)	$\sigma^2 e$
Total	(*er*-1)	TSS		

a. Estimation of combining ability effects

The individual effects are estimated as follows:

i) gca effect of line $g_i = \frac{x_{i}..}{tr} - \frac{x...}{ltr}$

ii) gca effect of tester $g_t = \frac{x_i}{lr} - \frac{x_{\cdots}}{ltr}$

iii) sca effect of crosses $s_{ij} = \frac{x_{ij\cdot}}{r} - \frac{x_{i\cdot\cdot}}{tr} - \frac{x_{j\cdot}}{lr} + \frac{x_{\cdots}}{ltr}$

Where,

$x_{i\cdot\cdot}$ = Total of female parent over all males and replications

$x_{j\cdot\cdot}$ = Total of male parent over all females and replications

$x_{\cdots}$ = Total of all cross combinations over all replications

$x_{ij\cdot}$ = It combination total over all replications

t = Number of testers

l = Number of lines

r = Number of replications

b. Estimation of standard errors for combining ability effects

The standard errors pertaining to gca effects of lines and testers and sca effects of different cross combinations were calculated as shown below:

S.E. $g_{(l)}$ lines $= \sqrt{\frac{\text{Error variance}}{rt}}$

S.E. $g_{(t)}$ testers $= \sqrt{\frac{\text{Error variance}}{rl}}$

S.E. $g_{(l \times t)}$ $= \sqrt{\frac{\text{Error variance}}{r}}$

S.E. $(g_l - g_t)$ line $= \sqrt{\frac{2\,\text{Error variance}}{rl}}$

S.E. $(g_l - g_t)$ tester $= \sqrt{\frac{2\,\text{Error variance}}{rt}}$

S.E. $(s_{lt} - s_{kl})$ $= \sqrt{\frac{2\,\text{Error Variance}}{r}}$

Cov. H.S. (line) = $M_l - M_{l \times t} / rt$

Cov. H.S (tester) = $M_t - M_{l \times t} / rl$

Cov. H.S (average) = $$\frac{1}{r(2lt - l - t)}\left[\frac{(l-1)(M_l) + (t-1)(M_t)}{l+t-2} - M_{l \times t}\right]$$

$$\text{Cov. (FS)} = \frac{(M_l - M_e) + (M_t - M_e) + (M_{l \times t} - M_e)}{3r} + \frac{6r\ Cov\ Hs - r(l+t)Cov.(HS)}{3r}$$

σ^2gca = $\text{Cov.HS} = \left(\frac{1+F}{4}\right)^2 \sigma^2 A$

σ^2sca = $M_{l \times t} - M_e / r$ or $\left[\frac{1-F}{2}\right]^2 \sigma^2 D$

σ^2gca : σ^2sca = $\frac{\sigma^2 gca}{\sigma^2 sca}$

3.5.5.8 ***Estimation of heterosis.*** The mean values of crosses were used for the estimation of heterosis percentage under three categories (Fonseca and Patterson, 1968). Estimates of heterosis were tested for significance at error degrees of freedom as suggested by Turner (1953).

a) Relative hetrosis (di)

The superiority of F_1 over mid parental value (Matzinger *et al.*, 1962) was estimated as follows,

di = $$\frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

't' for relative heterosis = $$\frac{\overline{F_1} - \overline{MP}}{\sqrt{\frac{Me}{r} \times \frac{3}{2}}}$$

b) Heterobeltiosis (dii)

The superiority of F_1 over better parent was estimated as follows,

$$\text{dii} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

$$\text{'t' for heterobeltiosis} = \frac{\overline{F_1} - \overline{BP}}{\sqrt{\frac{Me}{r} \times 2}}$$

c) Standard heterosis (diii)

The superiority of F_1 over the standard variety was estimated as follows,

$$\text{diii} = \frac{\overline{F_1} - \overline{SV}}{\overline{SV}} \times 100$$

$$\text{'t' for standard heterosis} = \frac{\overline{F_1} - \overline{SV}}{\sqrt{\frac{Me}{r} \times 2}}$$

The variety, TPT 4 was used as standard variety in the present study.

Where, .

$\overline{F_1}$ = mean value of hybrid

$\overline{MP}$ = value of mid parent

$\overline{BP}$ = mean value of better parent

$\overline{SV}$ = mean value of standard variety

Me = error variance

r = number of replications

CHAPTER IV

RESULTS

CHAPTER – IV

RESULTS

The results of two experiments conducted during the seasons, *kharif*, 2002 and *kharif*, 2003 are presented in this chapter. During the first season of experimentation data were recorded on 13 morphological, six biochemical and twelve physiological characters. Among the 31 characters studied, 14 characters that were contemplated to bear some association with aflatoxin content (a toxic substance produced by the fungus, *Aspergillus flavus*) were included in one group. They were pod volume, shell volume, free space in pod, shelling percentage, number of mature pods per plant, number of immature pods per plant, 100 seed weight, seed moisture percentage, oil percentage, protein content, carbohydrate content, reducing sugar content, non-reducing sugar content, pod weight per plant and kernel weight per plant. These characters were referred to as morphological and biochemical characters. Another group consisted of 12 physiological characters, which were SLA at 30 days, SLA at 60 days, SLA at 90 days, SLW at 30 days, SLW at 60 days, SLW at 90 days, CGR at 60 days, CGR at 90 days, LAR at 90 days, LAI at 90 days, SCMR at 30 days and harvest index.

The data recorded on these characters were subjected to character association, variability, heritability, genetic advance and divergence analyses. After I season of experimentation, a crossing programme in L X T fashion with nine parents was carried out during *rabi*, 2002. The 20 F_1 crosses bred along with nine parents were evaluated for their performance on 14 selected characters (pod volume, shell volume, free space in pod, shelling percentage, mature pods per plant, 100 seed weight, protein content, reducing sugar content, non-reducing sugar content, CGR at 60 DAS, CGR at 90 DAS, harvest index, aflatoxin content and kernel weight per plant) in the II season of experimentation. The data thus generated was used to estimate heterosis and combining ability effects.

As the crop was sown late, it experienced terminal moisture stress in both seasons of experimentation, which was required to establish an association of the pathogen with the developing pods. Water-deficit from 72 DAS to 99 DAS for 27 days and from 77 DAS to 118 DAS for 41 days during *kharif*, 2002 and 2003 respectively was utilized in imposing moisture stress in the end-of-seasons in both the years. Irrigations to the crop during the moisture stress period were withheld in first year while a life saving irrigation was given in the second year. During the two seasons (*kharif*, 2002 and *kharif*, 2003) of experimentation soil load of the pathogen, *A. flavus* was estimated before sowing, ten days after soil inoculation of the pathogen and a day after harvest. Initial population of the fungus during *kharif*, 2002 was 2.61 X 10^4 c.f.u. g^{-1} of soil and that during *kharif*, 2003 was 1.02 X 10^4 c.f.u. g^{-1} . The fungal population at 10 days after soil inoculation i.e. at 55 DAS in the two seasons (*kharif*, 2002 and *kharif*, 2003) was 15.03 X 10^4 c.f.u. g^{-1} and 12.97 X 10^4 c.f.u. g^{-1} respectively. A day after harvest, fungal population of 15.68 X 10^4 c.f.u. g^{-1} and 13.39 X 10^4 c.f.u. g^{-1} was observed during *kharif*, 2002 and *kharif*, 2003 respectively. This explains that the water stress and the soil load of the pathogen were sufficient to draw valid comparisons between the genotypes.

The experimental results are presented under appropriate sub headings as detailed hereunder.

4.1 MEAN PERFORMANCE

The mean performance of morphological and biochemical characters of group I are presented in table 2 and that of physiological characters of group II in table 4. The analyses of variance furnished in tables, 5 and 6 revealed the existence of significant

Table 2: Mean values of 54 groundnut genotypes for morphological and biochemical characters during *kharif*, 2002

S. No.	Genotypes	Shell volume (cc)	Pod volume (cc)	Free space in pod (cc)	Shelling per centage (%)	Mature pods per plant	Immature pods per plant	100 seed weight (g)	Seed mois-ture (%)	Oil per centage (%)	Protein content (mg g^{-1})	Carbo-hydrate content (mg g^{-1})	Reducing sugar content (mg g^{-1})	Non-reducing sugar content (mg g^{-1})	Afla-toxin content (ppb kg^{-1})	Kernel weight per plant (g)
1	ICG 50	0.90	2.03	0.40	67.69	18.67	4.43	33.56	10.10	51.97	179.92	120.57	0.60	10.80	88.33	12.03
2	ICG 1326	0.47	1.17	0.33	70.49	25.27	3.03	34.49	9.83	52.13	210.90	115.43	10.33	26.65	2.83	10.93
3	ICG 1416	1.23	2.10	0.20	68.39	17.10	7.47	34.10	9.80	50.70	247.72	124.31	0.40	4.37	34.00	9.03
4	ICG 2184	0.57	1.13	0.10	68.50	20.90	4.27	27.60	10.20	51.83	195.90	113.50	6.25	14.01	4.00	8.83
5	ICG 2411	0.47	1.37	0.30	71.22	23.63	4.33	31.09	10.03	52.77	212.99	123.31	1.52	25.27	4.83	10.63
6	ICG 3245	0.47	1.17	0.27	70.73	24.73	3.20	29.21	10.03	50.33	180.53	125.18	7.65	24.81	3.67	10.00
7	ICG 3509	1.40	3.17	0.53	65.58	16.93	3.53	36.33	10.23	49.73	238.61	118.63	3.00	21.82	75.50	10.33
8	ICG 3542	0.63	1.43	0.37	72.68	27.23	8.00	31.29	9.83	50.73	173.12	122.37	6.77	30.10	78.33	13.74
9	ICG 3643	0.57	1.50	0.37	68.66	24.73	3.60	28.03	9.97	50.17	235.76	123.77	0.80	12.18	8.83	10.11
10	ICG 4749	0.73	1.80	0.43	70.25	21.53	7.00	31.51	10.20	53.43	236.33	123.30	2.04	17.69	4.00	10.69
11	ICG 4893	0.53	1.93	0.77	72.11	24.50	10.93	32.15	10.47	53.90	220.96	121.91	0.12	12.41	5.00	12.47
12	ICG 5502	1.70	2.97	0.57	57.84	20.20	4.63	32.96	10.27	48.77	205.58	122.37	4.24	8.96	600.00	10.38
13	ICG 6690	1.17	2.80	0.87	60.99	13.80	3.10	30.27	9.83	49.90	178.82	125.64	4.45	10.57	21.67	7.78
14	ICG 7332	0.93	1.93	0.40	65.72	15.80	12.53	47.00	10.03	50.60	232.35	117.23	4.97	13.09	65.00	11.26
15	ICG 7633	1.23	2.73	0.73	70.83	25.03	4.93	32.03	9.60	52.23	194.76	120.97	3.72	38.59	12.00	14.24
16	ICG 7637	1.00	2.03	0.43	61.21	24.53	11.17	36.71	10.33	53.13	219.82	128.91	6.69	67.54	35.83	10.72
17	ICG 7749	0.97	2.23	0.53	63.95	21.73	15.03	40.74	10.83	50.37	206.72	126.11	2.92	27.57	20.00	10.97
18	ICG 8325	1.90	4.70	1.30	59.72	13.97	12.27	66.75	11.10	52.50	192.49	118.64	1.64	16.08	96.67	10.07
19	ICG 8666	1.00	2.40	0.43	62.85	17.73	6.60	33.22	11.07	51.47	190.21	117.70	0.16	2.76	3.67	11.08
20	ICG 10352	0.40	1.20	0.20	71.36	25.17	7.73	29.29	9.63	52.43	224.94	124.24	9.49	12.86	5.00	10.31
21	ICG 11386	0.90	2.03	0.27	59.60	32.10	17.50	47.59	10.50	53.53	230.07	113.03	1.76	5.97	12.00	13.83
22	ICG 13938	0.57	1.90	0.80	67.47	24.90	11.37	30.65	9.97	51.03	178.25	124.24	5.41	29.63	10.00	11.71
23	ICGV 86031	1.00	2.03	0.40	61.60	20.07	6.67	43.53	10.87	53.63	206.15	109.29	0.20	13.09	9.67	10.94
24	ICGV 86552	1.23	2.50	0.30	65.53	23.37	13.13	33.36	10.77	52.00	165.15	123.77	3.84	15.62	6.17	12.28
25	ICGV 86564	1.73	4.17	1.13	60.39	28.30	15.07	55.61	11.27	49.93	193.62	127.04	7.73	42.96	17.67	14.99
26	ICGV 86584	0.47	1.90	0.53	71.54	27.93	15.20	40.59	10.37	53.20	238.61	121.44	3.04	12.63	19.33	14.83
27	ICGV 88448	0.77	1.87	0.27	68.95	23.23	10.17	28.89	9.77	51.53	191.34	113.03	0.36	7.81	3.67	11.33
28	ICGV 89214	1.67	4.27	1.57	55.27	23.63	8.83	51.26	10.87	48.60	162.30	128.44	0.72	19.07	69.00	15.13
29	ICGV 96234	0.80	1.77	0.37	70.39	29.23	4.27	33.23	9.80	51.87	195.90	128.44	0.12	2.30	9.67	12.32
30	ICGV 96235	1.40	3.97	1.43	61.71	17.57	7.27	48.33	10.70	51.03	185.65	124.24	0.96	3.91	7.17	11.09
31	ICGS11	0.70	1.57	0.20	67.03	30.83	8.33	38.81	10.40	51.63	179.96	120.03	1.80	8.73	6.33	13.08
32	ICGS 21	0.77	2.17	0.80	64.28	25.17	12.53	33.83	10.13	52.23	206.72	126.11	1.00	16.77	269.67	11.25
33	BAU13	2.43	4.83	1.30	56.34	17.13	15.97	66.29	10.43	50.17	167.43	126.11	1.92	8.73	33.33	11.06
34	TG 39	0.97	2.67	0.93	65.99	18.00	9.07	52.17	10.13	52.63	233.49	131.71	2.12	4.37	5.67	10.86
35	TG 40	1.03	2.77	0.77	67.97	18.93	10.43	49.83	9.73	51.20	194.76	103.69	0.32	3.22	4.50	13.11

Table 2 (cont.)

S. No.	Genotypes	Shell volume (cc)	Pod volume (cc)	Free space in pod (cc)	Shelling per centage (%)	Mature pods per plant	Immature pods per plant	100 seed weight (g)	Seed mois- ture (%)	Oil per centage (%)	Protein content (mg g^{-1})	Carbo- hydrate content (mg g^{-1})	Reducing sugar content (mg g^{-1})	Non- reducing sugar content (mg g^{-1})	Afla- toxin content (ppb kg^{-1})	Kernel weight per plant (g)
36	**TG 41**	1.50	3.50	0.50	67.38	18.80	15.97	49.76	9.97	54.40	239.75	123.30	0.16	3.45	9.67	10.75
37	**TG 42**	1.73	4.23	1.30	66.80	16.10	13.00	63.87	10.27	51.07	171.98	127.51	6.21	4.14	20.83	11.78
38	**TG 45**	1.33	2.80	0.47	67.54	14.90	16.00	53.01	9.57	54.00	216.97	117.23	0.12	9.19	3.67	9.58
39	**TG 49**	1.43	3.10	0.73	62.64	18.13	15.57	52.97	10.10	51.33	194.76	119.57	1.16	22.97	3.67	10.79
40	**M13**	1.17	3.40	1.13	65.08	25.13	16.33	53.26	10.80	51.63	215.83	131.71	1.08	15.62	3.67	15.16
41	**JL 24**	1.07	2.43	0.37	66.86	23.53	6.33	35.21	9.90	51.93	218.11	105.56	0.48	19.30	4.50	12.38
42	**K 134**	0.87	1.60	0.10	70.56	23.70	6.20	29.48	9.90	51.60	203.88	125.64	0.20	6.20	3.67	11.22
43	**TPT 1**	0.90	1.80	0.13	68.11	25.53	5.90	34.48	9.80	48.53	246.01	122.37	6.45	18.84	28.33	12.81
44	**TPT 2**	1.20	2.27	0.20	68.36	19.13	7.40	35.55	10.40	50.20	189.64	116.30	2.00	9.65	11.00	10.82
45	**TPT 4**	0.77	2.40	0.53	69.43	25.20	7.00	41.11	9.80	49.60	232.35	104.62	2.96	6.66	3.67	15.23
46	**TCGS 29**	1.17	2.73	0.80	67.11	27.13	5.20	42.89	9.80	49.30	178.82	119.57	0.92	12.86	50.33	14.45
47	**TCGS 61**	2.23	3.40	0.43	59.29	25.87	10.10	54.29	10.63	52.27	169.14	127.04	2.48	25.27	626.67	14.29
48	**TCGS 91**	0.83	1.80	0.30	68.89	23.43	10.93	31.77	10.93	51.60	203.30	118.17	4.89	45.95	25.83	10.97
49	**TCGS 320**	1.27	2.40	0.57	68.37	24.77	11.80	31.54	9.90	52.63	173.69	121.44	0.16	3.22	21.50	13.10
50	**TCGS 407**	0.97	1.87	0.20	64.37	17.57	10.87	33.01	10.27	56.47	219.25	89.67	2.08	4.14	9.25	7.91
51	**TCGS 584**	1.00	2.73	0.87	66.79	12.97	4.23	46.78	9.97	49.63	238.04	119.10	2.16	9.65	5.00	8.68
52	**TCGS 596**	1.93	3.50	0.50	62.59	22.10	7.33	49.23	10.90	54.27	197.61	123.31	2.24	8.96	30.50	12.83
53	**TCGS 617**	1.83	3.90	1.03	62.84	19.10	11.67	58.85	10.37	53.27	226.08	122.84	4.12	30.32	12.92	13.59
54	**TCGS 634**	0.87	2.10	0.20	61.07	25.20	4.73	42.11	10.27	53.80	224.37	126.11	0.20	8.96	18.67	11.81
	Mean	**1.09**	**2.48**	**0.57**	65.90	**22.07**	9.08	40.58	**10.23**	51.88	**204.95**	**120.66**	2.76	15.89	47.15	11.69
	S.Ed	0.06	0.07	0.05	1.54	1.77	0.92	1.64	*0.11*	*0.40*	*8.47*	*4.22*	*0.27*	*1.40*	15.21	0.70
	C.D. 5%	0.16	0.19	0.15	4.33	4.97	2.59	4.60	0.30	1.13	23.75	11.82	0.77	3.91	42.64	1.96

differences among the genotypes for all the characters. The mean values along with rankings for morphological and biochemical characters related to quality are presented in table 3. The results on mean values for morphological and biochemical characters were discussed later in the chapter 4.3. However the results of morpho-biochemical characters related to quality and that of physiological characters are discussed in this chapter.

4.1.1 Morpho-biochemical characters related to quality

Fifty four groundnut genotypes were evaluated for some of the morphological and biochemical characters related to quality to ascertain their relative export worthiness (table 3). The genotypes differed significantly in their kernel weight per plant, shelling percentage, 100-seed weight, aflatoxin content, oil percentage, protein content, reducing sugar content and non-reducing sugar content. The results on relative ranking of genotypes for these characters and scores for seed size uniformity, testa colour and shape of kernel are presented as follows.

4.1.1.1 ***Kernel weight per plant.*** The order of ranking given for 54 genotypes for kernel weight per plant revealed that TPT 4 (15.23 g) was the best genotype and it was followed by M 13 (15.16 g), ICGV 89214 (15.13 g), ICGV 86564 (14.99 g) and ICGV 86584 (14.83 g) in that order.

4.1.1.2 ***Shelling percentage.*** The genotype ICG 3542 (72.68 %) ranked first for shelling percentage and the genotypes in descending order were ICG 4893 (72.11%), ICGV 86584 (71.54%), ICG 10352 (71.36%) and ICG 2411 (71.22%). Eleven genotypes recorded more than 70% shelling. Notable among them were ICG 7633, ICG 3245, K 134 and ICG 1326.

Table 3: Mean values of 54 groundnut genotypes for morphological and biochemical characters related to quality

S. No.	Genotypes	Kernel weight per plant (g)	rank	Shelling percentage (%)	rank	100-seed weight (g)	rank	Seed size uniformity score	Testa colour score	Shape of kernel score	Rank total for morphological characters
1	ICG 50	12.03	21	67.69	22	33.56	34	1	7	2	87
2	ICG 1326	10.93	35	70.49	9	34.49	30	1	1	4	80
3	ICG 1416	9.03	50	68.39	17	34.10	32	2	8	4	113
4	ICG 2184	8.83	51	68.50	16	27.60	54	2	1	5	129
5	ICG 2411	10.63	42	71.22	5	31.09	46	3	1	4	101
6	ICG 3245	10.00	48	70.73	7	29.21	51	4	1	4	115
7	ICG 3509	10.33	44	65.58	33	36.33	27	1	8	4	117
8	ICG 3542	13.74	10	72.68	1	31.29	45	2	1	4	63
9	ICG 3643	10.11	46	68.66	15	28.03	53	1	1	4	120
10	ICG 4749	10.69	41	70.25	11	31.51	44	2	1	4	103
11	ICG 4893	12.47	17	72.11	2	32.15	40	1	1	5	66
12	ICG 5502	10.38	43	57.84	52	32.96	39	5	10	3	152
13	ICG 6690	7.78	54	60.99	47	30.27	48	3	8	3	163
14	ICG 7332	11.26	26	65.72	32	47.00	17	2	10	4	91
15	ICG 7633	14.24	8	70.83	6	32.03	41	1	1	2	59
16	ICG 7637	10.72	40	61.21	45	36.71	26	7	3	3	124
17	ICG 7749	10.97	33	63.95	38	40.74	23	6	3	3	106
18	ICG 8325	10.07	47	59.72	49	66.75	1	9	4	1	111
19	ICG 8666	11.08	30	62.85	39	33.22	37	2	3	4	115
20	ICG 10352	10.31	45	71.36	4	29.29	50	1	1	5	106
21	ICG 11386	13.83	9	59.60	50	47.59	16	2	2	3	82
22	ICG 13938	11.71	24	67.47	24	30.65	47	1	1	5	102
23	ICGV 86031	10.94	34	61.60	44	43.53	19	4	4	3	108
24	ICGV 86552	12.28	20	65.53	34	33.36	35	3	1	4	97
25	ICGV 86564	14.99	4	60.39	48	55.61	5	4	2	1	64
26	ICGV 86584	14.83	5	71.54	3	40.59	24	5	2	4	43
27	ICGV 88448	11.33	25	68.95	13	28.89	52	3	1	4	98

Table 3 (cont.)

S. No.	Genotypes	Kernel weight per plant		Shelling percentage		100-seed weight		Seed size uniformity	Testa colour	Shape of kernel	Rank total for morphological characters
		(g)	rank	(%)	rank	(g)	rank	score	score	score	
28	**ICGV 89214**	15.13	3	55.27	54	51.26	11	7	3	1	79
29	**ICGV 96234**	12.32	19	70.39	10	33.23	36	3	2	3	73
30	**ICGV 96235**	11.09	29	61.71	43	48.33	15	8	2	3	100
31	**ICGS11**	13.08	14	67.03	27	38.81	25	2	1	4	73
32	**ICGS 21**	11.25	27	64.28	37	33.83	33	3	2	3	105
33	**BAU13**	11.06	31	56.34	53	66.29	2	9	8	2	105
34	**TG 39**	10.86	36	65.99	31	52.17	10	5	2	2	86
35	**TG 40**	13.11	12	67.97	21	49.83	12	3	1	1	50
36	**TG 41**	10.75	39	67.38	25	49.76	13	6	2	3	88
37	**TG 42**	11.78	23	66.80	29	63.87	3	4	1	2	62
38	**TG 45**	9.58	49	67.54	23	53.01	8	5	1	2	88
39	**TG 49**	10.79	38	62.64	41	52.97	9	4	1	2	95
40	**M13**	15.16	2	65.08	35	53.26	7	9	2	2	57
41	**JL 24**	12.38	18	66.86	28	35.21	29	1	1	4	81
42	**K 134**	11.22	28	70.56	8	29.48	49	1	1	3	90
43	**TPT 1**	12.81	16	68.11	20	34.48	31	1	1	4	73
44	**TPT 2**	10.82	37	68.36	19	35.55	28	1	1	4	90
45	**TPT 4**	15.23	1	69.43	12	41.11	22	2	1	4	42
46	**TCGS 29**	14.45	6	67.11	26	42.89	20	1	8	4	65
47	**TCGS 61**	14.29	7	59.29	51	54.29	6	4	2	2	72
48	**TCGS 91**	10.97	32	68.89	14	31.77	42	3	1	4	96
49	**TCGS 320**	13.10	13	68.37	18	31.54	43	2	9	3	88
50	**TCGS 407**	7.91	53	64.37	36	33.01	38	3	9	4	143
51	**TCGS 584**	8.68	52	66.79	30	46.78	18	2	2	4	108
52	**TCGS 596**	12.83	15	62.59	42	49.23	14	7	3	3	84
53	**TCGS 617**	13.59	11	62.84	40	58.85	4	8	1	1	65
54	**TCGS 634**	11.81	22	61.07	46	42.11	21	1	2	5	97

S. No.	Genotypes	Aflatoxin content		Oil percentage		Protein content		Non-reducing sugar content		Rank* total for biochemical characters	Combined rank total
		(ppb kg^{-1})	rank	(%)	rank	(mg g^{-1})	rank	(mg g^{-1})	rank		
1	ICG 50	88.33	50	51.97	32	179.92	44	10.80	31	157	244
2	ICG 1326	2.83	1	52.13	34	210.90	23	26.65	9	67	147
3	ICG 1416	34.00	43	50.70	16	247.72	1	4.37	46	106	219
4	ICG 2184	4.00	11	51.83	29	195.90	32	14.01	23	95	224
5	ICG 2411	4.83	14	52.77	42	212.99	22	25.27	10	88	189
6	ICG 3245	3.67	9	50.33	13	180.53	42	24.81	12	76	191
7	ICG 3509	75.50	48	49.73	7	238.61	4	21.82	14	73	190
8	ICG 3542	78.33	49	50.73	17	173.12	49	30.10	6	121	184
9	ICG 3643	8.83	22	50.17	11	235.76	8	12.18	30	71	191
10	ICG 4749	4.00	10	53.43	46	236.33	7	17.69	18	81	184
11	ICG 4893	5.00	17	53.90	50	220.96	16	12.41	29	112	178
12	ICG 5502	600.00	53	48.77	3	205.58	27	8.96	38	121	273
13	ICG 6690	21.67	38	49.90	8	178.82	46	10.57	32	124	287
14	ICG 7332	65.00	46	50.60	15	232.35	11	13.09	25	97	188
15	ICG 7633	12.00	30	52.23	36	194.76	35	38.59	4	105	164
16	ICG 7637	35.83	44	53.13	43	219.82	17	67.54	1	105	229
17	ICG 7749	20.00	35	50.37	14	206.72	25	27.57	8	82	188
18	ICG 8325	96.67	51	52.50	39	192.49	37	16.08	20	147	258
19	ICG 8666	3.67	8	51.47	23	190.21	39	2.76	53	123	238
20	ICG 10352	5.00	16	52.43	38	224.94	14	12.86	27	95	201
21	ICG 11386	12.00	29	53.53	47	230.07	12	5.97	44	132	214
22	ICG 13938	10.00	27	51.03	19	178.25	47	29.63	7	100	202
23	ICGV 86031	9.67	26	53.63	48	206.15	26	13.09	24	124	232
24	ICGV 86552	6.17	19	52.00	33	165.15	53	15.62	22	127	224
25	ICGV 86564	17.67	32	49.93	9	193.62	36	42.96	3	80	144
26	ICGV 86584	19.33	34	53.20	44	238.61	5	12.63	28	111	154
27	ICGV 88448	3.67	7	51.53	24	191.34	38	7.81	41	110	208

S. No.	Genotypes	Aflatoxin content		Oil percentage		Protein content		Non-reducing sugar content		Rank total for biochemical characters	Combined rank total
		(ppb kg^{-1})	rank	(%)	rank	(mg g^{-1})	rank	(mg g^{-1})	rank		
28	**ICGV 89214**	69.00	47	48.60	2	162.30	54	19.07	16	119	198
29	**ICGV 96234**	9.67	25	51.87	30	195.90	31	2.30	54	140	213
30	**ICGV 96235**	7.17	21	51.03	18	185.65	41	3.91	49	129	229
31	**ICGS11**	6.33	20	51.63	28	179.96	43	8.73	40	131	204
32	**ICGS 21**	269.67	52	52.23	35	206.72	24	16.77	19	130	235
33	**BAU13**	33.33	42	50.17	10	167.43	52	8.73	39	143	248
34	**TG 39**	5.67	18	52.63	41	233.49	9	4.37	45	113	199
35	**TG 40**	4.50	13	51.20	21	194.76	34	3.22	52	120	170
36	**TG 41**	9.67	24	54.40	53	239.75	3	3.45	50	130	218
37	**TG 42**	20.83	36	51.07	20	171.98	50	4.14	48	154	216
38	**TG 45**	3.67	6	54.00	51	216.97	20	9.19	35	112	200
39	**TG 49**	3.67	5	51.33	22	194.76	33	22.97	13	73	168
40	**M13**	3.67	4	51.63	27	215.83	21	15.62	21	73	130
41	**JL 24**	4.50	12	51.93	31	218.11	19	19.30	15	77	158
42	**K 134**	3.67	3	51.60	26	203.88	28	6.20	43	100	190
43	**TPT 1**	28.33	40	48.53	1	246.01	2	18.84	17	60	133
44	**TPT 2**	11.00	28	50.20	12	189.64	40	9.65	34	114	204
45	**TPT 4**	3.67	2	49.60	5	232.35	10	6.66	42	59	101
46	**TCGS 29**	50.33	45	49.30	4	178.82	45	12.86	26	120	185
47	**TCGS 61**	626.67	54	52.27	37	169.14	51	25.27	11	153	225
48	**TCGS 91**	25.83	39	51.60	25	203.30	29	45.95	2	95	191
49	**TCGS 320**	21.50	37	52.63	40	173.69	48	3.22	51	176	264
50	**TCGS 407**	9.25	23	56.47	54	219.25	18	4.14	47	142	285
51	**TCGS 584**	5.00	15	49.63	6	238.04	6	9.65	33	60	168
52	**TCGS 596**	30.50	41	54.27	52	197.61	30	8.96	37	160	244
53	**TCGS 617**	12.92	31	53.27	45	226.08	13	30.32	5	94	159
54	**TCGS 634**	18.67	33	53.80	49	224.37	15	8.96	36	133	230

1.1.3 ***100 seed weight.*** Only three genotypes viz., ICG 8325 (66.75 g), BAU 13 6.29 g) and TG 42 (63.87 g) recorded 100 seed weight, which was more than 60 g. The eight genotypes that produced bold seeds weighing between 50-60 g in descending order of ranking were TCGS 617, ICGV 86564, TCGS 61, M 13, TG 45, TG 49, TG 39 and ICGV 89214.

4.1.1.4 ***Seed size uniformity.*** The ratings for seed size uniformity ranged from 1 to 9. Relatively more uniform seed size with less mixed sizes was observed in ICG 50, ICG 1326, ICG 3509, ICG 3643, ICG 4893, ICG 7633, ICG 10352, ICG 13938, JL 24, K 134, TPT 2, TCGS 29, and TCGS 634.

4.1.1.5 ***Testa colour.*** Pink to light brown testa colours were considered as the most desirable and dark red to black, the most undesirable. Accordingly the ratings for genotypes were assigned and they ranged from 1 – 10. Thirty four out 54 genotypes were observed to possess the desirable testa colours.

4.1.1.6 ***Shape of kernel.*** The ratings for shape of kernels were assigned from 1 – 5. Among 14 genotypes which had ratings better than the average of 3, ICG 8325, ICGV 86564, ICGV 89214, TG 40, and TCGS 617 possessed elongated kernel shape which was considered preferable to round kernel shape of the genotypes like ICG 2184, ICG 4893 etc.

The total ranking for the aforesaid morphological characters indicated that TPT 4 vith a total rank of 42 emerged as the best genotype for morphological characters related o quality. The genotypes, ICGV 86584, TG 40, M 13 and ICG 7633 closely followed it.

4.1.1.7 ***Aflatoxin content.*** Fourteen out of 54 genotypes contained < 5 ppb kg^{-1} seed aflatoxin content in their seed. The best genotype that had recorded the lowest aflatoxin content of 2.83 ppb kg^{-1} was ICG 1326. The next best genotypes were TPT 4, K 134, M 13, TG 49, TG 45, ICGV 88448, ICG 8666 and ICG 3245.

4.1.1.8 ***Oil percentage.*** Low oil percentage was considered to be desirable in Hand Picked and Selected (HPS) varieties. Accordingly the genotypes were ranked in the ascending order. The lowest oil percentage assigned with rank 1 was present in TPT 1 (48.53%). The other low oil containing genotypes were ICGV 89214 and ICG 5502. The rest of the genotypes recorded more than 49% of oil.

4.1.1.9 ***Protein content.*** Protein content was highest in the genotype, ICG 1416 (247.72 mg g^{-1}). TPT 1, TG 41, ICG 3509 and ICGV 86584 followed it. Twenty six genotypes recorded protein content higher than the general mean (204.95 mg g^{-1}).

4.1.1.10 ***Non-reducing sugar content.*** Average non-reducing sugar content was 15.89 mg g^{-1}. Almost 20 genotypes have recorded more than the average value. The best genotype, which ranked I was ICG 7637 which was followed by ICGS 91, ICGV 86564, ICG 7633 and TCGS 617.

The genotypes, TPT 4, TPT 1, TCGS 584, ICG 1326, ICG 3643, ICG 3509 and TG 49 were observed to be best rankers in the descending order when total ranking for biochemical characters were taken into consideration.

A combined rank totaling for both morphological and biochemical characters related to quality revealed the superiority of TPT 4 over other genotypes involved in the study. The other best four genotypes were M 13, TPT 1, ICGV 86564 and ICG 1326.

.1.2 Physiological characters

4.1.2.1 ***Specific leaf area.*** Specific leaf area (SLA) was recorded at three stages i.e., at 30, 60 and 90 days after sowing (DAS). Mean SLA at 30 DAS was very high (213.37 cm^2 g^{-1}) and declined steeply at 60 DAS (178.63 cm^2 g^{-1}). At 90 DAS an increase (196 cm^2 g^{-1}) was recorded. TG 39 recorded the highest SLA at 30 DAS (283.17 cm^2 g^{-1}). Nine other genotypes exhibited superior performance over general mean. For SLA at 60 DAS, ICG 8666 was the best, which recorded 247.1 cm^2 g^{-1} leaf area. Ten genotypes excelled over general mean for SLA at 60 DAS. It was TPT 4, the only superior performer over general mean for SLA at 90 DAS with 238.2 cm^2 g^{-1} specific leaf area.

4.1.2.2 Specific leaf weight. In general, specific leaf weight (SLW) recorded at 30, 60 and 90 DAS indicated a raise in weight from 30 DAS to 60 DAS and thereafter declined at 90 DAS. At 30 DAS, ICG 8325 (6.33 g cm^{-2}) excelled other genotypes in recording the highest values. Ten genotypes each at 30 DAS and at 60 DAS and only two at 90 DAS were significantly superior over mean. The genotype, ICGV 86031 recorded significant values in all the three stages for SLW.

4.1.2.3 Crop growth rate. Crop growth rate (CGR) was recorded only at two periods; one at 60 DAS (30 – 60 DAS) and the other at 90 DAS (60 –90 DAS). An increasing trend in majority of the genotypes was observed from 60 to 90 DAS. ICG 7749 (14.47 g cm^{-2} day^{-1}) and ICGV 86552 (20.55 g cm^{-2} day^{-1}) were the superior genotypes over their respective general means at 60 DAS and at 90 DAS respectively. More number of genotypes (22) recorded significant values at 60 DAS where as only seven genotypes were significant at 90 DAS.

kharif, 2002

S. No.	Genotypes	SLA at 30 DAS ($cm^2 g^{-1}$)	SLA at 60 DAS ($cm^2 g^{-1}$)	SLA at 90 DAS ($cm^2 g^{-1}$)	SLW at 30 DAS ($g cm^{-2}$)	SLW at 60 DAS ($g cm^{-2}$)	SLW at 90 DAS ($g cm^{-2}$)	CGR at 60 DAS ($g cm^{-2} d^{-1}$)	CGR at 90 DAS ($g cm^{-2} d^{-1}$)	LAR at 90 DAS ($cm^2 g^{-1}$)	LAI at 90 DAS	SCMR at 30 DAS	Harvest index	Pod weight per plant (g)
1	**ICG 50**	226.07	205.50	197.17	4.40	4.87	5.07	5.90	6.67	35.38	1.54	42.17	0.36	17.77
2	**ICG 1326**	214.13	208.53	214.97	4.80	4.80	4.67	5.40	9.11	41.86	2.04	41.37	0.34	15.50
3	**ICG 1416**	194.77	131.03	182.40	5.27	7.67	5.50	11.93	8.47	35.24	2.37	41.27	0.30	13.12
4	**ICG 2184**	183.70	171.30	193.23	5.47	5.83	5.20	7.95	7.96	34.32	1.84	39.80	0.29	14.54
5	**ICG 2411**	261.27	149.73	217.00	3.87	6.70	4.77	8.12	5.64	45.21	2.03	41.73	0.29	16.26
6	**ICG 3245**	218.03	211.13	208.43	4.80	4.77	4.80	9.58	11.59	46.69	3.25	40.57	0.28	14.12
7	**ICG 3509**	266.07	192.30	166.00	3.73	5.20	6.07	8.73	8.68	36.81	2.11	38.53	0.31	16.40
8	**ICG 3542**	222.13	173.27	202.17	4.53	5.77	4.97	5.26	18.56	41.56	3.21	41.97	0.35	17.92
9	**ICG 3643**	201.73	164.27	212.60	4.97	6.10	4.77	7.91	6.01	45.60	2.12	39.30	0.33	16.04
10	**ICG 4749**	173.23	197.50	220.03	5.77	5.17	4.57	4.80	16.03	50.82	3.50	36.80	0.29	14.87
11	**ICG 4893**	183.17	173.00	211.77	5.60	5.77	4.80	9.01	5.94	42.45	2.12	34.93	0.36	17.35
12	**ICG 5502**	214.63	187.73	189.10	4.70	5.33	5.37	11.07	5.31	31.93	1.77	42.33	0.32	16.95
13	**ICG 6690**	253.77	203.50	204.40	3.93	4.90	4.90	5.34	8.86	40.97	2.01	39.40	0.25	12.12
14	**ICG 7332**	160.03	157.10	206.00	6.27	6.37	4.90	4.89	10.58	51.28	2.68	44.77	0.27	15.77
15	**ICG 7633**	239.47	243.27	202.73	4.33	4.17	4.93	5.31	11.97	42.14	2.45	36.67	0.39	20.15
16	**ICG 7637**	172.27	159.17	169.47	5.83	6.30	6.17	13.66	6.97	34.29	2.30	42.47	0.35	17.45
17	**ICG 7749**	187.67	179.00	171.57	5.33	5.60	5.83	14.47	6.28	48.92	3.32	44.87	0.27	17.51
18	**ICG 8325**	158.07	170.20	188.40	6.33	5.87	5.30	8.29	8.11	42.34	2.37	44.40	0.38	16.83
19	**ICG 8666**	234.10	247.10	226.37	4.43	4.10	4.43	2.34	19.50	47.61	3.44	36.00	0.31	16.64
20	**ICG 10352**	166.23	175.57	191.53	6.03	5.67	5.23	6.83	6.40	39.29	1.75	39.60	0.32	14.46
21	**ICG 11386**	222.50	143.80	192.20	4.50	7.00	5.20	10.75	9.47	41.89	2.75	38.97	0.30	21.21
22	**ICG 13938**	229.47	121.03	192.23	4.37	8.47	5.20	4.70	11.78	46.60	2.54	41.63	0.33	17.40
23	**ICGV 86031**	184.27	138.03	151.30	5.43	7.30	6.63	6.59	7.88	38.76	1.88	45.50	0.35	17.09
24	**ICGV 86552**	170.23	214.10	180.17	5.87	4.73	5.60	2.47	20.55	51.54	3.87	41.93	0.36	21.75
25	**ICGV 86564**	224.03	177.10	203.50	4.57	5.67	5.00	6.19	11.97	51.09	3.12	44.23	0.38	26.65
26	**ICGV 86584**	192.70	180.60	194.80	5.17	5.57	5.30	8.16	10.46	48.70	2.99	45.30	0.29	20.73
27	**ICGV 88448**	229.83	172.43	155.83	4.33	5.83	7.10	9.54	9.38	34.41	2.18	40.10	0.35	17.77
28	**ICGV 89214**	222.00	173.93	215.87	4.50	5.77	4.63	5.83	14.19	50.68	3.42	40.53	0.41	27.36
29	**ICGV 96234**	211.83	173.33	215.80	4.73	5.77	4.63	9.90	10.54	36.23	2.39	41.77	0.33	17.48
30	**ICGV 96235**	223.70	148.77	177.57	4.47	6.73	5.63	13.47	5.47	49.85	3.16	44.50	0.34	17.99
31	**ICGS11**	209.23	239.03	174.17	4.77	4.23	5.77	7.88	6.92	39.02	1.92	40.57	0.39	20.16
32	**ICGS 21**	203.50	190.77	194.27	4.90	5.33	5.17	9.88	14.18	45.67	3.55	44.10	0.31	17.51
33	**BAU13**	218.23	178.63	211.47	4.57	5.67	4.90	4.62	13.60	49.37	2.94	40.80	0.32	23.60
34	**TG 39**	283.17	187.67	201.67	3.70	5.37	5.00	7.62	7.70	33.39	1.67	42.53	0.40	16.47
35	**TG 40**	208.77	173.30	194.20	4.80	5.80	5.17	5.25	12.90	36.21	2.19	42.90	0.44	19.30

Table 4 (cont.)

S. No.	Genotypes	SLA at 30 DAS ($cm^2 g^{-1}$)	SLA at 60 DAS ($cm^2 g^{-1}$)	SLA at 90 DAS ($cm^2 g^{-1}$)	SLW at 30 DAS ($g cm^{-2}$)	SLW at 60 DAS ($g cm^{-2}$)	SLW at 90 DAS ($g cm^{-2}$)	CGR at 60 DAS ($g cm^{-2}d^{-1}$)	CGR at 90 DAS ($g cm^{-2}d^{-1}$)	LAR at 90 DAS ($cm^2 g^{-1}$)	LAI at 90 DAS	SCMR at 30 DAS	Harvest Index	Pod weight per plant (g)
36	**TG 41**	230.23	170.47	183.87	4.33	5.87	5.47	8.89	9.14	21.20	1.28	44.10	0.38	15.97
37	**TG 42**	205.57	181.33	185.63	4.90	5.50	5.40	9.94	8.05	26.49	1.59	42.63	0.43	17.60
38	**TG 45**	247.37	170.87	202.80	4.10	5.97	4.93	7.52	5.44	27.12	1.20	41.07	0.39	15.17
39	**TG 49**	243.33	193.47	197.37	4.10	5.20	5.20	9.99	6.54	28.37	1.57	41.50	0.40	17.26
40	**M13**	233.83	170.17	226.33	4.33	5.87	4.50	7.49	9.25	47.49	2.69	42.67	0.36	24.29
41	**JL 24**	198.87	222.80	192.30	5.03	4.53	5.20	7.51	10.15	42.61	2.52	40.97	0.33	19.23
42	**K 134**	200.53	153.93	170.73	5.00	6.53	6.00	5.95	12.68	36.22	2.22	41.30	0.28	14.60
43	**TPT 1**	187.90	139.03	174.27	5.30	7.20	5.77	8.03	18.70	44.04	3.82	40.53	0.33	20.15
44	**TPT 2**	259.87	232.93	187.23	3.87	4.27	5.37	10.58	7.28	43.42	2.58	41.03	0.28	17.50
45	**TPT 4**	163.43	182.87	238.20	6.10	5.50	4.30	9.94	8.84	47.45	3.02	38.03	0.32	21.93
46	**TCGS 29**	202.77	199.93	190.10	4.93	4.97	5.30	12.43	6.50	36.71	2.34	36.23	0.31	19.22
47	**TCGS 61**	192.87	178.17	190.27	5.20	5.63	5.30	12.02	9.05	41.84	2.82	39.33	0.35	24.72
48	**TCGS 91**	226.57	204.63	216.20	4.40	4.90	4.70	9.10	12.93	47.45	3.43	44.00	0.25	15.95
49	**TCGS 320**	211.40	133.77	227.57	4.73	7.50	4.43	9.69	9.13	40.99	2.56	38.93	0.32	21.50
50	**TCGS 407**	227.97	149.17	204.63	4.13	6.73	4.90	12.11	6.64	36.14	2.21	37.90	0.25	12.31
51	**TCGS 584**	248.13	159.67	189.07	4.03	6.27	5.33	8.81	6.13	19.51	0.94	42.80	0.35	12.68
52	**TCGS 596**	256.53	162.33	196.50	3.90	6.17	5.33	9.22	10.43	50.97	3.27	42.57	0.29	18.92
53	**TCGS 617**	230.20	159.33	188.10	4.37	6.27	5.37	9.16	6.89	38.85	2.06	41.97	0.35	27.64
54	**TCGS 634**	190.77	168.37	192.43	5.27	5.97	5.20	12.14	9.40	52.94	3.71	40.53	0.33	23.32
	Mean	**213.37**	**178.63**	**196.00**	**4.80**	**5.76**	**5.21**	**8.34**	**9.79**	**41.07**	**2.49**	**41.16**	**0.33**	**18.23**
	S.Ed	8.77	8.49	14.18	0.19	0.27	0.43	0.27	0.67	3.26	0.22	0.75	0.02	2.26
	C.D. 5%	24.60	23.81	39.76	0.54	0.75	1.20	0.75	1.88	9.15	0.62	2.09	0.06	6.33

Table 5: Mean sum of squares for morphological and biochemical characters

Source of variation	df	Mean squares														
		Shell volume	Pod volume	Free space in pod	Shelling %	Mature pods per plant	Immature pods per plant	100 seed weight	Moisture %	Oil %	Protein content	Carbohy-drate content	Reducing sugar content	Non-reducing sugar content	Aflatoxin content	Kernel weight per plant
Replications	2	0.02	0.02	0.02	20.61	8.8	2.73	8.72	0.16	0.03	2377.91	246.03	0.69	14.44	448.36	0.15
Genotypes	53	34.95**	2.62**	0.40**	54.87**	60.72**	52.93**	339.04**	0.55**	8.03**	1717.44**	169.53**	20.68**	475.75**	42802.81**	10.36**
Error	106	1.01	0.01	0.01	7.15	9.44	2.56	8.08	0.04	0.49	215.3	53.32	0.23	5.84	693.75	1.46

** Significant at 1 per cent level

Table 6: Mean sum of squares for physiological characters

Sourceof variation	df	Mean squares												
		SLA at 30 DAS	SLA at 60 DAS	SLA at 90 DAS	SLW at 30 DAS	SLW at 60 DAS	SLW at 90 DAS	CGR at 60 DAS	CGR at 90 DAS	LAR at 90 DAS	LAI at 90 DAS	Harvest index	SCMR at 30 DAS	Pod weight per plant
Replications	2	153.94	271.01	733.47	0.00	0.42	0.50	0.55	0.03	72.13	0.34	0.00	1.53	15.11
Genotypes	53	2535.81**	2382.55**	988.18**	1.34**	2.49**	0.86**	22.75**	42.04**	183.35**	1.52**	0.01**	18.32**	39.81**
Error	106	230.95	216.31	603.16	0.11	0.22	0.55	0.21	1.35	31.93	0.15	0.00	1.67	15.31

** Significant at 1 per cent level

4.1.2.4 Leaf area ratio. Leaf area ratio (LAR) was recorded only at 90 DAS. The genotype, TCGS 634 with 52.94 cm^2g^{-1} stood as the best genotype for LAR at 90 DAS. Six genotypes recorded significant values.

4.1.2.5 Leaf area index. Leaf area index (LAI) was also recorded at 90 DAS only. The highest value of 3.87 was recorded by the genotype, ICGV 86552 that was significant over the average. Eleven genotypes apart from ICGV 86552 were found to be significantly superior over the average (2.49).

4.1.2.6 SPAD chlorophyll metre reading (SCMR). Ten genotypes showed superior performance over the general mean (41.16) for SPAD chlorophyll metre reading (SCMR) recorded at 30 DAS. The best among them was ICGV 86031 (45.5).

4.1.2.7 Harvest index. Among the 54 genotypes studied only four exhibited better performance over general mean for harvest index. They were TG 39 (0.4), TG 40 (0.44), TG 42 (0.43) and TG 49 (0.4). The best among them was TG 40.

4.2 ASSOCIATION ANALYSIS

4.2.1 Correlation studies

4.2.1.1 *Correlations of morphological and biochemical characters with kernel yield*

Genotypic and phenotypic correlation coefficients for kernel yield with morphological and biochemical characters were estimated and the results are furnished in table 7. Genotypic and phenotypic correlations followed almost similar trend of association, the former being a little higher than the latter in most of the cases. As the

Table 7: Genotypic and phenotypic correlation coefficients for morphological and biochemical characters on kernel weight and aflatoxin content among 54 groundnut genotypes

Character	Correlation	Pod volume	Free space in pod	Shelling %	Mature pods per plant	Immature pods per plant	100 seed weight	Seed moisture %	Oil %	Protein content	Carbohydrate content	Reducing sugar content	Non-reducing sugar content	Aflatoxin content	Kernel yield per plant
Shell volume	g	0.9021	0.5806	-0.7707	-0.4191	0.3399	0.7461	0.4178	-0.1036	-0.3372	0.2306	-0.1739	-0.0276	0.3885	0.1486
	p	0.8972 **	0.5162 **	-0.6100 **	-0.3238 **	0.3075 **	0.7051 **	0.3666 **	-0.0993	-0.2749 **	0.1336	-0.1647 *	-0.0204	0.3705 **	0.1410
Pod volume	g		0.8355	-0.7232	-0.4400	0.4106	0.8415	0.4573	-0.1497	-0.2895	0.2714	-0.1998	-0.0544	0.1844	0.2421
	p		0.7945 **	-0.5882 **	-0.3470 **	0.3800 **	0.8054 **	0.4113 **	-0.1414	-0.2364 **	0.1669 *	-0.1948 *	-0.0518	0.1795 *	0.2076 **
Free space in pod	g			-0.5268	-0.3288	0.3200	0.6953	0.3551	-0.2542	-0.3251	0.3886	-0.0877	0.0251	0.0304	0.2708
	p			-0.4271 **	-0.2582 **	0.3046 **	0.6488 **	0.3116 **	-0.2224 **	-0.2709 **	0.2485 **	-0.0846	0.0187	0.0313	0.2118 **
Shelling percentage	g				0.3009	-0.3052	-0.6348	-0.6429	0.1242	0.2771	-0.1001	0.1423	-0.0450	-0.4164	-0.0887
	p				0.1398	-0.2291 **	-0.4666 **	-0.4929 **	0.0849	0.2111 **	-0.1552 *	0.1431	-0.0337	-0.3344 **	0.0495
Mature pods/plant	g					0.0191	-0.3428	-0.0021	0.0342	-0.0761	0.1715	0.1755	0.2904	0.0294	0.6497
	p					0.0017	-0.2824 **	-0.0170	0.0336	-0.0593	0.1031	0.1370	0.2179 **	0.0431	0.6106 **
Immature pods/plant	g						0.5822	0.3615	0.2995	-0.0211	0.0840	-0.1090	0.0616	-0.0472	0.2865
	p						0.5121 **	0.2798 **	0.2589 **	-0.0187	0.0418	-0.1026	0.0650	-0.0478	0.2295 **
100 seed weight	g							0.4044	0.0290	-0.0992	0.1899	-0.1343	-0.0793	0.0759	0.2708
	p							0.3662 **	0.0292	-0.0865	0.0954	-0.1267	-0.0774	0.0639	0.2415 **
Seed moisture percentage	g								0.0893	-0.2734	0.1919	-0.0657	0.1905	0.1233	0.2228
	p								0.0441	-0.1765 *	0.1202	-0.0518	0.1701 *	0.1086	0.1324
Oil percentage	g									0.2401	-0.2986	-0.2205	-0.0676	-0.1718	-0.1323
	p									0.1848 *	-0.1819 *	-0.2057 **	-0.0483	-0.1513	-0.1008
Protein content	g										-0.1924	-0.0337	-0.0482	-0.1828	-0.2132
	p										-0.1079	-0.0349	-0.0437	-0.1568 *	-0.1731 *
Carbohydrate content	g											0.1487	0.2610	0.1930	0.1999
	p											0.0976	0.1796 *	0.1141	0.0954
Reducing sugar content	g												0.5310	0.0232	-0.0571
	p												0.5174 **	0.0202	-0.0311
Non-reducing sugar content	g													0.0565	0.1639
	p													0.0514	0.1231
Aflatoxin content	g														0.0812
	p														0.0777

*Significant at 5% level **Significant at 1% level g = genotypic p = phenotypic genotypic correlations indicate the correlations of breeding values they were only referred as follows.

The genotypic correlations revealed that single plant kernel weight per plant recorded positive association with pod volume (0.2421), free space in pod (0.2708), mature pods per plant (0.6497), immature pods per plant (0.2865), 100 seed weight (0.2708), seed moisture percentage (0.2228), carbohydrate content (0.1999) and non-reducing sugar content (0.1639). The association of kernel weight per plant with protein content was negative (-0.2132). Kernel weight per plant did not establish any association with shell volume, shelling percentage, oil percentage, reducing sugar and aflatoxin contents.

4.2.1.2 *Correlations of morphological and biochemical characters with aflatoxin content*

Table 7 reads genotypic and phenotypic correlations of morphological and biochemical characters with aflatoxin content. The character, aflatoxin content, expressed positive association with shell volume (0.3885), pod volume (0.1844) and carbohydrate content (0.1930). Where as its relation with shelling percentage (-0.4164), protein content (-0.1828) and oil percentage (-0.1718) was negative. The other morphological and biochemical characters did not show any significant association with aflatoxin content.

4.2.1.3 *Inter correlations among morphological and biochemical characters*

4.2.1.3.1 Shell volume. Positive relationship was noticed between shell volume and the characters viz., pod volume (0.9021), free space in pod (0.5806), immature pods per plant (0.3399), 100 seed weight (0.7461), seed moisture percentage (0.4178), carbohydrate content (0.2306) and aflatoxin content (0.3885). Shell volume registered negative association with shelling percentage (-0.7707), mature pods per plant (-0.4191), protein content (-0.3372), and reducing sugar content (-0.1739).

4.2.1.3.2 Pod volume. Apart from shell volume (0.9021), free space in pod (0.8355), immature pods per plant (0.4106), 100 seed weight (0.8415), seed moisture percentage (0.4573) and carbohydrate content (0.2714) registered positive association with pod volume. Where as, negative relationship existed between pod volume and the characters like shelling percentage (-0.7232), mature pods per plant (-0.4400), protein content (-0.2895) and reducing sugar content (-0.1998).

4.2.1.3.3 Free space in pod. This character had positive correlation with shell volume (0.5806), pod volume (0.8355), immature pods per plant (0.3200), 100 seed weight (0.6953), seed moisture percentage (0.3551) and carbohydrate content (0.3886). It showed negative correlation with shelling percentage (-0.5268), mature pods per plant (-0.3288), oil percentage (-0.2542) and protein content (-0.3251).

4.2.1.3.4 Shelling percentage. Shelling percentage showed positive correlation with mature pods (0.3009) and protein content (0.2771). Where as its association was negative with most of the characters viz., shell volume (-0.7707), pod volume (-0.7232), free space in pod (-0.5268), immature pods per plant (-0.3052), 100 seed weight (-0.6348) and seed moisture percentage (-0.6429).

4.2.1.3.5 Mature pods per plant. Positive association was observed for mature pods per plant with shelling percentage (0.3009), carbohydrate content (0.1715), reducing sugar content (0.1755) and non-reducing sugar content (0.2904). Where as the correlations with 100 seed weight (-0.3428), shell volume, pod volume and free space in pod were negative.

4.2.1.3.6 Immature pods per plant. This character was positively associated with 100 seed weight (0.5822), seed moisture percentage (0.3615), oil percentage (0.2995), shell volume, pod volume and free space in pod but was negatively associated with shelling percentage (-0.3052).

4.2.1.3.7 100 seed weight. The character, 100 seed weight exhibited strong positive association with seed moisture content (0.4044), carbohydrate content (0.1899), shell volume, pod volume, free space in pod and immature pods per plant. However its association with shelling percentage and mature pods per plant was negative.

4.2.1.3.8 Seed moisture percentage. Seed moisture percentage registered positive correlation with carbohydrate content (0.1919), non-reducing sugar content (0.1905), shell volume, pod weight, free space in pod, immature pods per plant and 100 seed weight. Where as it expressed negative association with protein content (-0.2734) and shelling percentage.

4.2.1.3.9 Oil percentage. The character oil percentage was positively associated with protein content (0.2401) and immature pods per plant but negatively with carbohydrate content (-0.2986), reducing sugar content (-0.2205) and free space in pod.

4.2.1.3.10 Protein content. This character was positively associated with shelling percentage and oil percentage but negatively with carbohydrate content (-0.1924), pod volume, free space in pod and seed moisture percentage.

4.2.1.3.11 Carbohydrate content. Positive association was established by this character with non-reducing sugar content (0.2610), shell volume, free space in pod, 100 seed weight, mature pods per plant, seed moisture percentage and pod volume. However the character exhibited negative association with oil percentage and protein content.

4.2.1.3.12 Reducing sugar content. Reducing sugar content expressed positive correlation with non-reducing sugar content (0.5310) and mature pods per plant. Whereas its association with oil percentage, shell volume, pod volume were negative.

4.2.1.3.13 Non-reducing sugar content. Non-reducing sugar content exhibited positive relation with mature pods per plant (0.2904), seed moisture percentage (0.1905), carbohydrate content (0.2610), and reducing sugar content (0.5310).

4.2.1.4 *Correlation of kernel weight per plant with physiological characters*

Genotypic and phenotypic correlations were worked out and presented in table 8. A similar trend of association as was identified for morphological and biochemical characters were also observed both at genotypic and phenotypic levels with the former being higher than the latter in most of the cases.

Kernel yield per plant established positive association with SLA at 90 days after sowing (DAS) (0.3415), CGR at 90 DAS (0.3119), LAR at 90 DAS (0.4506), LAI at 90 DAS (0.4519), harvest index (0.3504) and pod weight per plant (0.8944). Its association with SLW at 90 DAS was negative (-0.2814).

4.2.1.5 *Inter correlations among physiological characters*

4.2.1.5.1 SLA at 30 DAS. Positive association was expressed between SLA at 30 DAS and SLA at 90 DAS (0.1768). With SLW at 30 DAS (-0.9906), SLW at 90 DAS (-0.1750), LAR at 90 DAS (-0.2863) and LAI at 90 DAS (-0.3080), the character exhibited negative association.

4.2.1.5.2 SLA at 60 DAS. This character expressed positive association with SLA at 90 DAS (0.3455) and CGR at 90 DAS (0.2090). Where as its association with SLW at 60 DAS (-0.9774), SLW at 90 DAS (-0.4048), CGR at 60 DAS (-0.2748) and SCMR at 30 DAS (-0.2995) was negative.

4.2.1.5.3 SLA at 90 DAS. SLA at 90 DAS showed positive relation with SLA at 30 DAS, SLA at 60 DAS, CGR at 90 DAS (0.2630) and pod weight per plant (0.2163). Its relationship with SLW at 60 DAS (-0.3533), SLW at 90 DAS (-0.1.000), CGR at 60 DAS (-0.4630) SCMR at 30 DAS (-0.5537) and harvest index (-0.2176) were negative.

4.2.1.5.4 SLW at 30 DAS. Positive association of SLW at 30 DAS with LAR at 90 DAS (0.2960) and LAI at 90 DAS (0.2831) was observed. The association of the character with SLA at 30 DAS was found to be negative (-0.9906).

4.2.1.5.5 SLW at 60 DAS. The character, SLW at 60 DAS exhibited positive association with SLW at 90 DAS (0.3985), CGR at 60 DAS (0.2096) and SCMR at 30 DAS (0.2456). Where as its association with SLA at 60 DAS (-0.9774) and SLA at 90 DAS was negative.

4.2.1.5.6 SLW at 90 DAS. SLW at 90 DAS was positively associated with SLW at 60 DAS, CGR at 60 DAS (0.4675), SCMR (0.5215) and harvest index (0.2296) and negatively with SLA at 90 DAS (-0.1000), SLA at 30 DAS and SLA at 60 DAS.

4.2.1.5.7 CGR at 60 DAS. Negative relationship was recorded between CGR at 60 DAS and the characters viz., CGR at 90 DAS (-0.6012), LAR at 90 DAS (-0.2328), harvest index (-0.1953), SLA at 90 DAS (-0.4630) and SLA 60 DAS (-0.2748). However,

Table 8: Genotypic and phenotypic correlation coefficients for physiological characters on kernel weight among 54 groundnut genotypes

Characters	Correlation	SLA at 60 DAS	SLA at 90 DAS	SLW at 30 DAS	SLW at 60 DAS	SLW at 90 DAS	CGR at 60 DAS	CGR at 90 DAS	LAR at 90 DAS	LAI at 90 DAS	SCMR at 30 DAS	Harvest index	Pod weight per plant	Kernel weight per plant
SLA at 30 DAS	g	0.1000	0.1768	-0.9906	-0.1179	-0.1750	-0.0423	-0.1522	-0.2863	-0.3080	-0.0275	0.0831	-0.1064	-0.1528
	p	0.1000 *	0.0365	-0.9643 **	-0.1278	-0.0265	-0.0435	-0.1324	-0.2192 **	-0.2489 **	-0.0200	0.0293	-0.0333	-0.0744
SLA at 60 DAS	g		0.3455	-0.1110	-0.9774	-0.4048	-0.2748	0.2090	0.1224	0.1093	-0.2995	0.0711	-0.0145	0.0751
	p		0.0561	-0.1222	-0.9639 **	-0.0628	-0.2584 **	0.1698 *	0.0398	0.0451	-0.2119 **	0.0731	0.0192	0.0805
SLA at 90 DAS	g			-0.1210	-0.3533	-1.0000	-0.4630	0.2630	0.0706	-0.0043	-0.5537	-0.2176	0.2163	0.3415
	p			-0.0285	-0.0652	-0.9491 **	-0.1714 *	0.1057	0.5078 **	0.3471 **	-0.2091 **	-0.0499	0.0662	0.1095
SLW at 30 DAS	g				0.0837	0.1200	-0.0011	0.1388	0.2960	0.2831	0.0230	-0.0677	0.0713	0.1242
	p				0.0883	0.0201	0.0058	0.1225	0.2303 **	0.2353 **	0.0181	-0.0176	-0.0052	0.0480
SLW at 60 DAS	g					0.3985	0.2096	-0.1413	-0.0827	-0.0717	0.2456	-0.0998	-0.0070	-0.0826
	p					0.0675	0.2020 **	-0.1248	-0.0112	-0.0234	0.1642 *	-0.0913	-0.0351	-0.0804
SLW at 90 DAS	g						0.4675	-0.2596	-0.0360	0.0290	0.5215	0.2296	-0.1537	-0.2814
	p						0.1625 *	-0.0924	-0.4698 **	-0.3214 **	0.1839 *	0.0125	-0.0572	-0.0899
CGR at 60 DAS	g							-0.6012	-0.2328	-0.0645	0.0845	-0.1953	-0.0301	-0.0835
	p							-0.5701 **	-0.1649 *	-0.0365	0.0664	-0.1460	-0.0248	-0.0692
CGR at 90 DAS	g								0.4887	0.7115	-0.0720	-0.0220	0.2895	0.3119
	p								0.3670 **	0.6475 **	-0.0674	-0.0358	0.1478	0.2241 **
LAR at 90 DAS	g									0.8420	-0.0129	-0.4217	0.5962	0.4506
	p									0.8516 **	-0.0336	-0.2690 **	0.2548 **	0.2690 **
LAI at 90 DAS	g										-0.0145	-0.3583	0.5638	0.4519
	p										-0.0331	-0.2627 **	0.2626 **	0.2952 **
SCMR at 30 DAS	g											0.1214	0.0930	-0.0417
	p											0.1108	-0.0126	-0.0449
Harvest index	g												0.3656	0.3504
	p												0.4195 **	0.3793 **
Pod weight per plant	g													0.8944
	p													0.7806 **

*Significant at 5% level **Significant at 1% level g = genotypic p = phenotypic with respect to SLW at 60 DAS (0.2096) and SLW at 90 DAS (0.4675) positive relationship was observed.

4.2.1.5.8 CGR at 90 DAS. The association of CGR at 90 DAS with LAR at 90 DAS (0.4887), LAI at 90 DAS (0.7115), pod weight per plant (0.2895), SLA 60 DAS (0.2090) and SLA at 90 DAS (0.2630) was observed to be positive. It was negative with SLW at 90 DAS (-0.2596) and CGR at 60 DAS (-0.6012).

4.2.1.5.9 LAR at 90 DAS. LAR at 90 DAS expressed positive relationship with LAI at 90 DAS (0.8420), pod weight per plant (0.5962), SLW at 30 DAS (0.2960) and CGR at 90 DAS (0.4887). The character exhibited negative relationship with harvest index (-0.4217), SLA at 30 DAS (-0.2863) and CGR at 60 DAS (-0.2328).

4.2.1.5.10 LAI at 90 DAS. The character, LAI at 90 DAS had positive association with pod weight per plant (0.5638), SLW at 30 DAS (0.2831), CGR at 90 DAS (0.7115) and LAR at 90 DAS (0.8420). Its association with harvest index (-0.3583), SLA at 30 DAS (-0.3080) was negative.

4.2.1.2.11 SCMR at 30 DAS. High positive correlation of SCMR at 30 DAS was observed with SLW 60 (0.2456) and SLW at 90 DAS (0.5215). The correlation with SLA at 60 DAS (-0.2995) and SLA at 90 DAS (-0.5537) were negative.

4.2.1.5.12 Harvest index. Harvest index exhibited positive relationship with pod weight per plant (0.3656), SLW at 90 DAS (0.2296) and negative relation with LAR at 90 DAS (-0.4217) and LAI at 90 DAS (-0.3583), CGR at 60 DAS (-0.1953) and SLA at 90 DAS (-0.2176).

4.2.1.5.13 Pod weight per plant. Pod weight per plant expressed positive association with CGR at 90 DAS (0.2895), SLA at 90 DAS (0.2163), LAR at 90 DAS (0.5962), LAI at 90 DAS (0.5638) and harvest index (0.3656).

4.2.2 Path coefficient analysis

The genotypic correlation coefficients of different component characters with kernel weight per plant and aflatoxin content were partitioned into direct and indirect effects by path analysis and the results are present in tables 9, 10, 11 and 12.

4.2.2.1 *Direct and indirect effects of morphological and biochemical characters on kernel yield*

The results on genotypic path analysis are presented in table 9.

4.2.2.1.1 Shell volume. Shell volume did not express any correlation but exhibited high direct positive effect on kernel weight per plant (0.3635). The indirect effects through mature pods (-0.4279) and shelling percentage (-0.3731) were negative and high. Moderate positive indirect effects were recorded through free space in pod (0.2029) and 100 seed weight (0.2228).

4.2.2.1.2 Pod volume. Pod volume had high positive correlation with kernel weight per plant. Where as it's direct effect was low (0.1353). Shell volume (0.3279) and free space in pod (0.3012) had positive and high indirect effects and shelling percentage (-0.3502) and mature pods per plant (-0.4491) expressed negative and high indirect effects on pod volume. The indirect effect of 100 seed weight (0.2513) was positive and moderate.

Table 9: Genotypic path analysis of morphological and biochemical characters on kernel weight per plant

Characters	Shell volume	Pod volume	Free space in pod	Shelling %	Mature pods per plant	Immature pods per plant	100 seed weight	Seed moisture %	Oil %	Protein content	Carbo-hydrate content	Reducing sugar content	Non-reducing sugar content	Aflatoxin content
Shell Volume	**0.3635**	0.3279	0.2111	-0.2802	-0.1524	0.1236	0.2712	0.1519	-0.0377	-0.1226	0.0838	-0.0632	-0.0100	0.1412
Pod Volume	0.1221	**0.1353**	0.1130	-0.0978	-0.0595	0.0555	0.1138	0.0619	-0.0203	-0.0392	0.0367	-0.0270	-0.0074	0.0249
Free space in pod	0.2093	0.3012	**0.3605**	-0.1899	-0.1185	0.1154	0.2507	0.1280	-0.0916	-0.1172	0.1401	-0.0316	0.0090	0.0110
Shelling Percentage	-0.3731	-0.3502	-0.2550	**0.4842**	0.1457	-0.1478	-0.3073	-0.3113	0.0602	0.1342	-0.0485	0.0689	-0.0218	-0.2016
Mature Pods/plant	-0.4277	-0.4491	-0.3355	0.3071	**1.0205**	0.0195	-0.3498	-0.0021	0.0349	-0.0777	0.1750	0.1791	0.2963	0.0300
Immature Pods/plant	-0.0108	-0.0130	-0.0101	0.0097	-0.0006	**-0.0317**	-0.0184	-0.0115	-0.0095	0.0007	-0.0027	0.0035	-0.0020	0.0015
100 seed Weight	0.2228	0.2513	0.2076	-0.1895	-0.1024	0.1739	**0.2986**	0.1207	0.0086	-0.0296	0.0567	-0.0401	-0.0237	0.0227
Seed moisture Percentage	0.0681	0.0745	0.0578	-0.1047	-0.0003	0.0589	0.0659	**0.1629**	0.0145	-0.0445	0.0313	-0.0107	0.0310	0.0201
Oil Percentage	0.0238	0.0344	0.0584	-0.0286	-0.0079	-0.0688	-0.0067	-0.0205	**-0.2299**	-0.0552	0.0686	0.0507	0.0155	0.0395
Protein Content	-0.0286	-0.0246	-0.0276	0.0235	-0.0065	-0.0018	-0.0084	-0.0232	0.0204	**0.0849**	-0.0163	-0.0029	-0.0041	-0.0155
Carbohydrate Content	-0.0755	-0.0888	-0.1272	0.0328	-0.0561	-0.0275	-0.0621	-0.0628	0.0977	0.0630	**-0.3272**	-0.0486	-0.0854	-0.0632
Reducing Sugar content	0.0283	0.0325	0.0143	-0.0231	-0.0285	0.0177	0.0218	0.0107	0.0359	0.0055	-0.0242	**-0.1626**	-0.0863	-0.0038
Non-reducing Sugar content	-0.0013	-0.0026	0.0012	-0.0022	0.0141	0.0030	-0.0039	0.0093	-0.0033	-0.0023	0.0127	0.0258	**0.0486**	0.0027
Aflatoxin Content	0.0278	0.0132	0.0022	-0.0298	0.0021	-0.0034	0.0054	0.0088	-0.0123	-0.0131	0.0138	0.0017	0.0040	**0.0716**
Correlation with kernel weight	0.1486	0.2421	0.2708	-0.0887	0.6497	0.2865	0.2708	0.2228	-0.1323	-0.2132	0.1999	-0.0571	0.1639	0.0812

Residual effects = 0.3428

Diagonal values denote direct effects

4.2.2.1.3 Free space in pod. This character recorded high positive correlation with kernel weight per plant. Its direct effect was also high (0.3605). The indirect effects of free space on kernel weight per plant were high and negative through mature pods per plant (-0.3355), moderate and negative through shelling percentage (-0.2550) and moderately positive through shell volume (0.2111) and 100 seed weight (0.2076).

4.2.2.1.4 Shelling percentage. Shelling percentage did not express any correlation with kernel weight per plant. How ever its direct effect on kernel yield was positive and high (0.4842). The indirect effect through shell volume (-0.2802) was negative and moderate. High positive indirect effect through mature pods per plant (0.3071) was also recorded. Most of the indirect effects were negligible.

4.2.2.1.5 Mature pods per plant. Mature pods per plant had the high positive correlation with kernel weight per plant and also exhibited very high direct effect on kernel weight plant (1.0205). Most of the indirect effects were negative and negligible.

4.2.2.1.6 Immature pods per plant. The character immature pods per plant though had positive and high correlation with kernel weight per plant, its direct effect was negative and negligible (-0.0317). Its indirect effects through most of the characters were low to negligible.

4.2.2.1.7 100 seed weight. This character established a high positive correlation with kernel weight per plant. The direct effects on kernel weight per plant were positive and moderate (0.2986). High negative indirect effects through shelling percentage (-0.3073) and mature pods per plant (-0.3498) and moderate positive indirect effects through shell volume (0.2712) and free space in pod (0.2507) were recorded.

4.2.2.1.8 Seed moisture percentage. The correlation coefficient of seed moisture percentage on kernel weight per plant was positive and high. Where as, the direct effect on kernel weight per plant (0.1629) was low. Seed moisture recorded high negative indirect effect on kernel weight through shelling percentage (-0.3113).

4.2.2.1.9 Oil percentage. Oil percentage did not record any correlation with kernel weight per plant. The direct effect was negative and moderate (-0.2299). Where as, the indirect effects through all the characters were low and negligible.

4.2.2.1.10 Protein content. Negative and high correlation was recorded for protein content with kernel weight per plant. Not only its direct effect (0.0849) but also the indirect effects via all the characters were negligible.

4.2.2.1.11 Carbohydrate content. Carbohydrate content had expressed positive correlation with kernel weight per plant. However its direct effect was negative and high (-0.3272). Indirect effects through most of the characters were negligible.

4.2.2.1.12 Reducing sugar content. Correlation was not established for reducing sugar content with kernel weight per plant. This was reflected in its negative low direct effect (-0.1626) on kernel weight per plant and negligible indirect effects through all the characters studied.

4.2.2.1.13 Non-reducing sugar content. Correlation of non-reducing sugar content with kernel weight per plant was positive and high. However its direct effect (0.0486) was negligible. Similarly the indirect effects via all the characters were also negligible with an exception through mature pods per plant (0.2963) wherein it was positive and moderate.

4.2.2.1.14 Aflatoxin content. Aflatoxin content exhibited no correlation with kernel weight per plant. It followed suit with direct (0.0716) and indirect effects on kernel weight per plant where in negligible effects were observed for both the effects.

4.2.2.2 *Direct and indirect effects of morphological and biochemical characters on aflatoxin content*

Genotypic direct and indirect effects of morphological and biochemical characters on aflatoxin content were worked out and the results are presented in table 10.

4.2.2.2.1 Shell volume. Shell volume recorded high positive correlation with aflatoxin content. The direct effect on aflatoxin content was also positive and very high (1.4484). Similar trend was observed for indirect effect through shelling percentage (0.3494), which was positive and high. Moderately positive indirect effect was recorded through the character, free space in pod (0.2765). Indirect effect through pod volume (-1.2871) was negative and very high. Through 100 seed weight (-0.2254) shell volume exhibited negative moderate indirect effects on aflatoxin content.

4.2.2.2.2 Pod volume. The character, pod volume exhibited high positive correlation with aflatoxin content where as it's direct effect (-1.4267) on aflatoxin content was negative and very high. The very high positive indirect effects through shell volume (1.3066) and moderate negative indirect effects through 100 seed weight (-0.2543). However it's indirect effect through free space in pod (0.3979) and shelling percentage (0.3279) were positive and high.

4.2.2.2.3 Free space in pod. The correlation coefficient between free space in pod and aflatoxin content was not established. But its direct effect was positive and high (0.4763). The indirect effect through pod volume (-1.1920) was very high negative and through 100

Table 10: Genotypic path analysis of morphological and biochemical characters on aflatoxin content

Character	Shell volume	Pod volume	Free space in pod	Shelling percent	Mature pods per plant	Immature pods per plant	100 seed weight	Seed moisture percent	Oil percent	Protein content	Carbo-hydrate content	Reducing sugar content	Non-reducing sugar content
Shell volume	**1.4484**	1.3066	0.8409	-1.1162	-0.6071	0.4923	1.0806	0.6051	-0.1501	-0.4884	0.3340	-0.2519	-0.0399
Pod volume	-1.2871	**-1.4267**	-1.1920	1.0318	0.6278	-0.5857	-1.2005	-0.6524	0.2136	0.4130	-0.3872	0.2850	0.0775
Free space in pod	0.2765	0.3979	**0.4763**	-0.2509	-0.1566	0.1524	0.3312	0.1691	-0.1211	-0.1549	0.1851	-0.0418	0.0119
Shelling per cent	0.3494	0.3279	0.2388	**-0.4533**	-0.1364	0.1384	0.2878	0.2914	-0.0563	-0.1256	0.0454	-0.0645	0.0204
Mature pods/plant	-0.0937	-0.0984	-0.0735	0.0673	**0.2235**	0.0043	-0.0766	-0.0005	0.0076	-0.0170	0.0383	0.0392	0.0649
Immature pods/plant	-0.0035	-0.0042	-0.0033	0.0031	-0.0002	**-0.0103**	-0.0060	-0.0037	-0.0031	0.0002	-0.0009	0.0011	-0.0006
100 seed weight	-0.2254	-0.2542	-0.2100	0.1917	0.1035	-0.1759	**-0.3021**	-0.1221	-0.0087	0.0300	-0.0574	0.0406	0.0240
Seed moisture percent	-0.0440	-0.0482	-0.0374	0.0678	0.0002	-0.0381	-0.0426	**-0.1054**	-0.0094	0.0288	-0.0202	0.0069	-0.0201
Oil percent	0.0050	0.0073	0.0124	-0.0061	-0.0017	-0.0146	-0.0014	-0.0043	**-0.0487**	-0.0117	0.0145	0.0107	0.0033
Protein content	-0.0530	-0.0455	-0.0511	0.0436	-0.0120	-0.0033	-0.0156	-0.0430	0.0377	**0.1572**	-0.0302	-0.0053	-0.0076
Carbohydrate content	0.0226	0.0266	0.0380	-0.0098	0.0168	0.0082	0.0186	0.0188	-0.0292	-0.0188	**0.0979**	0.0146	0.0255
Reducing sugar content	-0.0105	-0.0120	-0.0053	0.0086	0.0106	-0.0066	-0.0081	-0.0039	-0.0133	-0.0020	0.0089	**0.0601**	0.0319
Non-reducing sugar content	0.0037	0.0073	-0.0034	0.0061	-0.0392	-0.0083	0.0107	-0.0257	0.0091	0.0065	-0.0352	-0.0716	**-0.1348**
Correlation with aflatoxin content	0.3885	0.1844	0.0304	-0.4164	0.0294	-0.0472	0.0759	0.1233	-0.1718	-0.1828	0.1930	0.0232	0.0565

Residual effects = 0.7306

Diagonal values denote direct effects

seed weight (-0.2100) it was moderately negative. High positive indirect effect was observed through shell volume (0.8409). Through shelling percentage (0.2388) free space in pod exhibited positive moderate indirect effect on aflatoxin content.

4.2.2.2.4 Shelling percentage. This character had high negative association with aflatoxin content. The direct effect was also high and negative (-0.4533). Its indirect effect through pod volume (1.0318) was positive and very high and that through shelling percentage (-1.1162) very high and negative. Through free space in pod (-0.2509) shelling percentage expressed moderately negative indirect effect.

4.2.2.2.5 Mature pods per plant. Mature pods per plant did not show any correlation with aflatoxin content. It exhibited moderate direct effect (0.2235) on aflatoxin. The indirect effect through pod volume (0.6278) was positively high and that through shell volume negatively high (-0.6071).

4.2.2.2.6 Immature pods per plant. Correlation of immature pods per plant was not established with aflatoxin content. The direct effect on aflatoxin content was negligible. However, its indirect effect through shell volume (0.4923) was positively high and through shell volume negatively high (-0.5857).

4.2.2.2.7 100 seed weight. Correlation was not present between 100 seed weight and aflatoxin content. Where as it's direct effect on aflatoxin content was negative and high (0.3021). The indirect effect through shell volume (1.0806) was positive and very high. Whereas, through pod volume (-1.2005) it was negatively very high. Free space in pod (0.3312) the indirect effect was highly positive and through shelling percentage (0.2878) it was moderately positive.

4.2.2.2.8 Seed moisture percentage. Seed moisture percentage did not establish any correlation with aflatoxin content. The direct effect was negative and low. Seed moisture percentage expressed high positive indirect effects through shell volume (0.6051) and moderate positive through shelling percentage (0.2914). Its indirect effect through pod volume (-0.6524) was negative and high.

4.2.2.2.9 Oil percentage. Oil percentage exhibited negative correlation with aflatoxin content. Negligible direct (-0.0487) and indirect effects through most of the characters were recorded for this character. However the indirect effect through pod volume (0.2136) was moderately positive.

4.2.2.2.10 Protein content. This character was negatively correlated with aflatoxin content. However, its direct effect was positive but low (0.1572). The indirect effect on aflatoxin content through shell volume was negatively high (-0.4884) and through pod volume positively high (0.4130).

4.2.2.2.11 Carbohydrate content. Carbohydrate content exhibited positive high correlation with aflatoxin content but did not effect aflatoxin content either directly or indirectly through other characters except through shell volume (0.3340) and pod volume (-0.3872) which were positively and negatively high respectively.

4.2.2.2.12 Reducing sugar content. This character neither showed correlation not direct effect on aflatoxin content. The indirect effects though all other characters were also negligible with an exception to shell volume (-0.2519) and pod volume (0.2850) wherein it recorded moderate negative and positive indirect effects respectively.

4.2.2.2.8 Seed moisture percentage. Seed moisture percentage did not establish any correlation with aflatoxin content. The direct effect was negative and low. Seed moisture percentage expressed high positive indirect effects through shell volume (0.6051) and moderate positive through shelling percentage (0.2914). Its indirect effect through pod volume (-0.6524) was negative and high.

4.2.2.2.9 Oil percentage. Oil percentage exhibited negative correlation with aflatoxin content. Negligible direct (-0.0487) and indirect effects through most of the characters were recorded for this character. However the indirect effect through pod volume (0.2136) was moderately positive.

4.2.2.2.10 Protein content. This character was negatively correlated with aflatoxin content. However, its direct effect was positive but low (0.1572). The indirect effect on aflatoxin content through shell volume was negatively high (-0.4884) and through pod volume positively high (0.4130).

4.2.2.2.11 Carbohydrate content. Carbohydrate content exhibited positive high correlation with aflatoxin content but did not effect aflatoxin content either directly or indirectly through other characters except through shell volume (0.3340) and pod volume (-0.3872) which were positively and negatively high respectively.

4.2.2.2.12 Reducing sugar content. This character neither showed correlation not direct effect on aflatoxin content. The indirect effects though all other characters were also negligible with an exception to shell volume (-0.2519) and pod volume (0.2850) wherein it recorded moderate negative and positive indirect effects respectively.

4.2.2.2.13 Non-reducing sugar content. It did not register any correlation with aflatoxin content. Its direct effect on aflatoxin content was low and negative. The indirect effects through all other characters were negligible.

4.2.2.3 *Direct and indirect effects of physiological characters on kernel weight per plant*

The results on genotypic path analysis of physiological characters on kernel weight per plant are presented in table 11.

4.2.2.3.1 SLA at 30 DAS. SLA at 30 DAS had negative correlation with kernel weight per plant. The direct effect was also observed to be negative and moderate (-0.2926). High positive indirect effect was recorded through LAI at 90 DAS on kernel weight per plant (0.6149). Through LAR at 90 DAS (-0.3241) it expressed highly negative and through CGR at 90 DAS (-0.2269) moderately negative indirect effects..

4.2.2.3.2 SLA at 60 DAS. The character did not record correlation on kernel weight per plant. Where as its direct effect on kernel yield was positive and high. Indirectly SLA at 60 DAS affected kernel weight per plant through CGR at 60 DAS (-0.3068), which was negative and high. Through SLW at 60 DAS (-0.2374) and LAI at 90 DAS (-0.2181) it was negative and moderate.

4.2.2.3.3 SLA at 90 DAS. The correlation between SLA at 90 DAS and kernel weight per plant was positive and high. However the direct effect of SLA at 90 DAS on kernel weight per plant was negative and high (-0.3694). Positive high indirect effect was observed through SLW at 90 DAS (0.5840) and CGR at 90 DAS (0.3919). Whereas, the indirect effect through CGR at 60 DAS (-0.5168) was negative and very high.

Table 11: Genotypic path analysis of physiological characters on kernel weight per plant

Character	SLA at 30 DAS	SLA at 60 DAS	SLA at 90 DAS	SLW at 30 DAS	SLW at 60 DAS	SLW at 90 DAS	CGR at 60 DAS	CGR at 90 DAS	LAR at 90 DAS	LAI at 90 DAS	SCMR at 30 DAS	Harvest index	Pod weight per plant
SLA at 30 DAS	**-0.2926**	-0.0417	-0.0518	0.2899	0.0345	0.0512	0.0124	0.0445	0.0838	0.0901	0.0081	-0.0243	0.0311
SLA at 60 DAS	0.0437	**0.3063**	0.1058	-0.0340	-0.2993	-0.1240	-0.0842	0.0640	0.0375	0.0335	-0.0917	0.0218	-0.0044
SLA at 90 DAS	-0.0653	-0.1276	**-0.3694**	0.0447	0.1305	0.3735	0.1710	-0.0972	-0.0261	0.0016	0.2045	0.0804	-0.0799
SLW at 30 DAS	0.1569	0.0176	0.0192	**-0.1584**	-0.0133	-0.0190	0.0002	-0.0220	-0.0469	-0.0448	-0.0036	0.0107	-0.0113
SLW at 60 DAS	-0.0286	-0.2374	-0.0858	0.0203	**0.2429**	0.0968	0.0509	-0.0343	-0.0201	-0.0174	0.0597	-0.0242	-0.0017
SLW at 90 DAS	0.1011	0.2338	0.5840	-0.0693	-0.2301	**-0.5776**	-0.2700	0.1500	0.0208	-0.0168	-0.3012	-0.1326	0.0888
CGR at 60 DAS	-0.0472	-0.3068	-0.5168	-0.0012	0.2339	0.5219	**1.1162**	-0.6711	-0.2599	-0.0719	0.0943	-0.2180	-0.0336
CGR at 90 DAS	-0.2268	0.3114	0.3919	0.2068	-0.2106	-0.3869	-0.8959	**1.4901**	0.7281	1.0602	-0.1073	-0.0328	0.4313
LAR at 90 DAS	-0.3241	0.1385	0.0799	0.3351	-0.0936	-0.0408	-0.2635	0.5531	**1.1320**	0.9532	-0.0146	-0.4773	0.6749
LAI at 90 DAS	0.6149	-0.2181	0.0086	-0.5651	0.1432	-0.0579	0.1287	-1.4203	-1.6810	**-1.9963**	0.0289	0.7153	-1.1255
SCMR at 30 DAS	0.0004	0.0043	0.0080	-0.0003	-0.0035	-0.0075	-0.0012	0.0010	0.0002	0.0002	**-0.0144**	-0.0017	-0.0013
Harvest index	0.0091	0.0078	-0.0238	-0.0074	-0.0109	0.0251	-0.0214	-0.0024	-0.0461	-0.0392	0.0133	**0.1093**	0.0400
Pod weight per plant	-0.0943	-0.0128	0.1916	0.0632	-0.0062	-0.1362	-0.0267	0.2565	0.5283	0.4996	0.0824	0.3239	**0.8861**
Correlation with kernel weight	-0.1528	0.0751	0.3415	0.1242	-0.0826	-0.2814	-0.0835	0.3119	0.4506	0.4519	-0.0417	0.3504	0.8944

Residual effect =-- 0.3531 Diagonal values denote direct effects

4.2.2.3.4 SLW at 30 DAS. Correlation was not registered between SLW at 30 DAS kernel weight per plant. The direct effect of SLW at 30 DAS on kernel weight per plant was negative and low (-0.1584). The indirect effect via LAR at 90 DAS (0.3351) was positive and high and through SLA at 30 DAS (0.2899) and CGR at 90 DAS (0.2068) it was positive and moderate. The indirect effect through LAI at 90 DAS was negative and high (-0.5651).

4.2.2.3.5 SLW at 60 DAS. Although the correlation of SLW at 60 DAS with kernel weight per plant was not registered. SLW at 60 DAS expressed moderate positive direct effect on kernel weight per plant (0.2429). Where as through SLA at 60 DAS (-0.2993), SLW at 90 DAS (-0.2301) and CGR at 90 DAS (-0.2106) it exhibited moderate negative indirect effect on kernel weight per plant. Moderate positive indirect effect was recorded through CGR at 60 DAS (0.2339).

4.2.2.3.6 SLW at 90 DAS. High negative correlation was recorded between SLW at 90 DAS and kernel weight per plant. The direct effect on kernel weight per plant was also negative and high (-0.5776). The indirect effect through CGR at 60 DAS (0.5219) and SLA at 90 DAS (0.3735) were positive and high and through CGR at 90 DAS (-0.3869) it was negative and high.

4.2.2.3.7 CGR at 60 DAS. Though correlation was not recorded between CGR at 60 DAS and kernel weight per plant, the direct effect of CGR at 60 DAS on kernel weight per plant was observed to be very high and positive (1.1162). CGR at 60 DAS through CGR at 90 DAS (-0.8959), LAR at 90 DAS (-0.2635) contributed indirectly in a negative manner to kernel weight per plant.

4.2.2.3.8 CGR at 90 DAS. This character exhibited positive and high correlation with kernel weight per plant. The direct effect on kernel weight per plant was also positive and very high (1.4901). The indirect effect via LAR at 90 DAS (0.5531) was also very high and positive. Similarly moderately positive indirect effect was recorded through pod weight per plant (0.2565). In contrast, high negative indirect effects were observed through LAI at 90 DAS (-1.4203) and CGR at 60 DAS (-0.6711).

4.2.2.3.9 LAR at 90 DAS. This character had positive high association with kernel weight per plant. Its direct effect on kernel weight per plant was also positive and very high (1.1320). The indirect effects were also high and positive through CGR at 90 DAS (0.7281), and pod weight per plant (0.5283). Where as the indirect effects through LAI at 90 DAS (-1.6810) was very high and negative and that through CGR at 60 DAS (-0.2559) was moderate and negative.

4.2.2.3.10 LAI at 90 DAS. Although LAI at 90 DAS recorded high positive correlation with kernel weight per plant, its direct effect on kernel weight per plant was very high and negative (-1.9963). However it had also recorded very high positive indirect effects on kernel weight per plant through CGR at 90 DAS (1.0602) and high positive indirect effects through LAR at 90 DAS (0.9532) and pod weight per plant (0.4996).

4.2.2.3.11 SCMR at 30 DAS. This character did not record any relationship with kernel weight per plant. The indirect effect through SLA at 90 DAS (0.2045) was moderately positive and through SLW at 90 DAS (-0.3012) highly negative.

4.2.2.3.12 Harvest index. Harvest index had high positive correlation with kernel weight per plant. However the direct effect was low (0.1093) and the indirect effects through LAI at 90 DAS (0.7153) and pod weight per plant (0.3239) were positive and high. Harvest index through LAR at 90 DAS (-0.4773) exhibited high negative indirect effect. Whereas, its negative indirect effect through CGR at 60 DAS was moderate (-0.2180).

4.2.2.3.13 Pod weight per plant. Strong positive association was recorded for pod weight per plant with kernel weight per plant. The direct effect of pod weight per plant on kernel weight per plant was also high (0.8861) and positive. Similarly high and positive indirect effects were observed through CGR at 90 DAS (0.4313), LAR at 90 DAS (0.6749). The indirect effect through LAI at 90 DAS was negative and very high (-1.1255). The other indirect effects on kernel weight per plant were low and negligible.

4.2.2.4. Direct and indirect effects of physiological characters on aflatoxin content

An attempt was made to understand the relationship of physiological characters on aflatoxin content. Their direct and indirect effects on aflatoxin content are presented in table 12. None of the physiological characters except CGR at 60 DAS showed significant correlation with aflatoxin content. The association of CGR at 60 DAS with aflatoxin was positive and high. The physiological characters that exhibited high to very high positive direct effect on aflatoxin were SLA at 60 DAS (0.4459), SLA 90 DAS (1.3038), SLW at 90 DAS (1.1287), CGR at 60 DAS (1.0473), CGR at 90 DAS (1.0549) and LAR 90 DAS (0.7456). Moderate positive direct effect was observed by SCMR at 30 DAS (0.2451), where as low to negligible positive direct effects were recorded by SLW at 60 DAS and harvest index. High negative direct effects of SLA at 30 DAS (-1.5284), SLW at 30 DAS (-1.3467) and LAI at 90 DAS (-1.4122) on aflatoxin were also recorded.

SLA at 30 DAS expressed very high positive indirect effect through SLW at 30 DAS (1.3340) and high positive indirect effect through LAI at 90 DAS (0.4350). Whereas, through LAR at 90 DAS it was negatively moderate (-0.2134). SLA at 60 DAS exhibited high positive indirect effect through SLA at 90 DAS (0.4504) and through SLW at 90 DAS it was highly negative (-0.4569). Through SLW at 90 DAS (-1.1412), the character SLA at 90 DAS had a very high negative indirect effect on aflatoxin content. A high negative indirect effect was observed through CGR at 60 DAS (-0.4848).

Very high positive indirect effect was recorded on aflatoxin by SLW at 30 DAS through SLA at 30 DAS (1.5139). High negative indirect effect through LAI at 90 DAS (-0.3997) was also recorded. SLW at 60 DAS recorded high negative indirect effects on aflatoxin content through SLA at 60 DAS (-0.4358) and SLA at 90 DAS (-0.4606). Whereas, high positive indirect effect of SLW at 60 DAS was recorded through SLW at 90 DAS (0.4497) on kernel weight per plant. SLW at 90 DAS registered very high negative indirect effects through SLA at 90 DAS (-1.3182) and high positive indirect effect through CGR at 60 DAS (0.4896).

High negative indirect of CGR at 60 DAS through CGR at 90 DAS (-0.6342) and SLA at 90 DAS (-0.6036) was observed. Whereas, through SLW at 90 DAS (0.5277) it was positive and high. CGR at 90 DAS was observed to exhibit very high (-1.0048) and high (-0.6296) negative indirect effect through LAI at 90 DAS and CGR at 60 DAS respectively. High positive indirect effects through SLA at 90 DAS (0.3429) and LAR at 90 DAS (0.3643) was also recorded.

A very high negative and high positive indirect effects were recorded for LAR at 90 DAS through LAI at 90 DAS and CGR at 90 DAS respectively. The indirect effect of LAI at 90 DAS through SLA at 30 DAS (0.4708), CGR at 90 DAS (0.7505) and LAR at 90 DAS (0.6278) were positively high.

Genotypic path analysis of physiological characters on aflatoxin content

Character	SLA at 30 DAS	SLA at 60 DAS	SLA at 90 DAS	SLW at 30 DAS	SLW at 60 DAS	SLW at 90 DAS	CGR at 60 DAS	CGR at 90 DAS	LAR at 90 DAS	LAI at 90 DAS	SCMR at 30 DAS	Harvest index
SLA at 30 DAS	**-1.5284**	-0.2180	-0.2703	1.5139	0.1801	0.2675	0.0646	0.2326	0.4375	0.4708	0.0421	-0.1270
SLA at 60 DAS	0.0636	**0.4459**	0.1540	-0.0495	-0.4358	-0.1805	-0.1225	0.0932	0.0546	0.0487	-0.1335	0.0317
SLA at 90 DAS	0.2306	0.4504	**1.3038**	-0.1577	-0.4606	-1.3182	-0.6036	0.3429	0.0920	-0.0056	-0.7219	-0.2838
SLW at 30 DAS	1.3340	0.1494	0.1629	**-1.3467**	-0.1127	-0.1616	0.0015	-0.1869	-0.3987	-0.3812	-0.0310	0.0911
SLW at 60 DAS	-0.0164	-0.1358	-0.0491	0.0116	**0.1389**	0.0554	0.0291	-0.0196	-0.0115	-0.0100	0.0341	-0.0139
SLW at 90 DAS	-0.1975	-0.4569	-1.1412	0.1354	0.4497	**1.1287**	0.5277	-0.2930	-0.0407	0.0327	0.5887	0.2592
CGR at 60 DAS	-0.0443	-0.2878	-0.4848	-0.0012	0.2195	0.4896	**1.0473**	-0.6296	-0.2438	-0.0675	0.0885	-0.2046
CGR at 90 DAS	-0.1605	0.2204	0.2775	0.1464	-0.1491	-0.2739	-0.6342	**1.0549**	0.5155	0.7505	-0.0760	-0.0232
LAR at 90 DAS	-0.2134	0.0912	0.0526	0.2207	-0.0616	-0.0269	-0.1736	0.3643	**0.7456**	0.6278	-0.0096	-0.3144
LAI at 90 DAS	0.4350	-0.1543	0.0061	-0.3997	0.1013	-0.0410	0.0910	-1.0048	-1.1892	**-1.4122**	0.0204	0.5060
SCMR at 30 DAS	-0.0067	-0.0734	-0.1357	0.0056	0.0602	0.1278	0.0207	-0.0176	-0.0032	-0.0035	**0.2451**	0.0297
Harvest index	0.0044	0.0038	-0.0116	-0.0036	-0.0053	0.0122	-0.0104	-0.0012	-0.0225	-0.0191	0.0065	**0.0533**
Correlation with aflatoxin content	-0.0997	0.0350	-0.1358	0.0753	-0.0753	0.0792	0.2376	-0.0650	-0.0643	0.0314	0.0533	0.0043

Residual effect = 0.9644 Diagonal values denote direct effects

SCRM at 30 DAS recorded high negative indirect effects through SLA at 90 DAS (-0.7219) and highly positive indirect effect through SLW at 90 DAS (0.5887) on aflatoxin content. High positive indirect effect was observed on aflatoxin content by harvest index through LAI at 90 DAS (0.5060) and highly negative indirect effect through LAR at 90 DAS (-0.3144) was also recorded.

4.3 VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The results on range of variability, phenotypic (PCV) and genotypic coefficients of variation (GCV), heritability in broad sense ($h^2{}_{(b)}$) and genetic advance as percentage of mean (GAM) are furnished in table 13 for morphological and biochemical characters and in table 14 for physiological characters. The mean values for various characters from table 2 were presented at appropriate places.

4.3.1 Morphological and biochemical characters

4.3.1.1 *Shell volume.* The variability estimates of shell volume ranged from 0.4 - 2.43 cc with an overall mean of 1.09 cc. The genotypes exhibited significant difference for this character. The genotype, ICG 10352 (0.4 cc) had the lowest and BAU 13 (2.43 cc) had the highest shell volume. Notable among the genotypes that possessed the lowest shell volume were ICG 1326 (0.47 cc), ICG 2411 (0.467 cc), ICG 3245 (0.47 cc) and ICGV 86564 0.47) (table 2). A high magnitude of GCV of 42.77 and PCV of 43.70 were recorded for hell volume. The heritability of 95.80% and GAM of 86.24% were also high.

.3.1.2 *Pod volume.* Mean values for pod volume ranged from 1.13 cc to 4.83 cc with n overall mean of 2.48 cc indicating optimum variability. The lowest pod volume was bserved in ICG 2184 (1.13 cc) and the highest in BAU 13 (4.83 cc). The GCV and PCV

Genetic parameters for 34 genotypes of groundnut for morphological and biochemical characters

S. No.	Characters	Mean	Range		Coefficients of variation		Heritability (h2 $_{(b)}$) (%)	Genetic advance (GA)	GA as percent of mean (GAM)
			From	To	Genotypic (GCV)	Phenotypic (PCV)			
1	Shell volume (cc)	1.09	0.40	2.43	42.77	43.70	95.80	0.94	86.24
2	Pod volume (cc)	2.48	1.13	4.83	37.49	37.79	98.40	1.90	76.61
3	Free space in pod (cc)	0.57	0.10	1.57	63.32	65.36	93.80	0.73	126.36
4	Shelling percent	65.90	55.27	72.68	6.05	7.29	69.00	6.83	10.36
5	Mature pods/plant	22.07	12.97	32.10	18.73	23.34	64.40	6.84	30.98
6	Immature pods/plant	9.08	3.03	17.50	45.14	48.46	86.80	7.86	86.63
7	100 seed weight (g)	40.58	27.60	66.75	25.88	26.81	93.20	20.89	51.46
8	Seed moisture percent	10.23	9.57	11.27	4.06	4.45	83.00	0.78	7.61
9	Oil percent	51.68	48.53	56.47	3.07	3.35	83.70	2.99	5.78
10	Protein content (mg g^{-1})	204.95	162.30	247.72	10.92	13.06	69.90	38.55	18.81
11	Carbohydrate content (mg g^{-1})	120.66	89.67	131.71	5.16	7.95	42.10	8.32	6.89
12	Reducing sugar content (mg g^{-1})	2.76	0.12	10.33	94.54	96.09	96.80	5.29	191.61
13	Non-reducing sugar content (mg g^{-1})	15.89	2.30	67.54	78.74	80.20	96.40	25.31	159.26
14	Aflatoxin content (ppb kg^{-1})	47.15	2.83	626.67	251.25	257.38	95.30	238.24	505.24
15	Kernel weight/plant (g)	11.69	7.78	15.23	14.72	17.99	67.00	2.90	24.83

for this character were 37.49 and 37.79 respectively. This character recorded high values for heritability (98.40%) and GAM (76.61%).

4.3.1.3 *Free space in pod.* Free space in pod exhibited mean values ranging from 0.10 cc to 1.57 cc with an overall mean of 0.57 cc. It exhibited high estimates of GCV (63.31) and PCV (65.36). Further more, the heritability (93.80%) and GAM (126.36%) recorded for the character were also very high indicating great amount of variability for the character and success in improvement. The lowest free space in pod was observed in ICG 2184 (0.10) and K 134 (0.10), and the highest was found in ICGV 89214 (1.57 cc). The genotypes, ICG 1418, ICG 10352, ICGS 11, TPT 2, TCGS 407 and TCGS 634 also recorded a low free space in pod (0.20 cc).

4.3.1.4 *Shelling percentage.* The character shelling percentage expressed a low range in mean values ranging from 55.27% to 72.68%. Similar trend followed for all the other genetic parameters viz., GCV (6.05), PCV (7.29), GAM (10.36%) except heritability (69%), which was high. The highest shelling percentage was recorded in ICG 3542 (72.68%) and it was closely followed by ICG 4893 (72.11%), ICGV 86584 (71.54%) and ICG 10352 (71.36%).

4.3.1.5 *Mature pods per plant.* A good amount of variation was recorded for mature pods per plant, which was reflected in recording high range in mean values (12.97 to 32.10). Its overall mean was 22.07. The genotype, ICG 11386 produced more number of mature pods per plant (32.10) followed by ICGS 11 (30.80) and ICGV 86234 (29.20). The character recorded a moderate GCV (18.73) and high PCV (23.33). Its heritability was high (64.40%) but GAM was moderate (30.98%).

4.3.1.6 ***Immature pods per plant.*** This character registered a high range of variation in mean values ranging from 3.03 to 17.50 with an overall mean of 9.08. It also recorded high GCV (45.14) and PCV (48.46). Immature pods were more in the genotypes viz., ICG 11386 (17.50), TG 45 (16.00), M 13 (16.33) and BAU 13 (15.97). Less number of immature pods was observed in ICG 1326 (3.03), ICG 3245 (3.20) and ICG 6690 (3.10). High estimates of heritability (86.80%) and GAM (86.63%) were manifested for the traits.

4.3.1.7 ***100 seed weight.*** The variation of genotypes for 100 seed weight was quite impressive. This was evident from the high range (27.6 to 66.75 g), high GCV (25.88) and high PCV (26.81). The overall mean was also high 40.58 g. The genotypes that had weighed more on scale were ICG 8325 (66.75 g), BAU 13 (66.29 g), TG 42 (63.87 g), TCGS 617 (58.85 g) and ICGV 86564 (55.61 g). High heritability (93.20%) and GAM (51.46%) were registered for this character.

4.3.1.8 ***Seed moisture percentage.*** Seed moisture percentage was estimated to study its impact on biochemical characters including aflatoxin content during storage. Differences in seed moisture percentage in genotypes, even after uniform drying, were contemplated to be relevant in the present investigation. Though the genotypes differed significantly for seed moisture percentage the variation was negligible as indicated by low range (9.57 to 11.27), GCV (4.06) and PCV (4.45). Heritability estimates were recorded as high (83%) but GAM was low (7.60%).

4.3.1.9 ***Oil percentage.*** The mean values for oil percentage ranged from 48.53 to 56.47% with a high over all mean of 51.68 %. The high oil containing genotypes in descending order were TCGS 407 (56.47 %), TG 41 (54.40%), TG (45 (54%) and TCGS 596 (54.27%). In contrast TPT 1 (48.53 %), ICGV 89214 (48.60%) and ICG 5502 (48.77

%) processed low oil. Low GCV (3.07), PCV (3.35) and GAM (5.78%) were recorded for the character. The heritability value was very high (83.70%).

4.3.1.10 ***Protein content.*** Protein content registered an overall mean of 204.95 mg g^{-1} seed with the individual means ranging from 162.30 to 247.72 mg g^{-1}. The range, GCV (10.92) and PCV (13.06) indicate moderate variability for the character. Protein content had high heritability (69.90%) but GAM was low (18.80%). High protein lines observed in the study were ICG 1416 (247.72 mg g^{-1}) and TPT 1 (246.01 mg g^{-1}).

4.3.1.11 ***Carbohydrate content.*** The overall mean value recorded for carbohydrate content was 120.66 mg g^{-1} with a range of 89.67 to 131.71 mg g^{-1}. This charter exhibited low values for GCV (5.16), PCV (7.95) and GAM (6.89%). The heritability was moderate (42.10%). Higher carbohydrate content was recorded in M 13 (131.71 mg g^{-1}) and TG 39 (131.71 mg g^{-1}) where as TCGS 407 (89.67 mg g^{-1}) recorded the lowest estimate.

4.3.1.12 ***Reducing sugar content.*** High variation was observed for reducing sugar content. It was reflected in recording high range in mean values (0.12 to 10.33 mg g^{-1}) and high GCV (94.54) and PCV (96.09). It also recorded high estimates for heritability (96.80%) and GAM (191.61%). The overall mean was 2.76 mg g^{-1}. ICG 1326 (10.33 mg g^{-1}), ICG 10352 (9.49 mg g^{-1}), ICG 3245 (7.65 mg g^{-1}) and ICGV 86564 (7.73 mg g^{-1}) are some of the genotypes rich in reducing sugar content.

4.3.1.13 ***Non-reducing sugar content.*** With an overall mean of 15.89 mg g^{-1}, the mean values for non-reducing sugar content ranged from 2.30 to 67.54 mg g^{-1} indicating high variation, which was again reflected in high GCA (78.74 mg g^{-1}) and PCV (80.20 mg g^{-1}). Non-reducing sugar content was rich in the genotypes; ICG 7637 (67.54 mg g^{-1}), TCGS 91 (45.95 mg g^{-1}) and ICGV 86564 (42.96 mg g^{-1}). This character registered high heritability (96.40%) and high GAM (159.30%).

4.3.1.14 *Aflatoxin content.* The highest variation was recorded for aflatoxin with an overall mean of 47.15 ppb kg^{-1} seed and a range of 2.83 to 626.67 ppb kg^{-1}. The GCV (251.25) and PCV (257.38) were also very high. This character also possessed high estimates for heritability (238.24%) and GAM (505.24%). The low aflatoxin containing genotypes were, ICG 1326 (2.83 ppb kg^{-1}) followed by ICG 3245, ICG 8666, ICGV 88448, TG 49, TG 45, K 134 and TPT 4 which had recorded 3.67 ppb kg^{-1} aflatoxin content.

4.3.1.15 *Kernel weight per plant.* Kernel yield recorded an overall mean of 11.69 g with a range from 7.78 to 15.23 g. The GCV (14.72) and PCV (17.99) were moderate. The high yielding genotypes identified were TPT 4 (15.23 g), M 13 (15.16 g), ICGV 89214 (15.13 g), ICGV 86564 (14.99 g). The heritability estimate observed for the character was high (67%) and the GAM was moderate (24.83%).

In general high variability was recorded for aflatoxin content, reducing sugar content, non-reducing sugar content, free space in pod, immature pods per plant, shell volume and pod volume. Environmental influence was profound in the expression of the characters; aflatoxin content, mature pods per plant, immature pods per plant, kernel weight per plant, protein content, carbohydrate content and free space in pod as indicated by the differences between PCV and GCV. All the characters except carbohydrate content are highly heritable. Greater scope of improvement is present for aflatoxin content, reducing sugar content, non-reducing sugar content, free space in pod, shell volume, pod volume, mature pods per plant and 100 seed weight.

.3.2 Physiological characters

4.3.2.1 ***SLA at 30 DAS.*** SLA at 30 DAS registered an over all mean of 213.40 cm^2 g^{-1} with means ranging from 158.91 to 283.20 cm^2 g^{-1}. High SLA at 30 DAS was recorded by TG 39 (283.2 cm^2 g^{-1}) and it was followed by ICG 3509 (266.1 cm^2 g^{-1}) and ICG 2411 (261.3 cm^2 g^{-1}). Both the coefficients of variation; GCV (12.99) and PCV (14.82) were moderate. The character was highly heritable (76.90%) with moderate GAM (23.47%).

4.3.2.2 ***SLA at 60 DAS.*** An overall mean of 178.60 cm^2 g^{-1} and high range in mean values from 121.00 to 247.10 cm^2 g^{-1}, moderate GCV (15.04) and PCV (17.15) were recorded. The character had high heritability (76.90%) and moderate GAM (27.18%). ICG 8666 recorded the highest SLA at 60 DAS (247.10 cm^2 g^{-1}) and it was followed by ICG 7633 (243.30 cm^2 g^{-1}), ICGS 11 (239.00 cm^2 g^{-1}) and TPT 2 (232.90 cm^2 g^{-1}).

4.3.2.3 ***SLA at 90 DAS.*** High range of 151.30 to 238.20 cm^2 g^{-1} with overall mean of 196.00 cm^2 g^{-1} was recorded for SLA at 90 DAS. GCV was low (5.78) where as PCV was moderate (13.80). Both the heritability (17.50%) and GAM (4.90%) were low. TPT 4 registered high SLA at 90 DAS (238.20 cm^2 g^{-1}). The other genotypes that had recorded high values were TCGS 320 (227.60 cm^2 g^{-1}), ICG 8666 (226.40 cm^2 g^{-1}) and M 13 (226.30 cm^2 g^{-1}).

4.3.2.4 ***SLW at 30 DAS.*** This character ranged from a low value of 3.70 g cm^{-2} to a igh value of 6.33 g cm^{-2} with an overall mean of 4.8 g cm^{-2}. Besides having moderate CV (13.32) and PCV (15.03), this component character exhibited high heritability 78.50%) and a moderate GAM (24.30%). The top ranking genotypes for this character ere ICG 8325 (6.33 g cm^{-2}), ICG 7332 (6.27 g cm^{-2}) and TPT 4 (6.10 g cm^{-2}).

Table 14. Genetic parameters for 54 genotypes of groundnut for physiological characters

S. No.	Characters	Mean	Range		Coefficients of variation		Heritability (h2 (b)) (%)	Genetic advance (GA)	GA as percent of mean (GAM)
			From	To	Genotypic (GCV)	Phenotypic (PCV)			
1	SLA at 30 DAS ($cm^2 g^{-1}$)	213.40	158.91	283.20	12.99	14.82	76.90	50.07	23.47
2	SLA at 60 DAS ($cm^2 g^{-1}$)	178.60	121.00	247.10	15.04	17.15	76.90	48.56	27.18
3	SLA at 90 DAS ($cm^2 g^{-1}$)	196.00	151.30	238.20	5.78	13.80	17.50	9.78	4.99
4	SLW at 30 DAS ($g cm^{-2}$)	4.80	3.70	6.33	13.32	15.03	78.50	1.17	24.30
5	SLW at 60 DAS ($g cm^{-2}$)	5.76	4.10	7.67	15.10	17.13	77.70	1.58	27.41
6	SLW at 90 DAS ($g cm^{-2}$)	5.21	4.30	7.10	6.12	15.53	15.50	0.26	4.97
7	CGR at 60 DAS ($g m^{-2} d^{-1}$)	8.34	2.34	14.47	32.88	33.34	97.20	5.57	66.79
8	CGR at 90 DAS ($g m^{-2} d^{-1}$)	9.79	5.31	20.55	37.61	39.43	91.00	7.24	73.90
9	LAR at 90 DAS ($cm^2 g^{-1}$)	41.07	19.51	52.94	17.30	22.10	61.30	11.46	27.89
10	LAI at 90 DAS	2.49	0.94	3.87	27.10	31.19	75.50	1.21	48.51
11	SCMR at 30 DAS	41.16	34.93	45.50	5.72	6.53	76.80	4.25	10.33
12	Harvest index	0.33	0.25	0.44	11.82	16.67	50.30	0.06	17.26
13	Pod weight/plant (g)	18.23	12.12	27.64	15.68	26.59	34.80	3.47	19.05

4.3.2.5 ***SLW at 60 DAS.*** The mean values for this character ranged from 4.10 to 7.67 g cm^{-2} and recorded a mean of 5.76 g cm^{-2}. The heritability was high (77.70%) whereas the GAM was (27.40) moderate. The variability observed for this character was also moderate which was reflected in moderate estimates of GCV (15.10) and PCV (17.13).

4.3.2.6 ***SLW at 90 DAS.*** SLW at 90 DAS recorded a range in mean values from 4.30 g cm^{-2} to 7.10 g cm^{-2} with an overall mean of 5.21 g cm^{-2}. GCV (6.12) was low. Where as, PCV (15.53) was moderate. This character recorded low estimates of heritability (15.50%) and GAM (49.70%).

4.3.2.7 ***CGR at 60 DAS.*** The observed range of variation was from 2.34 g cm^{-2} day^{-1} to 14.47 g cm^{-2} day^{-1} with an overall mean of 8.34 g $cm^{-2}d^{-1}$. The highest growth rate was observed at 60 DAS in ICG 7749 (14.47 g cm^{-2} day^{-1}), ICG 7637 (13.66 g cm^{-2} day^{-1}) and ICGV 96235 (13.47 g cm^{-2} day^{-1}). This character exhibited high variation in terms of GCV (32.88) and PCV (33.34). Similarly the character recorded high heritability (97.20%) and high GAM (66.79%).

4.3.2.8 ***CGR at 90 DAS.*** CGR at 90 DAS followed a similar trend of recording higher values for all the genetic parameters as was expressed for CGR at 60 DAS. The overall mean was 9.79 g cm^{-2} day^{-1} and the mean values ranged from 5.31 to 20.55 g cm^{-2} day^{-1}. The GCV was 37.61 and PCV, 39.43. The estimates of heritability and GAM were 91.00% and 73.90% respectively. The genotypes ICGV 86564 was the highest to recorded 20.55 g cm^{-2} day^{-1} CGR at 90 DAS and it was followed by ICG 8666 (19.50 g cm^{-2} day^{-1}) and ICG 3542 (18.56 g cm^{-2} day^{-1}).

4.3.2.9 ***LAR at 90 DAS.*** Moderate to high variability was recorded for the character and it was expressed in recording high range from 19.50 to 52.94 cm^2 g^{-1}, GCV of 17.29 and PCV of 22.10 with an overall mean of 41.07 cm^2 g^{-1}. TCGS 634 exhibited high LAR at 90 DAS (52.94 cm^2 g^{-1}). The values recorded by the genotypes; ICGV 86552, ICGV 86564, ICG 7332, ICG 4749, ICGV 89214 and TCGS 596 were more than 50 cm^2 g^{-1}. The heritability was high (61.30%) and GAM was moderate (27.89%).

4.3.2.10 ***LAI at 90 DAS.*** Variability, heritability and GAM were high for this character. It recorded a mean value of 2.49, a range from 0.94 to 3.87, GCV of 27.10, PCV of 31.19, heritability of 75.50% and GAM of 48.51%. A value of more than 3.5 was recorded by the genotypes, ICGV 86552, TPT1, TCGS 634 and ICGS 21.

4.3.2.11 ***SCMR at 30 DAS.*** The mean values ranged from 34.93 to 45.50 with an overall mean of 41.16. Though the heritability was high (76.80%), the variation and GAM was low. The genotype, ICGV 86031 expressed higher mean value (45.50) and ICG 4893 the lower (34.93).

4.3.2.12 ***Harvest index.*** Harvest index recorded moderate values for all the genetic parameters with a mean of 0.33. The mean values ranged from 0.25 to 0.44. GCV was 1.82 and PCV was 16.67. The values for heritability and GAM were 50.30% and 17.26% espectively. Higher values were observed in the genotypes, TG 49 (0.44) and TG 42 0.43).

3.2.13 ***Pod weight per plant.*** Moderate to high values were recorded for the genetic rameters. The mean was 18.23 g with a range from 12.12 to 27.64 g. Moderate GCV 5.68) and high PCV (26.59) were observed. The heritability was 35% and GAM was

19.10%. The genotype, TCGS 617 recorded the highest pod weight (27.64 g) and it was followed by ICGV 89214 (24.36 g) and ICGV 86564 (26.65 g).

The results on genetic parameters for physiological characters in brief are as follows. Moderate to high variability was observed for all the physiological characters except for SLA at 90 DAS, SLW at 90 DAS, and SCMR at 30 DAS. High heritability was recorded for all the characters excepting those two characters (SLA at 90 DAS and SLW at 90 DAS), which showed less variability. The environmental influence in the expression of characters was more on pod weight per plant, SLA at 90 DAS and SLW at 90 DAS. GAM was high for CGR at 60 DAS, CGR at 90 DAS, LAI at 90 DAS, LAR at 90 DAS, SLW 60 DAS, SLA at 60 DAS, SLW at 60 DAS. When variability, heritability and GAM were considered together, CGR at 90 DAS, CGR at 60 DAS, LAI at 90 DAS, LAR at 90 DAS, SLW at 60 DAS, SLW at 30 DAS and SLA at 60 DAS were found to be a better choice of characters.

4.4 GENETIC DIVERGENCE

The quantitative assessment of genetic divergence was taken up by utilizing Mahalanobi's D^2 statistic. Fifty four genotypes of groundnut were subjected for the analysis

- to find out the most important characters contributing to total diversity among morphological, biochemical and physiological characters chosen for the study,
- to frame clustering pattern of genotypes based on D^2 values,
- to assess the contribution of different characters to total diversity and
- to identify suitable parents for hybridization considering the means and divergence.

4.4.1 Test with Wilk's criterion

Divergence studies were carried out separately for morpho-biochemical characters and physiological characters. Analyses of variance revealed significant differences among the genotypes for all the 15 morphological and biochemical characters and 12 physiological characters. Wilk's 'λ' criterion was used to test the differences among the genotypes based on the pooled effect of all the characters. The significance of 'V' statistic was tested by χ^2 at 795 degrees of freedom. The 'V' statistic was highly significant when all the characters were considered simultaneously for both groups of characters.

4.4.2 Grouping of genotypes into different clusters

The 54 genotypes of groundnut were grouped into different clusters using Tocher's method with the criterion that the intra cluster average D^2 values should be less than the inter cluster D^2 values, for morphological and biochemical characters at one time and physiological characters at the other.

When data on morphological and biochemical characters together were subjected to D^2 analysis, the 54 groundnut genotypes were grouped into eleven clusters. On the other hand, they were grouped into seventeen clusters when physiological characters were considered.

The grouping pattern for morphological and biochemical characters revealed that cluster I was the largest in which 33 genotypes were grouped. Cluster II followed it with next largest number with seven genotypes. Cluster VI accommodated five genotypes and cluster X with two. The remaining clusters had one genotype each. Table 15 contains the genotypes falling in different clusters and plates from 3 to 6 display the genotypes under different clusters.

TPT 2

ICGS 11

ICG 3643

ICG 50

ICGV 88448

K 134

ICGV 96234

ICG 4749

Plate 3: Groundnut genotypes evaluated for morphological and biochemical characters in cluster I

Plate 3 (cont.)

ICG 11386

ICGS 21

TCGS 320

ICG 7749

TCGS 29

TG 49

TG 45

TCGS 407

Plate 3 (cont.)

TCGS 634

JL 24

ICGV 63031

ICG 4893

ICGV 86552

ICG 1416

ICG 2411

ICG 8666

Plate 3 (cont.)

ICG 13938

TPT 4

ICG 3509

TG 39

TCGS 584

ICGV 86584

ICG 6690

ICG 7332

TG 40 in cluster I

ICG 3245 in cluster II

ICG 10352 in cluster II

ICG 2184 in cluster II

TCGS 91 in cluster II

ICG 3542 in cluster II

ICG 1326 in cluster II

TPT 1 in cluster II

Plate 4: Groundnut genotypes evaluated for morphological and biochemical characters in cluster I and II

TG 41 in cluster III

ICG 7633 in cluster IV

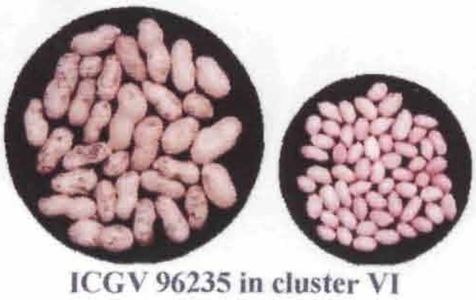
M 13 in cluster V

TCGS 617 in cluster VI

ICG 8325 in cluster VI

ICGV 89214 in cluster VI

TG 42 in cluster VI



ICGV 96235 in cluster VI

Plate 5: Groundnut genotypes evaluated for morphological and biochemical characters in cluster III, IV, V and VI

Table 15: **Clustering pattern of 54 groundnut genotypes on D^2 statistic for morphological and biochemical characters**

Cluster	No. of genotypes	Name of the genotypes
I	33	ICGV 96234, K 134, ICG 3643, ICGV 88448, ICGS 11, ICG 4749, ICG 50, TPT 2, TCGS 634, JL 24, ICG 4893, ICG 2411, ICG 8666, ICGV 86031, ICGV 86552, ICG 1416, TCGS 407, TCGS 320, ICG 7749, ICG 11386, ICGS 21, TCGS 29, TG 49, TG 45, TG 39, TCGS 584, ICG 7332, TPT 4, ICG 3509, ICGV 86584, ICG 13938, ICG 6690, TG 40
II	7	ICG 3542, ICG 3245, TPT 1, ICG 2184, ICG 1326, ICG 10352, TCGS 91
III	1	TG 41
IV	1	ICG 7633
V	1	M 13
VI	5	ICGV 89214, ICGV 96235, ICG 8325, TCGS 617, TG 42
VII	1	ICG 7637
VIII	1	TCGS 596
IX	1	ICGV 86564
X	2	ICG 5502, TCGS 61
XI	1	BAU 13

Table 16: **Clustering pattern of 54 groundnut genotypes on D^2 statistic for physiological characters**

Cluster	No. of genotypes	Name of the genotypes
I	22	ICGS 21, TCGS 91, ICG 3245, JL 24, ICGV 96234, TCGS 596, ICGV 88448, ICG 11386, TCGS 617, ICG 3509, M 13, TCGS 320, TG 42, ICGS 11, ICG 3643, ICG 2184, TG 41, TG 49, ICG 5502, TPT 2, TG 39, ICG 2411
II	11	ICG 50, ICG 1326, ICG 6690, ICG 10352, K 134, TG 40, BAU 13, ICGV 86564,ICGV 89214, ICG 7633, ICG 4749
III	2	TG 45, TCGS 584
IV	6	ICG 7749, ICGV 96235, TCGS 634, ICG 7637, TCGS 61, ICG 1416
V	1	ICGV 86584
VI	1	TCGS 29
VII	1	ICG 3542
VIII	1	TCGS 407
IX	1	ICG 4893
X	1	ICG 8325
XI	1	TPT 4
XII	1	ICGV 86031
XIII	1	ICG 7332
XIV	1	ICG 13938
XV	1	ICG 8666
XVI	1	TPT 1
XVII	1	ICGV 86552

For physiological characters, cluster I with 22 genotypes stood as the largest uster and cluster II with eleven genotypes, cluster IV with six genotypes and III with two notypes followed it in descending order. The other thirteen clusters held one genotype ach. The genotypes falling in different clusters were given in the table 16.

4.4.3 Clustering pattern in relation to geographic diversity

The constellation of genotypes into different clusters for both groups of characters s furnished in tables 15 and 16. The results in table 15 revealed that the distribution of enotypes into different clusters for morphological and biochemical characters was at andom and independent of each other. For instance, the genotypes developed at Tirupati, India had fallen in the clusters, I, II, VI, VIII and X. Cluster I consisted the genotypes rocured from ICRISAT, Kadiri, Tirupati, Junagadh, Tanzania, Argentina, Indonesia, Sudan, Nigeria, Trombay, Brazil and Zimbabwe. Like wise, cluster II possessed genotypes whose origin hails from India, Zaire and Zimbabwe. Therefore no relationship was observed between geographic origin and genetic diversity.

Distribution of genotypes for physiological characters in various clusters is shown in table 16. When clustering pattern was related to geographical origin, no regular demarcation was discernible in the pattern of constellation of genotypes into various clusters. For example, four genotypes from Tirupati, four from Trombay, seven from ICRISAT, two from Argentina, one each from Zaire, Jalgaon and Tanzania were grouped under cluster I. The genotypes from one center i.e., Tirupati had fallen in clusters I, III and V. Further more they had occupied solitary position in the clusters, VI, VIII, XI and XVI.

Table 17: Inter-cluster and intra-cluster (diagonal) distances of 54 groundnut genotypes for morphological and biochemical Characters

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**14.91**	20.91	19.21	18.23	20.54	28.88	27.71	21.08	32.29	34.56	37.03
II		**12.71**	30.14	20.68	30.49	37.70	22.30	30.70	35.04	38.91	46.75
III			**0.00**	23.68	12.55	21.40	34.44	17.72	28.31	36.34	29.61
IV				**0.00**	20.26	26.10	17.75	22.38	24.87	34.39	35.71
V					**0.00**	16.48	30.19	18.46	20.21	35.85	27.01
VI						**15.02**	35.91	19.24	19.92	33.97	18.96
VII							**0.00**	32.95	26.96	38.45	44.76
VIII								**0.00**	27.03	27.43	21.45
IX									**0.00**	37.69	28.34
X										**15.46**	32.67
XI											**0.00**

Table 18: Inter-cluster and intra-cluster (diagonal) distances of 54 groundnut genotypes for physiological characters

Clusters	I	II	III	IV	V	VI	VII	VII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII
I	8.00	11.37	10.19	11.95	9.35	11.39	13.70	10.18	9.31	9.07	10.08	11.28	14.21	15.20	19.11	12.49	19.88
II		7.96	12.74	18.42	10.14	17.50	9.25	16.87	11.45	10.43	12.95	9.77	9.48	10.69	12.59	11.66	13.32
III			4.30	15.55	14.12	14.20	16.38	11.17	10.44	10.88	12.60	12.06	16.36	16.41	20.26	16.25	22.31
IV				7.83	13.25	9.90	20.57	9.62	13.63	12.51	12.34	16.13	20.27	21.70	26.74	15.96	26.00
V					0.00	13.42	10.89	14.81	11.49	7.84	9.67	8.49	9.66	13.24	18.01	9.83	16.00
VI						0.00	19.93	8.72	9.51	13.40	8.41	18.14	21.05	22.65	25.01	17.06	26.37
VII							0.00	19.63	15.34	13.90	15.33	12.46	10.88	10.26	10.29	8.61	10.53
VII								0.00	11.04	13.33	12.51	16.36	20.36	20.32	24.73	16.76	26.50
IX									0.00	9.46	6.79	12.73	14.52	16.50	19.08	14.84	20.73
X										0.00	9.44	6.99	9.96	14.07	19.01	11.66	17.17
XI											0.00	13.65	14.97	18.16	20.08	12.89	20.42
XII												0.00	7.67	8.91	17.76	11.25	15.19
XIII													0.00	9.63	14.78	12.76	11.83
XIV														0.00	13.61	11.84	13.03
XV															0.00	15.28	9.41
XVI																0.00	13.11
XVII																	0.00

4.4. Inter and intra cluster distance (D^2) values

The inter and intra cluster distances for morphological and biochemical (table 17) and physiological characters (table 18) showed that the genotypes were highly divergent.

The maximum inter cluster distance, for morphological and biochemical characters, was observed between cluster II and XI (46.75) followed by cluster VII and cluster XI (44.76), while the minimum inter cluster distance was observed between cluster III and V (12.55) followed by V and VI (16.48). The clusters separated by maximum inter cluster distance showed maximum divergence. The intra cluster distance ranged from 0 (cluster III, IV, V, VII, VIII, IX and XI) to 15.46 (cluster X).

Perusal of the results furnished in table 18 for physiological characters indicated that intra cluster distances varied between 0 (cluster V to XVII) and 8 (cluster I). Most of the intra cluster distances were at par. Maximum inter cluster distance was observed between cluster IV and cluster XV (26.74) followed by cluster VI and XVII (26.37). Minimum inter cluster distance was observed between clusters IX and XI (6.79) and between clusters X and XII (6.99).

4.5 Cluster means

4.5.1 *Cluster means for 15 morphological and biochemical characters*

The estimated cluster mean values for 15 morphological and biochemical characters are presented in table 19. Analysis of the data indicated considerable differences between the clusters for most of the characters studied. The most remarkable differences between the clusters were noticed for shell volume, pod volume, free space in

Table 19: Cluster means for morphological and biochemical characters in 54 groundnut genotypes

Clusters	Shell volume (cc)	Pod volume (cc)	Free space in pod (cc)	Shelling % (%)	Mature pods per plant	Immature pods per plant	100 seed weight (g)	Seed moisture %	Oil %	Protein content ($mg\ g^{-1}$)	Carbo-hydrate content ($mg\ g^{-1}$)	Reducing sugar content ($mg\ g^{-1}$)	Non-reducing sugar content ($mg\ g^{-1}$)	Aflatoxin content ($ppb\ kg^{-1}$)	Kernel weight per plant (g)
I	0.94	2.21	0.48	66.69	21.88	8.87	38.00	10.15	51.82	208.81	118.85	1.62	11.86	24.92	11.45
II	0.61	1.39	0.24	70.11	24.61	6.15	31.16	10.04	51.09	204.96	120.18	7.40	24.75	21.14	11.08
III	1.50	3.50	0.50	67.38	18.80	15.97	49.76	9.97	54.40	239.75	123.30	0.16	3.45	9.67	10.75
IV	1.23	2.73	0.73	70.83	25.03	4.93	32.03	9.60	52.23	194.76	120.97	3.72	38.59	12.00	14.24
V	1.17	3.40	1.13	65.08	25.13	16.33	53.26	10.80	51.63	215.83	131.71	1.08	15.62	3.67	15.16
VI	1.71	4.21	1.33	61.27	18.07	10.61	57.81	10.66	51.29	187.70	124.33	2.73	14.70	41.32	12.33
VII	1.00	2.03	0.43	61.21	24.53	11.17	36.71	10.33	53.13	219.82	128.91	6.69	67.54	35.83	10.72
VIII	1.93	3.50	0.50	62.59	22.10	7.33	49.23	10.90	54.27	197.61	123.31	2.24	8.96	30.50	12.83
IX	1.73	4.17	1.13	60.39	28.30	15.07	55.61	11.27	49.93	193.62	127.04	7.73	42.96	17.67	14.99
X	1.97	3.18	0.50	58.56	23.03	7.37	43.62	10.45	50.52	187.36	124.71	3.36	17.12	613.33	12.34
XI	2.43	4.83	1.30	56.34	17.13	15.97	66.29	10.43	50.17	167.43	126.11	1.92	8.73	33.33	11.06

d mature pods per plant, immature pods per plant, 100 seed weight, protein content, ducing sugar content, non-reducing sugar content and aflatoxin content. The differences ween cluster means for shelling percentage, oil percentage, carbohydrate content and nel weight per plant were narrow.

The individual cluster means of each of the characters were compared with their spective overall averages. Based on the direction of association with kernel weight per plant and afltoxin content, higher and lower values above the overall means were utilized o identify the best clusters for the characters.

The cluster means for shell volume ranged from 0.61 cc (II) to 2.43 cc (XI). The lusters with lower shell volume than the overall mean were I (0.94 cc), II (0.61 cc), V 1.17 cc) and VII (1 cc). Pod volume was the highest in XI (4.83 cc) and the lowest in II 1.39 cc). Apart from the cluster XI, high cluster means for pod volume were recorded in III (3.5 cc), V (3.4 cc), VI (4.21 cc), VIII (3.5 cc) and IX (4.17 cc). Free space in pod anged between 0.24 (II) and 1.13 cc (V). The other clusters apart from II, which had low means, were I (0.48 cc), II (0.24 cc), III (0.5cc), IV (0.73), VII (0.43), VIII (0.5) and X 0.5 cc). The cluster IV (70.83 %) showed the highest mean for shelling percentage. Where as cluster XI showed the lowest value (56.34 %). The clusters on positive side over e overall mean were I (66.69 %), II (70.11 %), III (67.38 %), IV (70.83 %) and V (65.08). The highest, and the lowest mean number of mature pods per plant were recorded in usters IX (28.3) and XI (17.13) respectively. High values were recorded for II (24.61), IV (25.03), V (25.13) VII (24.53), IX (28.3) and X (23.03). Cluster IV (4.93) recorded the lowest mean number of immature pods. While cluster V recorded the highest (16.33). Lower mean number of immature pods per plant were recorded in I (8.87), II (6.15), VI (10.61), VIII (7.33) and X (7.37). The cluster mean values for 100 seed weight ranged from 31.16 g (II) to 66.29 g (XI). High mean values were recorded in III (49.76 g), V

8.26 g), VI (57.81 g), VIII (49.23 g) and IX (55.61 g). The lowest cluster mean for seed oisture percentage was observed in IV (9.6). The other low values were recorded for sters I (10.15 %), II (10.04 %), III (9.97 %), VII (10.33 %) and IX (11.27 %).

The values for oil percentage ranged from 49.9 % (IX) to 54.4 % (III). Lower lues than the overall mean were obtained by the clusters I (51.82 %), II (51.09 %), V (51.63 %), VI (51.29 %), IX (49.93 %), X (50.52 %) and XI (50.17 %). The range in otein content values was between 167.43 mg g^{-1} (XI) to 239.75 mg g^{-1} (III). Higher alues were recorded in I (208.81 mg g^{-1}), II (204.96 mg g^{-1}), V (215.83 mg g^{-1}) and VII 219.82 mg g^{-1}). The cluster means for carbohydrate content ranged from 118.85 mg g^{-1} (I) 131.71 mg g^{-1} (V). The lower values were observed in II (120.18 mg g^{-1}), III (123.3 mg), IV (120.97 mg g^{-1}) and VIII (123.31 mg g^{-1}). Cluster means for reducing sugar ontent were high in II (7.4 mg g^{-1}), IV (3.72 mg g^{-1}), VII (6.69 mg g^{-1}) and IX (7.73 mg g^{-}). The highest cluster means for non-reducing sugar content were recorded for VII (67.54 mg g^{-1}) and the lowest for III (3.45 mg g^{-1}). The other higher values than overall mean ere 24.75 mg g^{-1} (II), 38.59 mg g^{-1} (IV) and 42.96 mg g^{-1} (IX). With respect to latoxin content the lowest and the highest values were recorded in clusters V (3.67 ppb $^{-1}$) and X (613.33 ppb kg^{-1}) respectively. All the other clusters recorded cluster mean lues lower than the overall mean. The range in cluster mean values for kernel weight s from 10.72 g (VII) to 15.16 g (V). The clusters, IV (14.24 g), VIII (12.83 g) and IX .99 g) were the others apart from V, which recorded the higher values.

Based on the association analyses and on the direction of association, cluster ns that were higher or lower than the overall average were taken into account to identify the important clusters across all the 15 morphological, biochemical characters. Cluster II was considered to be the best as it exhibited higher cluster mean values than overall means for eleven characters. Clusters; IV and V (superior for nine characters each) and clusters; I and IX (superior for eight characters each) were the other clusters from which superior genotypes could be selected. The clusters X and XI were considered to be of little importance in the present study as they were better for only four and three characters respectively.

4.4.5.2 *Cluster means for physiological characters*

The cluster means for each of the fourteen physiological characters were presented in table 20. They had manifested appreciable variation. The differences were more pronounced for SLA at 30 DAS, SLA at 60 DAS, SLA at 90 DAS, SLW at 60 DAS, CGR at 60 DAS, LAR at 90 DAS, pod and kernel weights per plant.

The cluster means for SLA at 30 DAS ranged from 158.04 cm^2g-^{1} (X) to 247.74 cm^2g^{-1} (III). Lower values than the overall mean (199.9 cm^2g^{-1}) were recorded by the clusters, IV, V, IX, X, XI, XII, XIII, XVI and XVII. The range in cluster means for SLA at 60 DAS was from 121.05 cm^2g^{-1} (XIV) to 247.08 cm^2g^{-1} (XV). The cluster means higher than the average (173.19 cm^2g^{-1}) for SLA at 60 DAS were recorded in the clusters, I, II, V, VI, VII, XI, XV and XVII. At 90 DAS, SLA recorded lower cluster means in the clusters, III, IV, V, VI, X, XII, XIV, XVI and XVII than the average of 196.22 cm^2g^{-1}. The lowest and the highest values recorded in the clusters, XII and XI respectively were 151.32 cm^2g^{-1} and 238.22 cm^2g^{-1}. At 30 DAS, SLW recorded lower values than the average (5.12 g cm^2) in the clusters, I, II, III, VI, VII, VIII, XIV and XV. Its cluster means ranged from 4.14 g cm^2 (VII) to 6.33 g cm^2 (X). The overall cluster mean for SLW at 60 DAS was 5.96 g cm^2. The clusters, III, IV, VIII, XII, XIII, XIV and XVI recorded higher values than the overall mean. The range in cluster mean values was from 4.05 g cm^2 (XV) to 7.3 g cm^2 (XII). At 90 DAS, SLW recorded an overall mean of 5.2 g cm^2. The cluster means higher than the average were recorded in the clusters, VII, VIII, IX, XI, XIII and

Table 20: Cluster means for physiological characters in 54 groundnut genotypes

Clusters	SLA at 30 DAS ($cm^2 g^{-1}$)	SLA at 60 DAS ($cm^2 g^{-1}$)	SLA at 90 DAS ($cm^2 g^{-1}$)	SLW at 30 DAS ($g cm^{-2}$)	SLW at 60 DAS ($g cm^{-2}$)	SLW at 90 DAS ($g cm^{-2}$)	CGR at 60 DAS ($g m^{-2} d^{-1}$)	CGR at 90 DAS ($g m^{-2} d^{-1}$)	LAR at 90 DAS ($cm^2 g^{-1}$)	LAI at 90 DAS	SCMR at 30 DAS	Harvest index	Pod weight per plant (g)	Kernel weight per plant (g)
I	227.36	182.49	196.43	4.48	5.62	5.23	9.11	8.78	39.05	2.32	41.39	0.33	18.22	11.60
II	213.32	190.07	202.42	4.79	5.36	4.99	5.59	11.31	43.09	2.47	40.52	0.34	18.76	11.95
III	247.74	165.26	195.91	4.08	6.12	5.15	8.17	5.79	23.31	1.07	41.93	0.37	13.93	9.13
IV	193.68	160.75	180.62	5.21	6.03	5.61	12.95	7.61	43.85	2.95	42.16	0.32	19.02	11.32
V	192.69	180.60	194.82	5.19	5.56	5.30	8.16	10.46	48.70	2.99	45.30	0.29	20.73	14.83
VI	202.77	199.95	190.09	4.93	5.01	5.32	12.43	6.50	36.71	2.34	36.23	0.31	19.21	14.45
VII	222.11	173.28	202.17	4.50	5.78	4.95	5.26	18.56	41.56	3.21	41.97	0.35	17.92	13.74
VIII	228.00	149.17	204.63	4.14	6.73	4.92	12.11	6.64	36.14	2.21	37.90	0.25	12.31	7.91
IX	183.16	173.00	211.75	5.61	5.79	4.79	9.01	5.94	42.45	2.12	34.93	0.36	17.35	12.47
X	158.04	170.21	188.40	6.33	5.88	5.32	8.29	8.11	42.34	2.37	44.40	0.38	16.83	10.07
XI	163.45	182.85	238.22	6.12	5.48	4.30	9.94	8.84	47.45	3.02	38.03	0.32	21.93	15.23
XII	184.28	138.05	151.32	5.43	7.30	6.62	6.59	7.88	38.76	1.88	45.50	0.35	17.09	10.94
XIII	160.02	157.10	206.00	6.28	6.38	4.90	4.89	10.58	51.28	2.68	44.77	0.27	15.77	11.26
XIV	229.48	121.05	192.22	4.36	8.46	5.21	4.70	11.78	46.60	2.54	41.63	0.33	17.40	11.71
XV	234.11	247.08	226.38	4.42	4.05	4.46	2.34	19.50	47.61	3.44	36.00	0.31	16.64	11.08
XVI	187.91	139.07	174.23	5.33	7.02	5.78	8.03	18.70	44.04	3.82	40.53	0.33	20.14	12.81
XVII	170.24	214.10	180.14	5.88	4.74	5.59	2.47	20.55	51.54	3.87	41.93	0.36	21.75	12.28

XV. The minimum and maximum values were recorded in the clusters, XI (4.3 g cm^2) and XII (6.62 g cm^2). CGR at 60 DAS registered cluster means ranging from 2.34 g m^{-2} d^{-1} (XV) to 12.95 g m^{-2} d^{-1} (IV) with an overall mean of 7.65 g m^{-2} d^{-1}. The clusters that had recorded higher values over their average were clusters, I, III, IV, V, VI, VIII, IX, X, XI and XVI. At 90 DAS, CGR recorded the values ranging from 5.79 g m^{-2} d^{-1} (III) to 20.55 g m^{-2} d^{-1} (XVII) with an overall mean of 11.03 g m^{-2} d^{-1}. The superior cluster means were recorded for the clusters, II, VII, XIV, XV, XVI and XVII. The values ranged from 23.31 cm^{2}g^{-1} (III) to 51.54 cm^{2}g^{-1} (XVII) for LAR at 90 DAS with an overall mean of 42.62 cm^{2}g^{-1}. The clusters that had recorded higher values than 42.62 cm^{2}g^{-1} were II, IV, V, XI, XIII, XIV, XV, XVI and XVII. LAI at 90 DAS exhibited an overall mean value of 2.67 with cluster means ranging from 1.07 (III) to 3.87 (XVII). The inferior values below the average were recorded by the clusters, I, II, III, VI, VIII, IX, X, XII and XIV. The cluster mean value for SCMR at 30 DAS was low in the cluster IX (34.93) and high in the cluster XII (45.5). Lower values than the overall mean of 40.87 were recorded in the clusters, II, VI, VIII, IX, XI, XV, and XVI. Harvest index recorded cluster means ranging from 0.25 (VIII) to 0.38 (X) with an average value of 0.33. The clusters, I, II, VII, IX, X, XII, XIV, XVI and XVII recorded higher means than the overall average. The superior clusters for pod weight per plant over their overall mean (17.94 g) were I, II, IV, V, VI, XI, XVI and XVII. Their values differed between 12.31 g (VIII) and 21.93 g (XI). Kernel weight per plant registered cluster means ranging from 7.91 g (VIII) to 14.83 g (V). The superior clusters having cluster values higher than the overall mean of 11.93 g were II, V, VI, VII, IX, XVI and XVII.

The exercise as was done for morphological and biochemical characters was carried out for physiological characters also to identify the important clusters from which genotypes could be selected for crossing. Cluster XVI ranked first with superior performance for eleven characters. The clusters, II with ten characters, XVII and VI with

Table 21: Contribution of morphological and biochemical characters towards genetic divergence among 54 genotypes of groundnut

S. No.	Characters	Times ranked first	Contribution towards divergence %
1	Shell volume	39	2.73
2	Pod volume	506	35.36
3	Free space in pod	129	9.01
4	Shelling percentage	1	0.07
5	Mature pods/plant	5	0.35
6	Immature pods/plant	42	2.94
7	100 seed weight	63	4.40
8	Seed moisture percentage	13	0.91
9	Oil percentage	22	1.54
10	Protein content	12	0.84
11	Carbohydrate content	1	0.07
12	Reducing sugar content	245	17.12
13	Non-reducing sugar content	216	15.09
14	Aflatoxin content	135	9.43
15	Kernel weight/plant	2	0.14

Table 22: Contribution of physiological characters towards genetic divergence among 54 genotypes of groundnut

S. No.	Characters	Times ranked first	Contribution towards divergence %
1	SLA at 30 DAS	65	4.54
2	SLA at 60 DAS	58	4.05
3	SLA at 90 DAS	1	0.07
4	SLW at 30 DAS	2	0.14
5	SLW at 60 DAS	18	1.26
6	SLW at 90 DAS	3	0.21
7	CGR at 60 DAS	822	57.44
8	CGR at 90 DAS	173	12.09
9	LAR at 90 DAS	139	9.71
10	LAI at 90 DAS	14	0.98
11	SCMR at 30 DAS	73	5.10
12	Harvest index	9	0.63
13	Pod weight per plant	7	0.49
14	Kernel weight per plant	47	3.20

eight characters, V, IX, XI and XIV with seven characters and I, IV, VII, VIII and XV with six characters may also be considered for picking up the best genotypes.

4.4.6 Relative contribution of each character to total divergence

The relative ranking of different morphological and biochemical characters for D^2 is furnished in table 21 and depicted in fig. 3a. Among the total 1431 pair combinations, pod volume ranked first for 506 times and contributed 35.36% towards total divergence. It was followed by reducing sugar content (17.12%), non-reducing sugar content (15.09%), aflatoxin content (9.43%), free space in pod (9.01%), 100 seed weight (4.4%) and immature pods per plant (2.94%). The contribution of protein content (0.84%), mature pods per plant (0.35%), kernel weight per plant (0.14) and shelling percentage (0.07%) was minimum towards genetic divergence.

The relative contribution of physiological characters to total divergence is presented in table 22 and illustrated in fig. 3b. It was found that maximum contribution to total divergence in terms of percentage was found from CGR at 60 DAS (57.44%), CGR at 90 DAS (12.09%), LAR at 90 DAS (9.71%) SCMR at 30 DAS (5.1%) and SLA at 30 DAS (4.54%). However, LAI at 90 DAS (0.98%), harvest index (0.63%), pod weight per plant (0.49%), SLW at 90 DAS (0.21%), SLW at 30 DAS (0.14%) and SLA at 90 DAS (0.07%) contributed less to divergence.

4.5 COMBINING ABILITY ANYALYSIS

Four lines viz., ICG 1326 (L_1), ICG 3245 (L_2), ICG 3542 (L_3) and ICG 7633 (L_4) were crossed with five testers viz., ICGV 86564 (T_1), TG 42 (T_2), TG 49 (T_3), M 13 (T_4) and TPT 4 (T_5) (table 23) and the resultant 20 crosses were evaluated along with their

Table 23: Salient features of parents selected for crossing programme

S. No.	Lines (L) / Testers (T)	Genotypes	Origin	Genotypes falling in clusters for		Salient features
				Morphological and biochemical Characters	Physiological characters	
1	L_1	ICG 1326	Junagadh. India	II	II	Spanish bunch, resistant to *Aspergillus flavus*, medium duration, and high oil content.
2	L_2	ICG 3245	Zaire	II	I	Spanish bunch, medium duration, high oil content.
3	L_3	ICG 3542	India	II	VII	Spanish bunch, medium duration, low oil content.
4	L_4	ICG 7633	USA	IV	II	Spanish bunch, medium duration, resistant to *Aspergillus flavus.*
5	T_1	ICGV 86564	ICRISAT India	IX	II	Spanish bunch, long duration, high dry matter production, bold seeded, tolerant to leaf spot.
6	T_2	TG 42	Trombay, India	VI	I	Spanish bunch, early duration, high harvest index, bold seeded.
7	T_3	TG 49	Trombay, India	I	I	Spanish bunch, early duration, high harvest index, bold seeded.
8	T_4	M 13	Junagadh, India	V	I	Virginia runner, long duration, bold seeded, tolerant to leaf spot.
9	T_5	TPT 4	Tirupati, India	I	XI	Spanish bunch, medium duration, bold seeded, high yield.

parents for understanding the gene action, combining ability and heterosis for selected 14 morphological, biochemical and physiological characters. The selection criteria followed for selecting the 14 most important characters was explained in materials and methods. The results obtained by subjecting their mean values to statistical analysis are presented here under.

4.5.1 Analysis of variance

The analysis of variance revealed that the crosses taken for study differed significantly for all the selected characters (tables 24).

4.5.2 Analysis of variance for combining ability

The analysis of variance for combining ability using line X tester mating design (with parents) for 14 characters is given in table, 25. The estimates inferred that the parents (line and testers) and their interaction (line X tester) were highly significant for all the characters.

4.5.3 Components of variance

The additive and dominance genetic variances and their relative proportion for morphological, biochemical and physiological characters are presented in table 26 and illustrated in fig. 4. The results revealed that the additive genetic variance was higher in magnitude than the dominance genetic variance for pod volume and aflatoxin content. A perusal of the data indicated that the magnitude of dominance variance was higher for most of the characters (shell volume, free space in pod, shelling percentage, mature pods per plant, 100 seed weight, protein content, reducing sugar content, non-reducing sugar content, CGR at 60 and at 90 DAS, harvest index and kernel weight per plant).

Table 24. Analysis of variance for morphological, biochemical and physiological characters

Source of variation	df	Mean squares													
		Shell volume	Pod volume	Free space in pod	Shelling percent	Mature pods per plant	100 seed weight	Protein content	Reducing sugar content	Non-reducing sugar content	CGR at 60 DAS	CGR at 90 DAS	Harvest index	Aflatoxin content	Kernel weight per plant
Replications	2	0.0006	0.0022	0.0009	0.003	7.09	5.07	2.87	0.08	0.05	0.4	1.57	0.0004	0.36	0.15
Genotypes	28	0.29**	1.51**	0.05**	71.11**	160.75**	454.06**	3121.68*	21.48**	542.69**	25.36**	54.82**	0.01**	108.01**	34.43**
Error	56	0.0005	0.001	0.0002	0.28	1.75	1.18	1.51	0.25	1.9	0.15	0.36	0.00008	4.73	0.19

** Significant at 1 per cent level

Table 25: Analysis of variance of combining ability for morphological, biochemical and physiological characters

		Mean squares													
Source of variation	df	Shell volume	Pod volume	Free space in pod	Shelling %	Mature pods per plant	100 seed weight	Protein content	Reducing sugar content	Non-reducing sugar content	CGR at 60 DAS	CGR at 90 DAS	Harvest index	Aflatoxin content	Kernel weight per plant
Replications	2	0.0006	0.002	0.0009	0.003	7.09	5.07	2.87	0.08	0.05	0.39	1.57	0.0004	0.36	0.15
Treatments	28	0.29**	1.51**	0.54**	71.11**	160.75**	454.06**	3121.68**	21.48**	542.69**	25.36**	54.82**	0.011	108.01**	34.43**
Parents	8	0.40**	3.62**	1.23**	128.85**	195.76**	960.16**	1209.07**	7.98**	321.27**	5.30**	34.05**	0.014**	228.42**	14.76**
Parents (lines)	3	0.12**	0.21**	0.05**	10.38**	203.71**	31.38**	2059.60**	5.18**	374.20**	4.83**	20.82**	0.009**	399.69**	12.41**
Parents (testers)	4	0.23**	3.62**	1.72**	74.70**	135.33**	369.56**	776.45**	11.85**	209.04**	6.88**	38.22**	0.02**	119.85**	19.20**
Parents (L vs T)	1	1.89**	13.87**	2.80**	700.83**	413.61**	6108.89*	387.94**	0.92	611.40**	0.40	57.08**	0.0003	148.84**	4.05**
Parents vs crosses	1	0.98**	7.36**	1.53**	418.32**	965.10**	4467.59*	171.18**	139.18**	1139.07**	145.45**	166.97**	0.0001	210.01	232.26**
Crosses	19	0.21**	0.32**	0.20**	28.52**	103.67**	29.73**	4082.28**	20.97**	604.53**	27.48**	57.66**	0.01*	51.94**	32.30**
Lines	3	0.43	1.05*	0.06	9.70	203.26	53.68	5027.62	15.94	1221.21	18.96	15.14	0.01	82.18	17.04
Testers	4	0.17	0.10	0.20	70.59*	69.70	20.16	6026.43	19.08	422.50	33.89	53.85	0.007	80.03	62.07
Line X Tester	12	0.16**	0.21**	0.24**	19.21**	90.10**	26.93**	3197.89**	22.86**	511.03**	27.48**	69.56**	0.01**	35.02**	26.19**
Error	56	0.0005	0.001	0.0002	0.28	1.75	1.18	1.51	0.25	1.90	0.15	0.36	0.00008	4.73	0.19

*Significant at 5 per cent level ** Significant at 1 per cent level

Table 26. **Magnitude of genetic variance for morphological, biochemical and physiological characters**

Character	GCA variance	SCA variance	$\sigma^2 A$	$\sigma^2 D$	Ratio $\sigma^2 A : \sigma^2 D$
Shell volume	0.02	0.05	0.04	0.05	0.83 : 1
Pod volume	0.04	0.07	0.09	0.07	1.27 : 1
Free space in pod	0.01	0.09	0.02	0.09	0.25 : 1
Shelling percentage	2.96	6.32	5.91	6.32	0.94 : 1
Mature pods per plant	9.98	29.47	19.97	29.47	0.68 : 1
100 seed weight	2.66	8.66	5.33	8.66	0.44 : 1
Protein content	409.31	1065.50	818.61	1065.50	0.54 : 1
Reducing sugar content	1.28	7.52	2.55	7.52	0.34 : 1
Non-reducing sugar	60.76	169.80	121.51	169.80	0.72 : 1
CGR at 60 DAS	1.95	9.11	3.89	9.11	0.43 : 1
CGR at 90 DAS	2.53	23.06	5.05	23.06	0.23 : 1
Harvest index	0.0006	0.0036	0.0013	0.0036	0.35 : 1
Aflatoxin content	5.73	10.43	11.46	10.43	1.10 : 1
Kernel weight per plant	2.92	8.66	5.83	8.66	0.67: 1

4.5.4 Mean performance of parents

The mean performance of parents for all the 14 morphological, biochemical and physiological characters is presented in table 27. The importance of the characters as understood from the association analyses, for positive (+) and negative (-) selections were highlighted in the tables.

4.5.4.1 ***Shell volume.*** Shell volume ranged from 0.58 cc (L_1) to 1.03 cc (L_4) among the lines and from 1.01 cc (T_3 and T_5) to 1.65 cc (T_1) among testers. The line L_1 (0.58 cc) and L_2 (0.63 cc) and the testers, T_3 and T_4 (1.01 cc) recorded significantly lower shell volume.

4.5.4.2 ***Pod volume.*** Among the lines, pod volume ranged between 1.4 cc (L_2) and 2.02 cc (L_4) while the range was between 2.04 cc (T_5) and 4.43 cc (T_1). The lines L_3 (1.81 cc) and L_4 (2.02 cc) and the tester T_1 (4.43 cc) and T_2 (4.23 cc) were found to be significantly superior in volume when compared with respective means.

4.5.4.3 ***Free space in pod.*** This character varied from 0.17 cc (L_2 and L_3) to 0.42 cc (L_1) in lines and from 0.18 cc (T_5) to 1.8 cc (T_1) in testers. L_2 and L_3 (0.17 cc), T_3 (0.74 cc), T_4 (0.26 cc) and T_5 (0.18 cc) recorded significantly less free space in pod.

4.5.4.4 ***Shelling percentage.*** Minimum and maximum shelling percentage were recorded by L_4 (65.48 %) and L_3 (69.49 %) respectively among lines and by T_4 (50.14 %) and T_3 (62.62 %) respectively among testers. Two lines (L_2 and L_3) and two testers (T_3 and T_5) recorded significantly more shelling percentage than their means, which were 68.37 % (L_2), 69.49 % (L_3), 62.62 % (T_3) and 60.94 % (T_5).

Table 27: Mean performance of parents for morphological, biochemical and physiological characters

Parents	Shell volume (cc)	Pod volume (cc)	Free space in pod (cc)	Shelling %	Mature pods per plant	100 seed weight (g)	Protein content (mg g^{-1})	Reducing sugar content (mg g^{-1})	Non-reducing sugar content (mg g^{-1})	CGR at 60 DAS (g m^{-2} d^{-1})	CGR at 90 DAS (g m^{-2} d^{-1})	Harvest index	Aflatoxin content (ppb kg^{-1})	Kernel weight per plant (g)
LINES														
L_1	0.58$^-$	1.60	0.42	66.24	44.67$^+$	32.87	152.00	3.14	32.95	5.30$^+$	12.90$^+$	0.29	5.00$^-$	15.45 +
L_2	0.63$^-$	1.40	0.17$^-$	68.37$^+$	26.67	39.48$^+$	206.20$^+$	3.40	32.95	2.84	8.16	0.40$^+$	5.50$^-$	12.33
L_3	0.81	1.81$^+$	0.17$^-$	69.49$^+$	27.80	33.04	202.47$^+$	6.02$^+$	53.22$^+$	5.71$^+$	8.29	0.32	29.50	11.45
L_4	1.03	2.02$^+$	0.35	65.48	32.27	33.13	169.50	4.55	51.27$^+$	4.75	6.90	0.40$^+$	16.50	15.26$^+$
Mean	0.76	1.71	0.28	67.40	32.85	34.62	182.54	4.28	42.59	4.65	9.06	0.35	14.13	13.62
SEd	0.008	0.013	0.005	0.186	0.475	0.358	0.431	0.196	0.469	0.15	0.23	0.004	0.704	0.163
CD (5%)	**0.016**	**0.026**	**0.010**	**0.376**	**0.962**	**0.726**	**0.873**	**0.396**	**0.949**	**0.30**	**0.47**	**0.008**	**1.426**	**0.331**
TESTERS														
T_1	1.65	4.43$^+$	1.80	54.69	30.00$^+$	70.59$^+$	192.13$^+$	3.40	50.57	4.49	14.68$^+$	0.31	16.83	16.98$^+$
T_2	1.40	4.23$^+$	1.64	57.31	16.40	70.37$^+$	182.03$^+$	6.27$^+$	54.37$^+$	4.74	7.95	0.41$^+$	7.50$^-$	10.91
T_3	1.01$^-$	2.60	0.74$^-$	62.62$^+$	19.20	69.17$^+$	152.00	3.14	64.10$^+$	4.30	10.16	0.45$^+$	3.67$^-$	13.40$^+$
T_4	1.39	2.45	0.26$^-$	50.14	31.20$^+$	69.30$^+$	165.20	7.31$^+$	40.88	6.37$^+$	10.48	0.27	15.33	10.89
T_5	1.01$^-$	2.04	0.18$^-$	60.94$^+$	28.07$^+$	45.08	183.20$^+$	3.14	50.93	2.13	16.66$^+$	0.29	3.67$^-$	12.04
Mean	1.29	3.15	0.93	57.14	24.97	64.90	174.91	4.65	52.17	4.41	12.00	0.35	9.40	12.84
SEd	0.009	0.014	0.006	0.207	0.532	0.401	0.482	0.219	0.524	0.16	0.26	0.004	0.788	0.183
CD (5%)	**0.018**	**0.029**	**0.011**	**0.420**	**1.076**	**0.811**	**0.976**	**0.443**	**1.061**	**0.33**	**0.52**	**0.008**	**1.594**	**0.370**

$^+$ Significantly higher at 5 per cent level $^-$ Significantly lower at 5 per cent level

4.5.4.5 ***Mature pods per plant.*** Number of mature pods per plant varied between 26.67 (L_2) and 44.67 (L_1) in lines and between 16.4 (T_2) and 31.2 (T_4) in testers. L_1 (44.67), T_1 (30), T_4 (31.2) and T_5 (28.07) showed significant values over their means.

4.5.4.6 ***100 seed weight.*** The values of the character 100 seed weight ranged from 32.87 g (L_1) to 39.48 g (L_2) in lines and from 45.08 g (T_5) to 70.59 g (T_1) in testers. Significantly higher seed weight was recorded in L_2 (39.48 g) among lines and in T_1 (70.59g), T_2 (70.37 g), T_3 (69.17 g) and T_4 (69.3 g) among testers over their respective means.

4.5.4.7 ***Protein content.*** A range from 152 mg g^{-1} (L_1) to 206.2 mg g^{-1} (L_2) and from 152 mg g^{-1} (T_3) to 192.13 mg g^{-1} (T_1) for protein content among lines and testers respectively. Among lines, L_2 (206.2 mg g^{-1}) and L_3 (202.47 mg g^{-1}) and among testers, T_1 (192.13 mg g^{-1}), T_2 (182.03 mg g^{-1}) and T_5 (183.2 mg g^{-1}) recorded significantly higher protein content than their general mean.

4.5.4.8 ***Reducing sugar content.*** Reducing sugar content showed a range of 3.14 mg g^{-1} (L_1) to 6.02 mg g^{-1} (L_3) among lines and a range of 3.14 mg g^{-1} (T_3 and T_5) to 7.31 mg g^{-1} (T_4) among testers. The line L_3 (6.02 mg g^{-1}) and the testers T_2 and T_4 recorded significance for this character.

4.5.4.9 ***Non-reducing sugar content.*** The minimum and maximum non-reducing sugar content among lines were 32.95 mg g^{-1} (L_1 and L_2) and 53.22 mg g^{-1} (L_3) respectively. T_4 (40.88 mg g^{-1}) and T_3 (64.1 mg g^{-1}) were the minimum and maximum non-reducing sugar containing testers noticed. Significantly higher non-reducing sugar content over their respective general means of 42.59 mg g^{-1} (lines) and 52.17 mg g^{-1} (testers) was registered by L_3, L_4 in lines and T_2 and T_3 in testers.

4.5.4.10 ***CGR at 60 DAS.*** CGR at 60 DAS ranged from 2.84 g m^{-2} d^{-1} (L_2) to 5.71 g m^{-2} d^{-1} (L_3) in lines and from 2.13 g m^{-2} d^{-1} (T_5) to 6.37 g m^{-2} d^{-1} (T_4) in testers. Among lines, L_1 and L_3 and among testers T_4 were found to be significant over their respective means.

4.5.4.11 ***CGR at 90 DAS.*** A wide range of variation for CGR at 90 DAS was observed and it ranged from 6.9 g m^{-2} d^{-1} (L_4) to 12.9 g m^{-2} d^{-1} (L_1) among lines and from 7.95 g m^{-2} d^{-1} (T_2) to 16.66 g m^{-2} d^{-1} (T_5) among testers. However only one line (L_1) and two testers (T_1 and T_5) showed significant results when compared with general mean.

4.5.4.12 ***Harvest index.*** Harvest index showed a variation ranging from 0.29 (L_1) and 0.4 (L_2 and L_4) in lines and from 0.27 (T_4) and 0.45 (T_3) in testers. Two lines, L_2 and L_4 and two testers, T_2 and T_3 recorded significant superiority over general mean.

15.4.13 ***Aflatoxin content.*** Among lines L_1 (5 ppb kg^{-1}) and L_3 (29.5 ppb kg^{-1}) had e lowest and the highest aflatoxin content. Like wise, T_3 and T_5 (3.67 ppb kg^{-1}) were the west and T_1 (16.83 ppb kg^{-1}) was the highest among testers. L_1 and L_2 in lines and T_2, T_3 d T_5 in testers recorded significantly lower values than their means.

5.4.14 ***Kernel weight per plant.*** L_3 (11.45 g) and L_1 (15.45 g) were the lower and gher yielders among the lines and T_4 (10.89 g) and T1 (16.98 g) among testers were the er and higher yielders. L_1 and L_4 in lines and T_1 and T_3 in testers significantly out lded their general means.

Table 28: **Mean performance of crosses for morphological, biochemical and physiological characters**

Crosses	**Shell volume (cc)**	**Pod volume (cc)**	**Free space in pod (cc)**	**Shelling %**	**Mature pods per plant**	**100 seed weight (g)**	**Protein content (mg g^{-1})**
$L_1 X T_1$	0.82^{-}	2.11^{+}	0.23^{-}	68.46^{+}	50.20^{+}	33.21	204.33^{+}
$L_1 X T_2$	0.82^{-}	2.02^{+}	0.37	63.30	30.60	39.69^{+}	122.17
$L_1 X T_3$	0.99^{-}	1.82	0.02^{-}	70.38^{+}	37.73	31.61	191.83^{+}
$L_1 X T_4$	0.84^{-}	1.45	0.06^{-}	66.60	39.20^{+}	37.59^{+}	170.23
$L_1 X T_5$	0.20^{-}	1.62	0.94	65.63	39.07^{+}	36.61	192.67^{+}
$L_2 X T_1$	0.64^{-}	1.42	0.37	66.70	29.00	38.57^{+}	105.53
$L_2 X T_2$	0.64^{-}	1.64	0.37	62.06	29.07	35.93	125.70
$L_2 X T_3$	1.00^{-}	2.03^{+}	0.34	67.55^{+}	32.33	34.45	172.00
$L_2 X T_4$	1.07	2.02^{+}	0.12^{-}	71.18^{+}	30.33	42.03^{+}	179.47^{+}
$L_2 X T_5$	0.82^{-}	1.59	0.15^{-}	69.01^{+}	35.13	41.71^{+}	164.40
$L_3 X T_1$	0.79^{-}	1.64	0.23^{-}	65.57	33.20	37.97^{+}	192.63^{+}
$L_3 X T_2$	0.82^{-}	1.71	0.09^{-}	61.08	43.00^{+}	34.35	166.87
$L_3 X T_3$	0.61^{-}	1.62	0.53	65.54	30.80	34.70	205.90^{+}
$L_3 X T_4$	0.36^{-}	1.52	0.74	72.50^{+}	45.20^{+}	31.80	203.17^{+}
$L_3 X T_5$	0.81^{-}	2.04^{+}	0.40	65.73	37.20	31.11	151.67
$L_4 X T_1$	1.02	2.45^{+}	0.24^{-}	67.35^{+}	35.33	34.06	176.70
$L_4 X T_2$	1.05	2.45^{+}	0.58	63.78	26.80	33.56	141.60
$L_4 X T_3$	1.41	2.41^{+}	0.42	61.71	35.27	34.81	155.97
$L_4 X T_4$	1.01^{-}	2.05^{+}	0.03^{-}	66.49	38.47^{+}	37.75^{+}	216.33^{+}
$L_4 X T_5$	0.82^{-}	2.01^{+}	0.77	68.17^{+}	35.53	37.67^{+}	266.27^{+}
Mean	1.06	1.88	0.35	66.44	35.67	35.96	175.27
SEd	0.02	0.03	0.01	0.42	1.06	0.80	0.96
CD (5%)	**0.04**	**0.06**	**0.02**	**0.84**	**2.15**	**1.62**	**1.95**

$^{+}$Significantly higher at 5 per cent level $^{-}$ Significantly lower at 5 per cent level

Table 28 (cont.)

Crosses	Reducing sugar content (mg g^{-1})	Non-reducing content (mg g^{-1})	CGR at 60 DAS (g m^2 d^{-1})	CGR at 90 DAS (g m^2 d^{-1})	Harvest index	Aflatoxin content (ppb kg^{-1})	Kernel weight per plant (g)
L$_1$ X T$_1$	10.46^{+}	46.39^{+}	9.76^{+}	7.51	0.38^{+}	1.33^{-}	19.18^{+}
L$_1$ X T$_2$	4.45	82.24^{+}	5.45	16.13^{+}	0.28	13.83	11.98
L$_1$ X T$_3$	9.15^{+}	40.49	11.62^{+}	16.43^{+}	0.28	12.17	15.35
L$_1$ X T$_4$	7.60	41.90	11.80^{+}	10.36	0.33	7.83	13.99
L$_1$ X T$_5$	7.60	38.10	5.06	10.94	0.30	10.83	16.91
L$_2$ X T$_1$	4.45	33.92	5.04	21.14^{+}	0.27	6.33	13.42
L$_2$ X T$_2$	4.18	24.58	6.94	8.49	0.43^{+}	6.50	15.27
L$_2$ X T$_3$	7.60	27.02	3.26	14.38	0.37^{+}	5.00	14.94
L$_2$ X T$_4$	4.71	22.48	13.98^{+}	11.52	0.36	3.83^{-}	17.25
L$_2$ X T$_5$	7.48	36.02	4.25	13.64	0.47^{+}	3.67^{-}	21.61^{+}
L$_3$ X T$_1$	10.46^{+}	25.63	3.11	14.47	0.40^{+}	6.00	18.04^{+}
L$_3$ X T$_2$	3.14	40.49	3.23	15.52^{+}	0.38^{+}	12.5	14.91
L$_3$ X T$_3$	7.48	38.10	8.91^{+}	8.86	0.30	12.17	14.14
L$_3$ X T$_4$	13.61^{+}	43.60^{+}	6.80	14.54	0.40^{+}	11.67	22.67^{+}
L$_3$ X T$_5$	4.18	40.38	8.86^{+}	16.47^{+}	0.30	10.33	14.44
L$_4$ X T$_1$	6.93	33.94	8.07^{+}	22.28^{+}	0.33	6.00	18.98^{+}
L$_4$ X T$_2$	9.16^{+}	39.82	9.12^{+}	11.14	0.31	6.00	12.95
L$_4$ X T$_3$	8.78^{+}	39.82	6.50	20.15^{+}	0.31	17.17	15.32
L$_4$ X T$_4$	5.37	36.02	7.96	6.69	0.43^{+}	6.00	19.77^{+}
L$_4$ X T$_5$	7.60	70.90^{+}	6.47	13.00	0.41^{+}	3.67^{-}	23.31^{+}
Mean	7.22	40.09	7.31	13.68	0.35	8.14	16.72
SEd	0.44	1.05	0.33	0.51	0.01	1.58	0.37
CD (5%)	**0.89**	**2.12**	**0.66**	**1.04**	**0.02**	**3.19**	**0.74**

$^{+}$Significantly higher at 5 per cent level $^{-}$ Significantly lower at 5 per cent level

4.5.5 Mean performance of crosses

The mean performance of crosses for 14 characters is presented in table 28.

4.5.5.1 ***Shell volume.*** Among the crosses shell volume ranged from 0.2 cc (L_1 X T_5) to 1.41 cc (L_4 X T_3). Out of 20 crosses, 16 were significantly lesser in shell volume as compared to the mean (1.06 cc).

4.5.5.2 ***Pod volume.*** Pod volume ranged from 1.42 cc (L_2 X T_1) to 2.45 cc (L_4 X T_1 and L_4 X T_2). Ten crosses had higher values significantly differing from the mean value of crosses (1.88 cc).

4.5.5.3 ***Free space in pod.*** The cross, L_1 X T_3 recorded smaller free space in pod (0.02 cc) and L_1 X T_5 recorded greater space (0.94 cc). Nine crosses had smaller values significantly deviating from the mean (0.35 cc).

4.5.5.4 Shelling percentage. The values of shelling percentage varied between 61.08% (L_3 X T_2) and 72.5 % (L_3 X T_4). Eight crosses had significantly higher percentage as compared with the mean (66.44 %).

4.5.5.5 ***Mature pods per plant.*** The minimum and maximum number of mature pods per plant were possessed by the crosses L_2 X T_1 (29) and L_1 X T_1 (50.2) respectively. Six crosses registered significantly more number of mature pods per plant than mean (35.67).

4.5.5.6 ***100 seed weight.*** The mean performance for this character varied between 31.11 g (L_3 X T_5) and 42.03 g (L_2 X T_4). A total of eight crosses recorded highly significant values than mean of 35.96 g.

4.5.5.7 ***Protein content.*** Seed protein content of the crosses ranged from 105.53 mg g^{-1} (L_2 X T_1) to 266.27 mg g^{-1} (L_4 X T_5). A total of nine crosses recorded significantly higher protein content over the mean (175.27 mg g^{-1}).

4.5.5.8 ***Reducing sugar content.*** Among the 20 crosses, the cross L_3 X T_2 (3.14 mg g^{-1}) showed the lowest value. Where as, the cross L_3 X T_4 (13.61 mg g^{-1}) possessed the highest value. Six crosses registered significantly higher values as compared to the mean (7.22 mg g^{-1}).

4.5.5.9 ***Non-reducing sugar content.*** Non-reducing sugar varied between 22.48 mg g^{-1} (L_2 X T_4) and 82.24 mg g^{-1} (L_1 X T_2). Four crosses recorded highly significant values for non-reducing sugar content over the mean (40.09 mg g^{-1}).

4.5.5.10 ***CGR at 60 DAS.*** The variation for this character was between 3.11 g m^{-2} d^{-1} (L_3 X T_1) and 11.8 g m^{-2} d^{-1} (L_1 X T_4). Seven out of 20 crosses registered significantly more CGR as compared to the general mean of 7.31 g m^{-2} d^{-1}.

4.5.5.11 ***CGR 90 DAS.*** The range in variation for CGR at 90 DAS was between 7.51 g m^{-2} d^{-1} (L_1 X T_1) and 22.28 g m^{-2} d^{-1} (L_4 X T_1). Seven crosses excelled their general mean (13.68 g m^{-2} d^{-1}) for CGR at 90 DAS.

4.5.5.12 ***Harvest index.*** Harvest index showed a variation in range from 0.27 (L_2 X T_1) to 0.47 (L_2 X T_5). Nine crosses were found to be significantly superior over mean (0.35).

4.5.5.13 ***Aflatoxin.*** Among the crosses, aflatoxin ranged from 1.33 ppb kg^{-1} (L_1 X T_1) to 17.17 ppb kg^{-1} (L_4 X T_3). Four crosses showed significant lower aflatoxin content when compared with mean (8.14 ppb kg^{-1}).

Table 29: **Proportional contribution of lines, testers and line X tester interaction towards variation in the crosses of groundnut**

S. No.	Characters	Contribution percent of		
		Lines	Testers	Line X Tester interaction
1	Shell volume	32.86	17.82	49.32
2	Pod volume	52.45	6.72	40.83
3	Free space in pod	4.97	20.99	74.04
4	Shelling percentage	5.37	52.11	42.53
5	Mature pods per plant	30.96	14.16	54.89
6	100 seed weight	28.51	14.28	57.22
7	Protein content	19.45	31.08	49.48
8	Reducing sugar content	12.00	19.16	68.84
9	Non-reducing sugar content	31.90	14.71	53.39
10	Aflatoxin content	24.98	32.44	42.58
11	CGR at 60 DAS	10.89	25.96	63.15
12	CGR at 90 DAS	4.15	19.66	76.19
13	Harvest index	15.75	15.53	68.72
14	Kernel weight per plant	8.33	40.46	51.21

4.5.5.14 *Kernel weight per plant.* The cross, producing lower kernel weight per plant was L_4 X T_2 (12.95 g) and the maximum kernel yield per plant was produced by the cross, L_4 X T_5 (23.31 g). Seven crosses out yielded the general mean significantly (16.72 g).

4.5.6 Proportional contribution of lines, testers and line X tester interaction

Results on the proportional contribution of lines, testers and line X tester interaction towards variation in the crosses are furnished in table 29 and depicted in fig. 5. Contribution to the total variation was mainly due to line X tester interaction for all most all the characters except pod volume and shelling percentage. Variation in crosses was contributed by lines to the tune of 52.45 % for pod volume. Similarly for shelling percentage 52.11 % of total variation was contributed by testers. On relative terms, lines had contributed more than testers to variation for more characters except for free space in pod and shelling percentage for which testers contributed more than lines. For biochemical characters, excepting non-reducing sugar content, testers' contribution was greater than that of lines. When physiological characters were considered, lines contributed more than testers.

4.5.7 General combining ability effects

Estimates of general combining ability (GCA) effects of parents (lines and testers) are presented in table 30 for 14 morphological, biochemical and physiological characters. Fig. 6 illustrates gca effects of parents for aflatoxin content and fig. 7 for kernel weight.

4.5.7.1 ***Shell volume.*** The gca effects ranged from –0.148 (L_3) to 0.234 (L_4) in lines and from –0.163 (T_5) to 0.176 (T_3) in the testers. The lines L_1 (-0.092) and L_3 (-0.148) and the testers T_1 (-0.01) and T_5 (-0.163) exhibited negative and significant gca effects.

Table 30: General combining ability effects of parents for morphological, biochemical and physiological characters

Parents	Shell volume	Pod volume	Free space in pod	Shelling %	Mature pods per plant	100 seed weight	Protein content	Reducing sugar content	Non-reducing sugar content	CGR at 60 DAS	CGR at 90 DAS	Harvest index	Aflatoxin content	Kernel weight per plant
LINES														
L_1	-0.092 **	-0.078 **	-0.027 **	0.432 **	3.687 **	-0.217	0.975 **	0.632 **	9.732 **	1.429 **	-1.409 **	-0.036 **	1.058 *	-1.240 **
L_2	0.006 **	-0.140 **	-0.079 **	0.863 **	-4.500 **	2.578 **	-25.852 **	-1.536 **	-11.289 **	-0.616 **	0.152	0.025 **	-3.075 **	-0.223 *
L_3	-0.148 **	-0.175 **	0.048 **	-0.355 **	2.207 **	-1.973 **	8.775 **	0.555 **	-2.452 **	-1.127 **	0.289 *	0.004	2.392 **	0.119 *
L_4	0.234 **	0.393 **	0.058 **	-0.939 **	-1.393 **	-0.389	16.102 **	0.348 **	4.009 **	0.314 **	0.968 **	0.007 **	-0.375	1.344 **
SEd	0.006	0.009	0.004	0.131	0.336	0.254	0.305	0.138	0.332	0.104	0.163	0.003	0.498	0.115
TESTERS														
T_1	-0.010 **	0.022 *	-0.083 **	0.581 **	1.260 **	-0.008	-5.472 **	0.855 **	-5.121 **	-0.814 **	2.666 **	-0.007	-3.225 **	0.682 **
T_2	0.005 **	0.076 **	0.001	-3.886 **	-3.307 **	-0.078	-36.188 **	-1.987 **	6.689 **	-1.126 **	-0.862 **	-0.001	1.567 **	-2.942 **
T_3	0.176 **	0.091 **	-0.022 **	-0.145	-1.640 **	-2.066 **	6.153 **	1.033 **	-3.734 **	0.263*	1.274 **	-0.037 **	3.483 **	-1.784 **
T_4	-0.009	-0.122 **	-0.112 **	2.754 **	2.627 **	1.332 **	17.028 **	0.603 **	-4.093 **	2.825 **	-2.907 **	0.027 **	-0.808	1.700 **
T_5	-0.163 **	-0.067 **	0.216 **	0.697 **	1.060 **	0.819 **	18.478 **	-0.504 **	6.259 **	-1.148 **	-0.171	0.018 **	-1.017	2.345 **
SEd	0.006	0.010	0.004	0.147	0.376	0.283	0.341	0.155	0.371	0.116	0.182	0.003	0.557	0.129

* Significant at 5 per cent level ** Significant at 1 per cent level

4.5.7.2 ***Pod volume.*** For pod volume, the lower value of gca was shown by the line L_3 (-0.175) and the highest by L_4 (0.393). Where as for tester the range was from –0.122 (T_4) to 0.091 (T_3). Significantly negative values of gca were obtained by L_1 (-0.078), L_2 (-0.14) L_3 (-0.175), T_4 (-0.122) and T_5 (-0.067).

4.5.7.3 Free space in pod. The gca effects for this character varied between –0.079 (L_2) and L_4 (0.058) among lines and between –0.112 (T_4) and 0.216 (T_5) among testers. The lines L_1 (-0.027) and L_2 (-0.079) showed negative significant effects and the testers T_1 (-0.083), T_3 (-0.022) and T_4 (-0.112) were negatively significant.

4.5.7.4 ***Shelling percentage.*** Among the lines, the gca values ranged from –0.939 (L_4) to 0.863 (L_2) and for testers the range was from –3.886 (T_2) to 2.754 (T_4). The gca effects were positive and significant in lines L_1 (0.432) and L_2 (0.863). They were significantly positive in the testers, T_1 (0.581), T_4 (2.754) and T_5 (0.697).

4.5.7.5 ***Mature pods per plant.*** For number of mature pods per plant, the gca values fell between –4.5 (L_2) and 3.687 (L_1) for lines and between –3.307 (T_2) and 2.627 (T_4) for testers. Positive significant effects were observed for L_1 (3.687), L_3 (2.207), T_1 (1.26), T_4 (2.627) and T_5 (1.06).

4.5.7.6 ***100 Seed weight.*** Among the lines, gca effects for 100 seed weight ranged from –1.973 (L_3) to 2.578 (L_2) among lines and from –2.066 (T_3) to 1.332 (T_4) among testers. T_4 (1.332) and T_5 (0.819) had positive significant effects.

4.5.7.7 ***Protein content.*** The gca effects ranged from –25.852 (L_2) to 16.102 (L_4) in lines and from –36.188 (T_2) to 18.478 (T_5) in testers. The lines, L_4 (16.102), L_1 (0.975), nd L_3 (8.775) and the testers, T_3 (6.153), T_4 (17.028) and T_5 (18.478) had positive and gnificant gca effects.

5.7.8 ***Reducing sugar content.*** Among lines, minimum gca for reducing sugar ntent was recorded by L_2 (-1.536) and maximum by L_1 (0.632). Among testers, T_2 987) showed minimum value for reducing sugar content while, T_3 (1.033) had the aximum. The lines, L_1 (0.632), L_3 (0.555), L_4 (0.348) and the testers, T_1 (0.855), T_3 033) and T_4 (0.603) showed significant values.

4.5.7.9 ***Non-reducing sugar content.*** The gca effects for non-reducing sugar content anged from –11.289 (L_2) to 9.732 (L_1) in lines and from –5.121 (T_1) to 6.689 (T_2) in esters. Significantly higher values over their respective means for non-reducing sugar ontent were recorded in L_1 (9.732) and L_4 (4.009) among lines and in T_2 (6.689) and T_5 259) among testers.

4.5.7.10 ***CGR at 60 DAS.*** The line L_3 had the lowest values of –1.127, while L_1 xhibited the highest value 1.429 for gca effects. The gca of the testers ranged from -1.148 (T_5) to 2.825 (T_4). The lines L_1 (1.429) and L_4 (0.314) recorded positive and ignificant gca effects. Like wise, T_3 (0.263) and T_4 (2.825) showed positive and ignificant values.

4.5.7.11 ***CGR at 90 DAS.*** For CGR at 90 DAS, the gca values fell between –1.409 L_1) and 0.968 (L_4) for lines and between –2.907 (T_4) and 2.666 (T_1) for testers. Positive nd significant gca effects were observed by L_3 (0.289) and L_4 (0.968) in lines and by T_1 2.666) and T_3 (1.274) in testers.

4.5.7.12 ***Harvest index.*** Among the lines, gca effects for harvest index ranged from -0.036 (L_1) to 0.025 (L_2) and from –0.037 (T_3) to 0.027 (T_4) among testers. Positive significant gca effects were recorded by L_2 (0.025), L_4 (0.007), T_4 (0.027) and T_5 (0.018).

4.5.7.13 ***Aflatoxin content.*** A minimum gca effect for aflatoxin content of –3.075 and a maximum of 2.392 were recorded by L_2 and L_3 respectively among lines. Where as T_1 (-3.225) and T_3 (3.483) among testers had the minimum and maximum gca effects respectively. L_2 (-3.075) in lines and T_1 (-3.225) in testers showed significant gca effects for aflatoxin content.

4.5.7.14 ***Kernel weight per plant.*** For kernel weight per plant, the lowest value of gca was shown by the line L_1 (-1.24) and the highest by L_4 (1.344) in lines. Where as in testers, the range was from -2.942 (T_2) to 2.345 (T_5). Significantly positive values for gca were obtained by L_3 (0.119) L_4 (1.344), T_1 (0.682), T_4 (1.7) and T_5 (2.345).

4.5.8 Specific combining ability effects of crosses

The specific combining ability (sca) effects of crosses for 14 characters were present in table 31. Fig. 8 and 9 depicts sca effects of 20 F_1 crosses for aflatoxin content and kernel weight per plant respectively.

4.5.8.1 Shell volume. The specific combining ability effects for shell volume ranged from -0.368 (L_1 X T_5) to 0.297 (L_3 X T_5). Out of twenty crosses, eight had negative significant sca effects.

4.5.8.2 Pod volume. The range of sca effects was noticed from –0.343 (L_2 X T_1) to 0.401 (L_3 X T_5). Eight combiners were found to have significant positive sca effects.

Table 31: Specific combining ability effects of 20 F_1 crosses for morphological, biochemical and physiological characters

Crosses	Shell volume	Pod volume	Free space in pod	Shelling %	Mature pods per plant	100 seed weight	Protein content	Reducing sugar content	Non-reducing sugar content	CGR at 60 DAS	CGR at 90 DAS	Harvest index	Aflatoxin content	Kernel weight per plant
L_1 X T_1	0.095 **	0.281 **	-0.007	1.005 **	9.580 **	-2.528 **	33.558 **	1.753 **	1.689 *	1.839 **	-7.430 **	0.074 **	-4.642 **	3.017 **
L_1 X T_2	0.080 **	0.141 **	0.042 **	0.312	-5.453 **	4.022 **	-17.892 **	-1.419 **	25.722 **	-2.163 **	4.721 **	-0.033 **	3.067 **	-0.556 *
L_1 X T_3	0.079 **	-0.074 **	-0.281 **	3.651 **	0.013	-2.063 **	9.433 **	0.269	-5.601 **	2.622 **	2.885 **	0.001	-0.517	1.649 **
L_1 X T_4	0.114 **	-0.232 **	-0.152 **	-3.028 **	-2.787 **	0.518	-23.042 **	-0.855 **	-3.829 **	0.233	0.990 **	-0.010	-0.558	-3.191 **
L_1 X T_5	-0.368 **	-0.117 **	0.397 **	-1.941 **	-1.353	0.052	-2.058 *	0.252	-17.981 **	-2.531 **	-1.166 **	-0.031 **	2.650 *	-0.919 **
L_2 X T_1	-0.187 **	-0.343 **	0.183 **	-1.178 **	-3.433 **	0.044	-38.415 **	-2.093 **	10.237 **	-0.842 **	4.636 **	-0.104 **	4.492 **	-3.764 **
L_2 X T_2	-0.199 **	-0.173 **	0.098 **	-1.355 **	1.200	-2.533 **	12.468 **	0.486	-10.913 **	1.373 **	-4.486 **	0.053 **	-0.133	1.714 **
L_2 X T_3	-0.006	0.202 **	0.092 **	0.397	2.800 **	-2.025 **	16.427 **	0.883 **	1.950 *	-3.700 **	-0.725	0.029 **	-3.550 **	0.229
L_2 X T_4	0.242 **	0.398 **	-0.036 **	1.125 **	-3.467 **	2.157 **	13.018 **	-1.577 **	-2.234 *	4.462 **	0.596	-0.048 **	-0.425	-0.948 **
L_2 X T_5	0.150 **	-0.084 **	-0.337 **	1.011 **	2.900 **	2.357 **	-3.498 **	2.300 **	0.961	-1.292 **	-0.020	0.071 **	-0.383	2.770 **
L_3 X T_1	0.124 **	-0.088 **	-0.088 **	-1.097 **	-5.940 **	3.988 **	14.058 **	1.830 **	-6.887 **	-2.261 **	-2.167 **	0.050 **	-1.308	0.518
L_3 X T_2	0.132 **	-0.072 **	-0.312 **	-1.120 **	8.427 **	0.444	19.008 **	-2.649 **	-3.841 **	-1.829 **	2.411 **	0.027 **	0.400	1.016 **
L_3 X T_3	-0.242 **	-0.177 **	0.155 **	-0.401	-5.440 **	2.779 **	15.700 **	-1.328 **	4.196 **	2.468 **	-6.382 **	-0.020 **	-1.850	-0.920 **
L_3 X T_4	-0.311 **	-0.064 *	0.454 **	3.666 **	4.693 **	-3.519 **	2.092 **	5.235 **	10.049 **	-2.207 **	3.472 **	0.016 *	1.942	4.134 **
L_3 X T_5	0.297 **	0.401 **	-0.210 **	-1.047 **	-1.740 *	-3.692 **	-50.858 **	-3.088 **	-3.517 **	3.829 **	2.666 **	-0.072 **	0.817	-4.748 **
L_4 X T_1	-0.032 *	0.150 **	-0.088 **	1.270 **	-0.207	-1.503 *	-9.202 **	-1.490 **	-5.038 **	1.264 **	4.960 **	-0.019 **	1.458	0.229
L_4 X T_2	-0.013	0.104 **	0.171 **	2.163 **	-4.173 **	-1.933 **	-13.585 **	3.582 **	-10.968 **	2.619 **	-2.646 **	-0.046 **	-3.333 **	-2.173 **
L_4 X T_3	0.169 **	0.049 *	0.034 **	-3.647 **	2.627 **	1.309 *	-41.560 **	0.176	-0.545	-1.390 **	4.222 **	-0.010	5.917 **	-0.958 **
L_4 X T_4	-0.046 **	-0.102 **	-0.267 **	-1.763 **	1.560 *	0.844	7.932 **	-2.804 **	-3.986 **	-2.488 **	-5.057 **	0.043 **	-0.958	0.005
L_4 X T_5	-0.078 **	-0.201 **	0.149 **	1.977 **	0.193	1.284 *	56.415 **	0.536	20.536 **	-0.006	-1.480 **	0.032 **	-3.083 **	2.897 **
SEd	**0.012**	**0.020**	**0.008**	**0.293**	**0.752**	**0.567**	**0.682**	**0.310**	**0.741**	**0.232**	**0.364**	**0.006**	**1.114**	**0.258**

* Significant at 5 per cent level ** Significant at 1 per cent level

4.5.8.3 ***Free space in pod.*** Free space in pod had sca effects between –0.337 (L_2 X T_5) and 0.454 (L_3 X T_4). Out of 20 cross combinations, nine had negative significant sca effects.

4.5.8.4 ***Shelling percentage.*** Among the crosses, sca effects differed from –3.647 (L_4 X T_3) to 3.666 (L_3 X T_4). Eight out of ten positive crosses showed significant sca effects.

4.5.8.5 ***Mature pods per plant.*** The minimum and maximum sca effects recorded among crosses for this character were –5.94 (L_3 X T_1) and 9.58 (L_1 X T_1) respectively. Seven out of ten positive sca effects were significant.

4.5.8.6 **100 Seed weight.** The cross combination, L_3 X T_5 (-3.692) and L_1 X T_2 (4.022) showed the lowest and the highest sca effects for 100 seed weight. Seven cross combinations showed significantly positive sca effects.

4.5.8.7 ***Protein content.*** Protein content exhibited minimum and maximum sca effects of -50.858 (L_3 X T_5) and 56.415 (L_4 X T_5) respectively. All the eleven positive sca effects were significant.

4.5.8.8 ***Reducing sugar content.*** The sca effects for reducing sugar content varied between –3.088 (L_3 X T_5) and 5.235 (L_3 X T_4). Six crosses out of twenty were having positive and significant sca effects.

4.5.8.9 ***Non-reducing sugar content.*** The lowest and the highest sca effects for this character were exhibited in L_1 X T_5 (-17.981) and L_1 X T_2 (25.722) respectively. Altogether seven cross combinations showed positive significant gca effects for non-reducing sugar.

4.5.8.10 ***CGR at 60 DAS.*** The sca effects for this character expressed a range from -3.7 (L_2 X T_3) to 4.462 (L_2 X T_4). Eight out of nine positive sca effects were significant.

4.5.8.11 ***CGR at 90 DAS.*** The lowest sca effects of –7.43 (L_1 X T_1) and the highest effect of 4.96 (L_4 X T_1) and the highest effect of 4.96 (L_4 X T_1) were registered for CGR at 90 DAS. Eight crosses expressed positive significant sca effects for this character.

4.5.8.12 ***Harvest index.*** The cross combinations L_2 X T_1 (-0.104) and L_1 X T_1 (0.074) exhibited the minimum and maximum gca effects for harvest index. Significantly positive sca effects for this character were established in nine cross combinations.

4.5.8.13 ***Aflatoxin content.*** Among the crosses, the range of sca effects for aflatoxin content was from –4.642 (L_1 X T_1) to 5.917 (L_4 X T_3). Only four combinations had negative significant values.

4.5.8.14 ***Kernel weight per plant.*** The minimum and maximum sca effects for this character were –4.748 (L_3 X T_5) and 4.134 (L_3 X T_4) respectively. Positive significant sca effects were recorded for seven crosses.

4.6 HETEROSIS

The percentage of heterosis over mid parent (relative heterosis (di)), better parent heterobeltiosis (dii)) and standard variety, TPT 4 (standard heterosis (diii)) for all the 14 characters were furnished from tables 32 to 35. They were graphically represented for the two most important characters; aflatoxin content and kernel weight per plant in fig. 10 and 11 respectively.

Table 32: Percentage of heterosis for shell volume, pod volume, free space in pod and shelling percentage

Crosses	Shell volume			Pod volume			Free space in pod			Shelling percentage		
	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)
$L_1 X T_1$	-26.35 **	-50.20 **	-19.08 **	-30.13 **	-52.41 **	3.27 *	-78.98 **	-87.04 **	27.27 **	13.22 **	3.35 **	12.33 **
$L_1 X T_2$	-17.17 **	-41.43 **	-19.08 **	-30.78 **	-52.28 **	-0.98	-64.34 **	-77.60 **	100.00 **	2.46 **	-4.44 **	3.86 **
$L_1 X T_3$	24.27 **	-2.30	-2.30	-13.40 **	-30.00 **	-10.78 **	-96.55 **	-97.30 **	-89.09 **	9.23 **	6.25 **	15.48 **
$L_1 X T_4$	-14.86 **	-39.71 **	-17.11 **	-28.51 **	-40.90 **	-28.92 **	-82.44 **	-85.71 **	-67.27 **	14.45 **	0.54	9.28 **
$L_1 X T_5$	-74.48 **	-79.93 **	-79.93 **	-11.07 **	-20.59 **	-20.59 **	210.50 **	123.02 **	410.91 **	3.20 **	-0.92	7.68 **
$L_2 X T_1$	-43.99 **	-61.34 **	-37.17 **	-51.29 **	-67.92 **	-30.39 **	-62.44 **	-79.44 **	101.82 **	8.40 **	-2.44 **	9.45 **
$L_2 X T_2$	-36.84 **	-54.29 **	-36.84 **	-41.69 **	-61.18 **	-19.44 **	-59.04 **	-77.39 **	101.82 **	-1.25 *	-9.23 **	1.83 *
$L_2 X T_3$	22.36 **	-0.99	-0.99	1.58	-21.79 **	-0.33	-25.27 **	-54.05 **	85.45 **	3.14 **	-1.20	10.85 **
$L_2 X T_4$	5.61 **	-23.44 **	5.26 **	4.58 **	-17.80 **	-1.14	-43.08 **	-53.16 **	-32.73 **	20.12 **	4.10 **	16.80 **
$L_2 X T_5$	0.00	-19.08 **	-19.08 **	-7.65 **	-22.06 **	-22.06 **	-15.09 **	-18.18 **	-18.18 **	6.73 **	0.93	13.24 **
$L_3 X T_1$	-35.41 **	-51.82 **	-21.71 **	-47.38 **	-62.95 **	-19.61 **	-76.99 **	-87.41 **	23.64 **	5.59 **	-5.65 **	7.59 **
$L_3 X T_2$	-26.09 **	-41.67 **	-19.41 **	-43.38 **	-59.61 **	-16.18 **	-90.41 **	-94.70 **	-52.73 **	-3.67 **	-12.11 **	0.22
$L_3 X T_3$	-32.72 **	-39.47 **	-39.47 **	-26.48 **	-37.69 **	-20.59 **	16.48 **	-28.38 **	189.09 **	-0.79	-5.69 **	7.54 **
$L_3 X T_4$	-67.32 **	-74.16 **	-64.47 **	-28.64 **	-38.04 **	-25.49 **	241.54 **	181.01 **	303.64 **	21.21 **	4.33 **	18.97 **
$L_3 X T_5$	-10.79 **	-19.74 **	-19.74 **	6.07 **	0.00	0.00	128.30 **	120.00 **	120.00 **	0.79	-5.41 **	7.86 **
$L_4 X T_1$	-23.69 **	-38.06 **	0.66	-24.10 **	-44.73 **	19.93 **	-77.95 **	-86.85 **	29.09 **	12.09 **	2.86 **	10.51 **
$L_4 X T_2$	-13.19 **	-24.76 **	3.95 *	-21.54 **	-42.05 **	20.26 **	-41.51 **	-64.56 **	216.36 **	3.88 **	-2.60 **	4.65 **
$L_4 X T_3$	37.91 **	37.01 **	38.82 **	4.47 **	-7.18 **	18.30 **	-22.70 **	-43.24 **	129.09 **	-3.66 **	-5.76 **	1.25
$L_4 X T_4$	-16.80 **	-27.75 **	-0.66	-8.35 **	-16.44 **	0.49	-90.16 **	-91.35 **	-83.64 **	15.02 **	1.55 *	9.10 **
$L_4 X T_5$	-19.61 **	-20.13 **	-19.08 **	-1.15	-1.63	-1.63	191.82 **	123.08 **	321.82 **	7.85 **	4.12 **	11.86 **
SEd	0.02	0.02	0.02	0.02	0.03	0.03	0.01	0.01	0.01	0.36	0.42	0.42

* Significant at 5 per cent level ** Significant at 1 per cent level

.1 Shell volume

The cross combination L_1 X T_5 exhibited the lowest heterosis over mid parent (-74.48), better parent (-79.93) and standard variety, TPT 4 (-79.93). On the other hand the cross, L_4 X T_3 expressed maximum heterosis over mid parent (37.91), Better parent (37.01) and standard variety (38.82). A total of 15 crosses showed negative significant relative heterosis, 17 crosses expressed significant negative heterobeltiosis and 13 crosses expressed significant negative standard heterosis over the standard variety, TPT (T5).

4.6.2 Pod volume

Heterosis over mid parent for pod volume differed from –51.29 (L_2 X T_1) to 6.07 (L_3 x T_5) with only three crosses showing positive significant relative heterosis. Heterosis over better parent ranged from –67.92 (L_2 X T_1) to 0.001 (L_3 X T_5). None of the crosses exhibited positive significant heterobeltiosis. Heterosis over standard variety showed a minimum value of –30.39 (L_2 X T_1) and a maximum value of 20.26 (L_4 X T_2). Four cross combinations were positively significant for standard heterosis.

4.6.3 Free space in pod

Mid parental heterosis for this character varied from –96.55 (L_1 X T_3) to 241.54 (L_3 X T_4). Fifteen out of 20 cross combinations expressed negatively significant relative heterosis. Heterosis over better parent varied between –97.3 (L_1 X T_3) and 181.01 (L_3 X T_4) with 16 negative and significant crosses. Heterosis over standard parent exhibited a range from –89.09 (L_1 X T_3) to 410.91 (L_1 X T_5) with six superior crosses, which were negative and significant.

4.6.4 Shelling percentage

The minimum and maximum percentages of relative heterosis for this character were recorded by L_3 X T_2 (-3.67) and L_3 X T_4 (21.21) respectively. Fifteen combinations registered positively significant relative heterosis. The crosses L_3 X T_2 (-12.11) and L_1 X T_3 (6.25) had the minimum and maximum percentage of heterobeltiosis over the better parent, respectively. Seven cross combinations showed significant and positive heterobeltiosis. The lowest and the highest standard heterosis were recorded by L_3 X T_2 (0.22) and L_3 X T_4 (18.97) respectively. Eighteen heterotic crosses were significant for standard heterosis.

4.6.5 Mature pods per plant

The cross, L_1 X T_2 recorded the minimum percentage of heterosis over mid parent (0.22) and better parent (-31.49). Similarly the cross L_3 X T_2 recorded the maximum percentage of heterosis over mid parent (94.57) and over better parent (54.68). Sixteen crosses for relative heterosis and thirteen crosses for heterobeltiosis showed positive significant values. The cross L_4 X T_2 (-4.51) had the lowest standard heterosis and L_1 X T_1 (78.86) the highest. Seventeen out of 19 positive standard heterotic values were significant.

4.6.6 100 Seed weight

The lowest relative heterosis (-38.04) and heterobeltiosis (-54.3) were recorded by the cross, L_1 X T_3. Like wise, the highest relative heterosis (-1.34) and heterobeltiosis (-7.47) were shown by L_2 X T_5. Where as the cross, L_3 X T_5 registered the lowest standard heterosis (-30.98) and the highest (-6.77) by L_2 X T_4. All the cross combinations possessed

Table 33: Percentage of heterosis for mature pods per plant, 100 seed weight, protein content and reducing sug content

Crosses	Mature pods per plant		100 seed weight			Protein content			Reducing sugar content		
	Relative heterosis (di)	Standard heterosis (diii)	Relative heterosis (di)	Heterobel-tiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobel-tiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobel-tiosis (dii)	Standard heterosis (diii)
$L_1 X T_1$	34.46 **	78.86 **	-35.81 **	-52.96 **	-26.34 **	18.75 **	6.35 **	11.54 **	219.88 **	207.65 **	233.12 **
$L_1 X T_2$	0.22	9.03 *	-23.12 **	-43.60 **	-11.96 **	-26.85 **	-32.89 **	-33.32 **	-5.49	-29.08 **	41.61 **
$L_1 X T_3$	18.16 **	34.44 **	-38.04 **	-54.30 **	-29.87 **	26.21 **	26.21 **	4.71 **	191.51 **	191.51 **	191.51 **
$L_1 X T_4$	3.34	39.67 **	-26.41 **	-45.75 **	-16.61 **	7.34 **	3.05 **	-7.08 **	45.50 **	4.01	142.04 **
$L_1 X T_5$	7.42 **	39.19 **	-6.06 **	-18.78 **	-18.78 **	14.96 **	5.17 **	5.17 **	142.04 **	142.04 **	142.04 **
$L_2 X T_1$	2.35	3.33	-29.91 **	-45.36 **	-14.43 **	-47.01 **	-48.82 **	-42.39 **	30.78 **	30.78 *	41.61 **
$L_2 X T_2$	34.98 **	3.56	-34.59 **	-48.94 **	-20.30 **	-35.25 **	-39.04 **	-31.39 **	-13.48	-33.28 **	33.23 *
$L_2 X T_3$	40.99 **	15.20 **	-36.59 **	-50.20 **	-23.59 **	-3.96 **	-16.59 **	-6.11 **	132.42 **	123.53 **	142.04 **
$L_2 X T_4$	4.84	8.08 *	-22.73 **	-39.36 **	-6.77 **	-3.36 **	-12.96 **	-2.04 **	-12.02	-35.54 **	50.00 **
$L_2 X T_5$	28.38 **	25.18 **	-1.34	-7.47 **	-7.47 **	-15.56 **	-20.27 **	-10.26 **	128.75 **	120.00 **	138.22 **
$L_3 X T_1$	14.88 **	18.29 **	-26.73 **	-46.22 **	-15.78 **	-2.37 **	-4.86 **	5.15 **	122.08 **	73.75 **	233.12 **
$L_3 X T_2$	94.57 **	53.21 **	-33.56 **	-51.18 **	-23.79 **	-13.20 **	-17.58 **	-8.92 **	-48.90 **	-49.92 **	0.00
$L_3 X T_3$	31.06 **	9.74 *	-32.10 **	-49.84 **	-23.03 **	16.17 **	1.70 **	12.39 **	63.32 **	24.25 **	138.22 **
$L_3 X T_4$	53.22 **	61.05 **	-37.85 **	-54.11 **	-29.46 **	10.52 **	0.35	10.90 **	104.30 **	86.31 **	333.55 **
$L_3 X T_5$	33.17 **	32.54 **	-20.34 **	-30.98 **	-30.98 **	-21.35 **	-25.09 **	-17.21 **	-8.66	-30.51 **	33.23 *
$L_4 X T_1$	13.49 **	25.89 **	-34.33 **	-51.75 **	-24.45 **	-2.28 **	-8.03 **	-3.55 **	74.28 **	52.16 **	120.81 **
$L_4 X T_2$	10.14 *	-4.51	-35.15 **	-52.31 **	-25.55 **	-19.44 **	-22.21 **	-22.71 **	69.27 **	46.15 **	191.83 **
$L_4 X T_3$	37.05 **	25.65 **	-31.94 **	-49.67 **	-22.77 **	-2.98 **	-7.98 **	-14.87 **	128.06 **	92.61 **	179.51 **
$L_4 X T_4$	21.22 **	37.05 **	-26.30 **	-45.53 **	-16.27 **	29.27 **	27.63 **	18.09 **	-9.53	-26.55 **	70.91 **
$L_4 X T_5$	17.79 **	26.60 **	-3.67 *	-16.43 **	-16.43 **	50.99 **	45.34 **	45.34 **	97.49 **	66.79 **	142.04 **
SEd	0.92	1.06	0.69	0.80	0.80	0.84	0.96	0.96	0.38	0.44	0.44

* Significant at 5 per cent level ** Significant at 1 per cent level

significant negative values for all the three forms of heterosis except the cross L_2 X T_5 which did not show significant relative heterosis.

4.6.7 Protein content

The lowest heterosis percentage over mid parent (-47.01), better parent (-48.82) and the standard variety (-42.39) were established by the cross, L_2 X T_1. Like wise, the highest relative heterosis (50.99), heterobeltiosis (45.34) and standard heterosis (45.34) were registered for the cross, L_4 X T_5. Eight crosses each for relative heterosis and standard heterosis and seven crosses for heterobeltiosis were positive and significant.

4.6.8 Reducing sugar content

The cross, L_3 X T_2 not only recorded a minimum heterosis over mid (-48.9) but also over better parent (-49.92) and standard variety (0.001). Where as the cross L_1 X T_1 recorded a maximum heterosis over both mid parent (219.88) and better parent (207.65). The cross L_3 X T_3 registered maximum heterosis over standard variety (333.55). A total of 14, 13 and 19 crosses registered significant positive heterosis percentage respectively for relative heterosis, heterobeltiosis and standard heterosis.

4.6.9 Non-reducing sugar content

Among the crosses, L_1 X T_2 had the highest percentage of heterosis over mid parent (88.36), better parent (51.24) and standard variety (61.46). The crosses, L_3 X T_1 (-50.61), L_2 X T_3 (-57.84) and L_2 X T_4 (-55.87) recorded a minimum relative heterosis, heterobeltiosis and standard heterosis respectively. Among 20 crosses, only four for relative heterosis, two each for heterobeltiosis and standard heterosis showed positive significant values.

Table 34: Percentage of heterosis for non-reducing sugar content, CGR at 60 DAS and CGR at 90 DAS

Crosses	Non-reducing sugar content			CGR at 60 DAS			CGR at 90 DAS		
	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)
L_1 X T_1	11.10 **	-8.27 **	-8.91 **	99.39 **	84.10 **	359.09 **	-45.55 **	-48.85 **	-54.92 **
L_1 X T_2	88.36 **	51.24 **	61.46 **	8.49	2.77	156.27 **	54.73 **	25.06 **	-3.16
L_1 X T_3	-16.55 **	-36.83 **	-20.50 **	142.07 **	119.17 **	446.55 **	42.51 **	27.39 **	-1.36
L_1 X T_4	13.52 **	2.51	-17.73 **	102.17 **	85.29 **	454.70 **	-11.42 **	-19.72 **	-37.84 **
L_1 X T_5	-9.15 **	-25.19 **	-25.19 **	36.20 **	-4.59	137.93 **	-26.00 **	-34.35 **	-34.35 **
L_2 X T_1	-18.77 **	-32.93 **	-33.40 **	37.43 **	12.18	136.83 **	85.08 **	43.95 **	26.87 **
L_2 X T_2	-43.70 **	-54.79 **	-51.74 **	83.03 **	46.31 **	226.33 **	5.36	4.05	-49.06 **
L_2 X T_3	-44.31 **	-57.84 **	-46.95 **	-8.78	-24.26 **	53.13 **	57.02 **	41.52 **	-13.67 **
L_2 X T_4	-39.11 **	-45.01 **	-55.87 **	203.69 **	119.58 **	557.37 **	23.64 **	9.92	-30.83 **
L_2 X T_5	-14.11 **	-29.27 **	-29.27 **	71.28 **	49.77 **	100.00 **	9.95 **	-18.11 **	-18.11 **
L_3 X T_1	-50.61 **	-51.83 **	-49.67 **	-39.07 **	-45.56 **	46.08 **	25.95 **	-1.45	-13.15 **
L_3 X T_2	-24.73 **	-25.53 **	-20.50 **	-38.25 **	-43.46 **	51.72 **	91.05 **	87.14 **	-6.84 *
L_3 X T_3	-35.04 **	-40.55 **	-25.19 **	78.15 **	56.19 **	319.12 **	-3.96	-12.79 *	-46.80 **
L_3 X T_4	-7.33 **	-18.08 **	-14.40 **	12.64 *	6.81	219.75 **	54.84 **	38.66 **	-12.75 **
L_3 X T_5	-22.45 **	-24.12 **	-20.71 **	126.30 **	55.32 **	316.77 **	31.98 **	-1.16	-1.16
L_4 X T_1	-33.34 **	-33.79 **	-33.36 **	74.68 **	69.85 **	279.62 **	106.42 **	51.71 **	33.71 **
L_4 X T_2	-24.61 **	-26.76 **	-21.81 **	92.00 **	91.80 **	328.68 **	50.04 **	40.11 **	-33.11 **
L_4 X T_3	-30.96 **	-37.87 **	-21.81 **	43.52 **	36.68 **	205.49 **	136.14 **	98.23 **	20.93 **
L_4 X T_4	-21.81 **	-29.73 **	-29.27 **	43.17 **	25.03 **	274.29 **	-23.07 **	-36.22 **	-59.86 **
L_4 X T_5	38.74 **	38.29 **	39.20 **	88.08 **	36.12 **	204.23 **	10.36 **	-21.97 **	-21.97 **
SEd	0.91	1.05	1.05	0.28	0.33	0.33	0.45	0.51	0.51

* Significant at 5 per cent level ** Significant at 1 per cent level

4.6.10 CGR at 60 DAS

The cross combination, L_3 X T_1 recorded a minimum heterosis percentage over mid parent (-39.07), better parent (-45.56) and standard variety (46.08). Like wise, maxmimum heterotic values were recorded by L_2 X T_4 over mid parent (203.69), better parent (119.58) and standard variety (557.37). Altogether, 16 crosses for relative heterosis, 13 for heterobeltiosis and all the 20 crosses for standard heterosis showed positive and significant heterotic values.

4.6.11 CGR at 90 DAS

Mid parental heterosis for CGR at 90 DAS varied between –45.55 (L_1 X T_1) and 136.14 (L_4 X T_3). Similarly the minimum and maximum heterosis percentages over better parent (-48.85 and 98.23 respectively) were recorded by the same crosses, L_1 X T_1 and L_4 X T_3 respectively. In case of standard heterosis, minimum and maximum heterosis percentages were recorded by L_4 X T_4 (-59.86) and L_4 X T_1 (33.71) respectively. Positive significant heterosis percentage over mid, better and standard parents was recorded in fourteen, nine and three crosses respectively.

4.6.12 Harvest index

Harvest index had relative heterosis percentages ranging between –26.85 (L_4 X T_3) and 35.92 (L_2 X T_5) with ten positively significant crosses. The minimum and maximum percentages of heterobeltiosis were exhibited by L_1 X T_3 (-38.24) and L_3 X T_1 (25). Heterobeltiosis was positive and significant in six crosses. The lowest percentage of standard heterosis was recorded by L_1 X T_3 (-2.33) and the highest by L_2 X T_5 (62.79). Fourteen cross combinations exhibited positive and significant standard heterosis.

Table 35: Percentage of heterosis for harvest index, aflatoxin content and kernel weight per plant

Crosses	Harvest index			Aflatoxin content			Kernel weight per plant		
	Relative heterosis (di)	Heterobel-tiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobel-tiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobel-tiosis (dii)	Standard heterosis (diii)
L_1 X T_1	26.37 **	22.34 **	33.72 **	-87.79 **	-92.08 **	-63.64	18.31 **	12.98 **	59.35 **
L_1 X T_2	-19.81 **	-31.45 **	-1.16	121.33 **	84.44 **	277.27 **	-9.08 **	-22.42 **	-0.44
L_1 X T_3	-25.00 **	-38.24 **	-2.33	180.77 **	143.33 **	231.82 **	6.39 **	-0.65	27.50 **
L_1 X T_4	18.34 **	13.64 **	16.28 **	-22.95	-48.91 **	113.64 *	6.25 *	-9.43 **	16.23 **
L_1 X T_5	4.60	3.41	5.81	150.00 **	116.67 **	195.45 **	23.03 **	9.45 **	40.46 **
L_2 X T_1	-25.23 **	-33.33 **	-6.98 *	-43.28 **	-62.38 **	72.73	-8.44 **	-20.97 **	11.46 **
L_2 X T_2	5.74 **	4.03	50.00 **	0.00	-13.33	77.27	31.39 **	23.84 **	26.86 **
L_2 X T_3	-13.28 **	-18.38 **	29.07 **	9.09	-9.09	36.36	16.14 **	11.49 **	24.15 **
L_2 X T_4	6.47 **	-10.83 **	24.42 **	-63.20 **	-75.00 **	4.55	48.60 **	39.90 **	43.31 **
L_2 X T_5	35.92 **	16.67 **	62.79 **	-20.00	-33.33	0.00	77.40 **	75.29 **	79.56 **
L_3 X T_1	26.32 **	25.00 **	39.53 **	-74.10 **	-79.66 **	63.64	26.92 **	6.26 **	49.88 **
L_3 X T_2	4.55 *	-7.26 **	33.72 **	-32.43 **	-57.63 **	240.91 **	33.37 **	30.25 **	23.90 **
L_3 X T_3	-22.41 **	-33.82 **	4.65	-26.63 **	-58.76 **	231.82 **	13.76 **	5.47	17.45 **
L_3 X T_4	35.59 **	25.00 **	39.53 **	-47.96 **	-60.45 **	218.18 **	103.01 **	98.02 **	88.37 **
L_3 X T_5	0.00	-5.21	5.81	-37.69 **	-64.97 **	181.82 **	22.93 **	19.94 **	19.94 **
L_4 X T_1	-6.98 **	-17.36 **	16.28 **	-64.00 **	-64.36 **	63.64	17.72 **	11.78 **	57.66 **
L_4 X T_2	-23.27 **	-24.19 **	9.30 **	-50.00 **	-63.64 **	63.64	-1.06	-15.16 **	7.59 *
L_4 X T_3	-26.85 **	-30.88 **	9.30 **	70.25 **	4.04	368.18 **	6.91 **	0.39	27.31 **
L_4 X T_4	27.72 **	6.61 **	50.00 **	-62.30 **	-63.64 **	63.64	51.20 **	29.53 **	64.25 **
L_4 X T_5	18.84 **	1.65	43.02 **	-63.64 **	-77.78 **	0.00	70.74 **	52.70 **	93.63 **
SEd	0.01	0.01	0.01	1.36	1.58	1.58	0.32	0.37	0.37

* Significant at 5 per cent level   ** Significant at 1 per cent level

4.6.13 Aflatoxin content

Aflatoxin content had relative heterosis ranging from –74.1 (L_3 X T_1) to 180.77 (L_1 X T_3). Heterobeltiosis for this character varied between –92.08 (L_1 X T_1) and 143.33 (L_1 X T_3). Where as standard heterotic percentages ranged from –63.64 (L_1 X T_1) to 368.18 (L_4 X T_3). Relative heterosis was negative and significant in 12 crosses. Similar negative and significant values were obtained for heterobeltiosis in 13 crosses. Contrastingly none of the crosses exhibited negative standard heterosis.

4.6.14 Kernel weight per plant

The cross combination, L_1 X T_2 recorded the lowest relative heterosis (-9.08), heterobeltiosis (-22.42) and standard heterosis (-0.44). A similar trend was observed in the cross L_3 X T_4 where in all the three forms of heterosis viz., relative heterosis (103.01), heterobeltiosis (98.02) and standard heterosis (88.37) were the highest. Seventeen crosses exhibited positive heterosis over mid parent, 13 over better parent and 19 over standard heterosis.

CHAPTER V

DISCUSSION

CHAPTER V

DISCUSSION

It is predicted that in a liberalized economy the cropping pattern will shift in favour of rice, wheat, chickpea, cotton etc. and crops like groundnut face declaration in their area expansion (Gulati and Sharma, 1997). It has to be accepted that crop scientists have failed to suggest an alternative crop to the dry land farmer who cannot dispense the cultivation of groundnut even in the near future. As there is no other alternative to groundnut in these areas, breeding for its improvement still shows promise. The liberalization promotes global trade, which warrants the production of quality produce. Though Indian groundnuts are price-competitive, they may not get access to markets of developed countries for non-compliance with the health and safety standards. The changed scenario adds yet another objective of breeding for quality produce, which includes resistance to aflatoxin content also, to the already existing two priorities; yield and drought tolerance.

Yield, drought tolerance and quality, however, are not unitary characters but are the result of interaction of a number of factors inherent both in the plant as well as in the environment in which the plant grows. So before attempting an exhaustive breeding programme for the three objectives, it is essential to have a knowledge on the association of various plant characters with yield and quality, variation and diversity existing for the characters, their gene actions, combining ability effects and heterosis. Such a study through advanced biometrical procedures such as correlations, path analyses, coefficient of variation, heritability, genetic advance, genetic divergence, combining ability analysis and heterosis will be of immense value for effective selection from the breeding material to design a crossing programme and to select the best cross combinations. Experiments were executed with this background and the results on these aspects and their bearing on genetic improvement of groundnut are discussed.

A total of 54 groundnut genotypes were evaluated for 31 morphological, biochemical and physiological characters in the first year of experimentation to select suitable parents. The nine selected parents were mated in L X T design to generate 20 crosses, which were evaluated in the second year of experimentation along with nine parents. The genetic analyses are discussed in this chapter.

The physiological aspects of improvement of drought resistance in groundnut is possible only by understanding the inter-relationship between various physiological characters under targeted environments. The better understanding of these physiological characters will help for pyramiding genes that regulate different specific physiological characters into single cultivars to fit into the moisture deficit environments. In the present investigation end-of-season drought was the target environment. As the crop was sown late, water deficit occurred from 72 DAS to 99 DAS for 27 days during *kharif*, 2002 and from 77 DAS to 118 DAS for 41 days during *kharif*, 2003. Approximately two weeks of water deficit was enough to observe genotypic differences and measuring physiological characters during this period might provide useful information for breeding groundnut cultivars for resistance to end of season water deficit (Clavel *et al.*, 2004).

Sufficient load of the pathogen, *A. flavus* was maintained through soil inoculation in the rhizosphere of the genotypes to cause pre-harvest infection and to screen the genotypes to aflatoxin resistance.

5.1 MEAN PERFORMANCE

Data were recorded on 18 morphological and biochemical characters and on 14 physiological characters. However, data on ten morphological and biochemical characters related to quality were utilized to evaluate the 54 genotypes for quality and the data on the rest of the characters were used in various biometrical analyses.

5.1.1 Morphological and biochemical characters related to quality

Besides high yield, the kernels of confectionary types should possess good morpho-biochemical characters. Higher values for 100 seed weight, kernels with elongated shape, tapering ends, and pink to light brown testa colours were considered desirable by Nigam *et al.* (1989). Misra *et al.* (2000) opined that high seed uniformity, low oil, high protein and high sucrose contents were desirable to assess the export worthiness of hand picked and selected (HPS) genotypes. They also reported that tapering ends of kernels for easy blanching, low oil for better health, higher protein for more nutritional food value and sucrose (non-reducing sugar) from organoleptic point of view, were the ost desirable attributes to the end user of confectionery groundnuts. As per the commendations of Natural Resources Institute of UK Ministry for Overseas Development (Chandrasekhar, 1991) freedom from aflatoxin (< 5 ppb) was considered as e overriding principle in deciding the quality in groundnut.

With this back ground a comprehensive evaluation of genotypes for their net hand-cked and selected worth with an integrated evaluation of morphological and biochemical aracters was carried out. For this evaluation each genotype was ranked according to merical value and desirability of the character. Among the morphological characters, gh kernel yield, high shelling percentage, high 100-seed weight, maximum uniformity in ed size, light pink or light brown colour testa and elongated shape of kernels with tapering ends were considered desirable characters while among the biochemical characters, low aflatoxin content, low oil percentage, high protein content, and high non-reducing sugar content were considered desirable and accordingly the ranks were assigned.

The genotype, TPT 4 with a rank total of 42 was adjudged the best for morphological characters (table 3). Further more, its kernel yield was the highest among the 54 genotypes tested. With a rank total of 43, the genotype ICGV 86564 ranked second. Next in order were TG 40, M 13, and ICG 7633 with rank totals of 50, 57 and 59, respectively. Among the best five, except TG 40 all the genotypes recorded significantly higher kernel weight. Kernel weight was significantly higher in all the best five genotypes evaluated for morphological characters related to quality except TG 40 whose kernel weight was higher than mean but not significant. The best 18 (1/3 proportion of total genotypes) genotypes were superior for both kernel weight and the rest of the morphological characters related to quality.

For biochemical characters, TPT 4 with a rank total of 59 was identified as the best genotype. Its kernel weight was also the highest. The second best genotype, TPT 1 with a rank total of 60 recorded moderate kernel weight, which was at par with the average. TCGS 584 stood third (91) but its kernel weight was inferior. The genotypes, ICG 1326 and ICG 3643 ranked 4th and 5th respectively. But their kernel weights were not significantly superior over mean. Hence TPT 4 was adjudged as the best genotype for biochemical characters related to quality. It was also observed that most of the high yielders were not superior for biochemical characters.

On the basis of a combined evaluation of genotypes for morpho-biochemical characters, the genotype, TPT 4 with a combined rank total of 101 and M 13 with 130 were identified as the I and II best genotypes respectively. Incidentally the former was the highest kernel yielder and the later also produced significantly higher kernel weight per plant. TPT 1 was identified as the third, ICGV 86564 the fourth, and ICG 1326 as the fifth best genotypes with combined rank totals of 133, 144, and 147 respectively. However the kernel weight of ICG 1326 was low, that of TPT 1 was at par with mean and that of ICGV 86564 was significantly superior over the average.

Thus a combination of kernel yield as well as superior quality characters was difficult to find. In view of the relative desirability of quality characters vis-à-vis kernel weight per plant, the genotypes TPT 4, M 13 and ICGV 86564 were identified for cultivation and trading as HPS varieties. The worthiness of M 13 (Vindhiya Varman and Senthil, 1998) and ICGV 86564 (Venkataravana *et al.*, 2000) for many characters were reported earlier. The other genotypes found superior for respective quality characters might be used in the breeding programs for gene pyramiding to produce genotypes with high yield and quality as well.

5.1.2 Physiological characters

Specific leaf area (SLA) indicates leaf density and is the mean area of leaf displayed per unit of leaf weight. Arjunan *et al.* (1997) opined that more leaf area in turn higher dry matter production results in accumulation of photosynthates for high pod yield. According to Desai *et al.* (1999) leaf area in groundnut ranged from 4 cm^2 in young seedlings up to 80 cm^2 in the fully developed plants. In the present study, SLA in the initial stages of crop growth (30 DAS) was higher than other stages (table 4). It declined at 60 DAS and again rose at pod filling stage (90 DAS). Incidentally there was a dry spell of 27 days from 72 to 99 DAS, which facilitated to evaluate the growth parameters for end-of-season *drought. Water-deficit did not affect SLA as the genotypes produced more leaf* area at 90 DAS. TPT 4 was the only genotype that showed significant performance over general mean at 90 DAS. A steady increase was observed in this genotype from 30 – 90 DAS and the stress did not affect it. Similar consistent performance was recorded in ICG 8325 and ICG 10352. These three genotypes may be selected for maintenance of leaf area till harvest.

Specific leaf weight (SLW) is the ratio of leaf weight to leaf area and is one of the many characters considered useful for selection of varieties. SLW in most of the genotypes studied, increased up to 60 DAS and there after declined. A similar increase in SLW up to 60 – 70 DAE was recorded by Madhavi (1988). The peak values of SLW realized by the genotypes were also found to be different in most of the stages. Eight genotypes out of 54 exhibited increasing trend in SLW from 30 – 90 DAS. Among them ICGV 86031 recorded significant values and exhibited increasing trend in all the three stages. The next best genotype on which drought had no effect was ICGV 88448. Both the genotypes can be utilized to improve SLW.

Crop growth rate (CGR) is the increase in dry matter per unit land area per unit time and is used to estimate the productivity efficiency in crops. According to Duncan *et al.* (1978) selection for higher yield through traditional breeding had resulted in varieties which portioned more of the assimilate to fruit, but had not resulted in corresponding increase in crop growth rates. In this study an increase was registered in CGR of most of the genotypes. Dry spell at later part of the life cycle did not reduce the crop growth rate from 60 – 90 DAS. The marked increase in CGR at later part of the growing season could be due to a combination of decreased leaf area and increased leaf weight (Sivakumar and Shaw, 1978). CGR as observed by Madhavi (1988) increased in the initial stages from 45 to 60 DAE. Desai *et al.* (1999) summarized that CGR in groundnut increased from a very low value early in the season to a maximum (19.6 ± 4.2 g m^{-2} day^{-1}) at about 60-90 days after planting. In contrast, Vindhiya Varman *et al.* (1990) reported an increase up to 50 –

30 DAS but decreased thereafter. Two genotypes, ICGS 21 and TCGS 91 showing higher values in both the stages were suggested as parents to improve CGR in groundnut.

Leaf area ratio (LAR) indicates the ratio between photosynthesizing surface to that of respiring material. TCGS 634 and ICGV 86552 were adjudged as the best genotypes that maintained photosynthesizing surface even during water deficit.

Leaf area index describes the size of assimilatory apparatus of a crop stand or the crop canopy expansion. A decrease in LAI in mung bean was reported to be due to senescence and shadowing, which limited the photosynthesis in lower leaves (Madhavilatha, 1998). According to Duncan *et al.* (1978) maximum light interception ccurred when the LAI was three. In the present study, LAI values greater than three for 15 genotypes indicated that growth rate was significantly maximum in these genotypes. The highest was recorded by ICGV 86552. It was interesting to note that this genotype ecorded significant values for all the growth parameters at one or the other stage. It roved its importance in selection for drought as it recorded significant values during tress (at 90 DAS) for all growth parameters studied except for SLA.

Ten genotypes showed significant values for SCMR recorded at 30 DAS and CGV 86031 was found to be the best. Only four genotypes showed significant superiority ver mean for harvest index and all of them were from Trombay. They were TG 40, TG 2, TG 49 and TG 39 in the decreasing order of superiority. They invariably should find a lace in breeding programs intended to improve harvest index.

5.2 ASSOCIATION ANALYSIS

5.2.1 Correlations

Correlation studies provide reliable information on nature and extent of relationship between different characters. Information on the association of traits of economic worth is of great value to plant breeders as it will help in assessing the scope of simultaneous improvement of two or more characters. These relationships may be positive or negative. Negative associations are limiting factors in selection for higher yield. But for selecting those characters like days to maturity, anti-nutritional factors, toxic contents etc. where lower values are important, negative correlations show immense importance. It is, therefore, imperative to find out the characters that are positively correlated to yield and negatively correlated to aflatoxin content in groundnut. Further more, information on relationship of physiological characters with drought tolerance is necessary to suggest a holistic approach to solve the problem envisaged in the present investigation. The association between two characters that can be directly observed measures the phenotypic correlation, whereas genotypic correlation is the correlation of breeding value. Hence, even though genotypic and phenotypic correlations both were worked out on kernel yield as well as on aflatoxin content, discussion is restricted to genotypic correlations only.

The genotypic and phenotypic correlations amongst the characters followed almost similar trend of association, the former being a little higher in most of the cases, indicating the strong inherent association between the characters existed in the study (Venkataravana *et al.* 2000 a).

5.2.1.1 *Correlations of morphological and biochemical characters with kernel weight per plant.*

The characters in order of strong and positive correlation with kernel weight per plant were; pod volume, mature pods per plant, immature pods per plant, 100 seed weight, free space in pod, seed moisture percentage, carbohydrate content and non-reducing sugar content (table 7). Kernel weight per plant showed negative and high correlation with protein content. The rest of the associations were negligible. These observations corroborates with that of Venkataravana *et al.* (2000 a) who reported that kernel yield was positively associated with mature pods and 100 kernel weight. They along with Ali *et al.* (1996) and Bera and Das (1998) also reported positive association of oil percentage with kernel yield. But the association reported by Layrisse *et al.* (1980) was negative. Vindhiya Varman and Raveendran (1996) observed negative association of mature pods with kernel weight. Where as high positive phenotypic correlation between kernel yield and mature pod number per plant was reported by Jayalakshmi (2003). The association of seed yield per plant with shelling percentage and 100 seed weight observed by Uddin *et al.* (1995) at genotypic level was negative.

5.2.1.2 *Correlations of morphological and biochemical characters with aflatoxin content.*

The character, shelling percentage exhibited negative and strong association with aflatoxin content (table 7). Strong positive association of aflatoxin content was observed with shell and pod volume. Ghewande *et al.* (1993) reported infection and colonization in bold-seeded groundnuts. Large pod surface might invite infection than small pod surface. Carbohydrate content also expressed a high positive correlation with aflatoxin content. But carbohydrate components, reducing and non-reducing sugars, did not establish significant relationship with aflatoxin. Similar non-significant correlation between sugar content and aflatoxin content by Ghewande *et al.* (1993) and non-significant correlation between total carbohydrate and aflatoxin by Zafar Iqbal *et al.* (2004) were reported earlier.

Protein content and oil percentage exhibited negative and strong association with aflatoxin content. The results were contradictory with that of Ghewande *et al.* (1987) for protein and with that of Reddy *et al.* (1992) for lipids. Where as the results of Zafar Iqbal *et al.* (2004) indicated that protein and fat were not related to aflatoxin content. The positive inter correlation between protein content and oil percentage and their negative inter correlation with carbohydrate content might have led to the negative association of aflatoxin content with protein content and oil percentage. Carbohydrates seemed to be preferred to protein and oil by the pathogen in producing aflatoxin in groundnut.

5.2.1.3 *Inter correlations among morphological and biochemical characters.*

Shell volume, which was positively associated with aflatoxin content, had also expressed strong positive correlation with pod volume, 100 seed weight, free space in pod, immature pods per plant, seed moisture percentage and carbohydrate content. However, it showed strong negative correlation with shelling percentage, mature pods per plant, protein content and reducing sugar content. Similar trend of correlations were observed for pod volume with all the characters that are related either positively or negatively with shell volume in addition to positive and strong correlation with kernel weight per plant.

The correlation of shell volume and pod volume with morphological and biochemical characters indicated that large poded varieties not only produced high kernel weight per plant having high test weight but also possessed higher quantities of carbohydrate content and aflatoxin contents. The large pods with greater free space in pod contained more seed moisture percentage and produced more number of immature pods. All these characters might have favoured the pathogen to grow in them and produce more aflatoxin content. This can be further substantiated by the negative and strong correlation of the two characters, shell volume and pod volume with mature pods and shelling percentage. The results also revealed that the higher the shell and pod volume, the higher was the carbohydrate content and the lower was the protein content. Further more, the pathogen might have preferred carbohydrates to protein. It can be summarized that the large pods not only produced high kernel weight per plant but also contained more aflatoxin in their seeds.

The character, free space in pod showed positive strong association with kernel weight, which might be due to its positive and high association with pod volume and 100 seed weight. The higher the space, higher was the moisture percentage in seeds. The free space in pod increased with immature pods per plant and decreased with mature pods per plant and shelling percentage.

Shelling percentage was strongly and positively associated with mature pods per plant and protein content. Similar positive relationship between shelling percentage and mature pods was observed by Rama Reddy (1991), Suresh Kumar (1993) and Venkataravana *et al.* (2000 a). Its association with shell volume, pod volume, free space in pod, immature pods per plant, 100 seed weight, seed moisture percentage and aflatoxin content was negative and high. It can be inferred that bold seeded nature as observed from negative correlation of shelling percentage with shell volume, pod volume and 100 seed weight was associated with low shelling percentage (Varisai Muhammad *et al.*, 1973). However positive association of shelling percentage with 100 kernel weight was reported by Venkataravana *et al.* (2000 a). High shelling percentage in turn compact filling of the pod seemed to be related to low free space in pod and facilitated uniform drying which resulted in low seed moisture percentage in seed.

Very strong positive correlation was established between mature pods per plant and kernel weight per plant, which makes it the most important character to bank upon for realizing higher kernel yields. Observations of a similar relationship between mature pods and kernel weight were also made by Ursal *et al.* (1995) and Venkataravana *et al.* (2000 a). Gupta (2000) reported that in the seed of groundnut, carbohydrates reached a maximum just beyond middle maturity and then remained constant, sugar content increased throughout maturation, and lipid content reach its maximum at full maturity and then declined at over maturity. In the present investigation the association of mature pods was also positive and high with non-reducing sugar content but positive and weak with carbohydrate content and reducing sugar content. Whereas, its association with oil percentage was non-significant. It indicated that more the pods were mature, the more was the accumulation of carbohydrate content and its components (reducing and non sugars) in seed. Mature pods per plant were positively and strongly correlated with shelling percentage but negatively and highly with 100 seed weight, shell volume, pod volume and free space in pod. Which in turn indicated that mature pods were produced more in small seeded varieties rather than in large seeded varieties.

Immature pods exhibited correlations, which were in contrast to the correlations expressed by mature pods per plant though the correlation between them was insignificant. The correlation between immature pods per plant and 100 seed weight was strong and positive. As the pod volume, shell volume and free space in pod, which were strongly associated with 100 seed weight, exhibited high positive correlation with immature pods per plant, the correlation of immature pods per plant with 100 seed weight was also found to be high and positive. It is interesting to note that immature pods per plant exhibited positive and high relationship with oil percentage. This was again substantiated by the observations of Gupta (2000) who reported a raise before and a decline after maturity in oil content. Comparison of the correlations observed with mature pods per plant and immature pods per plant for biochemical characters revealed that the varieties in which more number of mature pods per plant were present contained more quantities of carbohydrate and its components (reducing and non-reducing sugars) in their seeds whereas, the genotypes producing more immature pods per plant produced more oil percentage.

A strong positive correlation was observed between 100 seed weight and kernel weight per plant. The results were not in agreement with that of Uddin *et al.* (1995) who had reported negative association of 100 seed weight with seed yield per plant at genotypic level. However they were in agreement with those of Mathews *et al.* (2000). This was because of its positive association with pod volume, shell volume, free space in pod, immature pods per plant and seed moisture percentage. It showed high negative correlation with shelling percentage and mature pods per plant. Whereas, the observations of Singh *et al.* (2000) on the association between 100 kernel weight and mature kernels and that of Venkataravana *et al.* (2000 a) on the association of 100 seed weight with mature pods and shelling percentage were highly significant and positive.

Seed moisture percentage was strongly and positively associated with shell volume, pod volume, free space in pod, immature pods per plant, 100 seed weight and kernel weight per plant. Its association with shelling percentage was highly negative. Though the pods were uniformly shade dried, there were differences in seed moisture percentage. It can be inferred that the large pods, which were characterized by higher test weight, shell volume, pod volume, free space in pod and immature pods retained moisture and were not completely dried. This might also be the reason for the positive and strong association between seed moisture percentage and 100 seed weight.

Oil percentage expressed strong positive correlation with protein content but negative and high association with carbohydrate and reducing sugar contents. Similar positive correlation between oil and protein was reported by Makne and Bhale (1987). Where as, Layrisse *et al.* (1980) reported negative relationship between oil and protein and positive relationship between protein and sugar content. Such reports on inverse correlation between oil and protein content were also observed by many workers (Dwivedi *et al*, 1990; Misra *et al.*, 1992 and Sadhana Kumari and Snehalatha Reddy, 1998). Its negative association with aflatoxin might be attributed to the fact that the pathogen, *Aspergillus flavus*, producing aflatoxin preferred carbohydrates to protein which was indicated by the positive correlation of aflatoxin content with carbohydrate content and negative correlation with protein content. Earlier reports indicated positive (Reddy *et al.*, 1992 and Holbrook *et al.*, 1994) and non-significant (Zafar Iqbal *et al.*, 2004) association of oil with aflatoxin content.

Protein content exhibited an increasing tendency with oil content but it was at the cost of carbohydrate accumulation. Penning de Vries *et al.* (1974) opined that an increase in protein content requires more photosynthate, thus decreasing available photosynthate for starch synthesis and thus grain yield. The negative correlation between protein and kernel weight indicated the difficulty in simultaneous selection for both high yield and protein content. This negative correlation might be implicated to be a function of the fact that an increase in kernel weight was associated with a disproportionately large deposition of carbohydrates relative to protein (Diehl *et al.*, 1978). For simultaneous improvement of protein and kernel weight, it can be suggested that selection should be made initially for high yield and with in families, plants having the highest percentage of protein should be identified for further selection and intermating. Kitbite (1990) suggested that the inverse phenotypic correlation between grain yield and protein was not caused by genetic factors such as linkage or pleiotropy, but arise from the intrinsic physiological and mathematical relationships, the two characters have. Protein content was also observed to be inversely related with aflatoxin content and carbohydrate content. Ghewande *et al.* (1989) observed positive and Zafar Iqbal *et al.* (2004) a non-significant relationship between protein and aflatoxin content. This might be due to the positive correlation of carbohydrate content with aflatoxin content and kernel weight per plant.

Carbohydrate content had positive strong correlation with non-reducing sugar content and aflatoxin content. It recorded strong positive correlation with kernel weight per plant. Its association with shell volume, pod volume, free space in pod and 100 seed weight indicated that larger the pod size, greater was the carbohydrate content in seed. Hence, the character was a natural favorite of the pathogen. On contrary, earlier reports indicated that total carbohydrates (Zafar Iqbal *et al.*, 2004) and sugar content (Ghewande *et al.*, 1993) were not related to aflatoxin content.

Reducing sugar content registered a strong positive relationship with non-reducing sugar content and mature pods per plant. However its association with oil percentage, shell volume, pod volume and free space in pod was negative. The results revealed that the smaller the size of the pod, greater was the accumulation of reducing sugars in the seed.

Non-reducing sugar content was positively correlated with kernel weight. This might be due to its positive association with carbohydrate content and mature pods per plant.

5.2.1.4 Correlations of physiological characters with kernel weight per plant

A perusal of the correlation coefficients (table 8) between physiological characters and kernel weight per plant revealed that the physiological characters; LAI at 90 DAS, LAR at 90 DAS, harvest index, SLA at 90 DAS and CGR at 90 DAS in that order including pod weight per plant were positively and strongly associated with kernel weight per plant. However, SLW at 90 DAS expressed negative association with kernel weight per plant. The crop experienced moisture stress at 90 DAS, hence, the significance of most of the growth parameters was observed at 90 DAS.

SLA at 30, 60 and 90 DAS followed a similar trend of association with most of the characters. The associations among themselves were positive. But with SLW at 30, 60 and 90 DAS, CGR at 90 DAS and SCMR at 30 DAS the correlations were negative. Nageswara Rao *et al.* (2001a) showed significant correlation between SLA and SCMR and suggested that SCMR could be used as rapid, low-cost, non-destructive technique to screen large breeding population for SLA. Time of sampling (at 30 DAS) of SCMR might have influenced its relationship with SLA in a similar way it influenced SLA as was reported in the studies of Wright and Hammer, (1994) and Nageswara Rao *et al.* (1995). The results of Reddy *et al.* (2004) also supports the inverse relationship obtained between SLA and SCMR. SLA at 30 DAS showed negative correlation with LAR at 90 DAS and LAI at 90 DAS. Where as, SLA at 90 DAS showed negative relationship with harvest index. Positive significant association of SLA with harvest index was reported by Jayalakshmi (1997) and Arjunan *et al.* (1997). SLA at 90 DAS exhibited positive and high correlation with pod weight per plant and kernel weight per plant. Jayalakshmi (2003) also observed highly significant and positive correlation between kernel yield and SLA. It can be inferred that SLA at later stages of crop growth was more important than at early stages.

The negative association of SLW at 30, 60 and 90 DAS with SLA at three different periods might be due to the presence of thicker and smaller leaves in the material studied. Their association with SCMR at 30 DAS indicated that thicker leaves were dark green in colour and contained more chlorophyll. However SLW at any stage did not contribute to kernel weight per plant. The association between SLW at 90 DAS and kernel weight per plant was negative and high. But the relationship observed by Subramanyam and Pandey (1981) between SLW and yield was positive and that observed by Madhavi (1988) at 30 days after emergence was also positive but non-significant. Pallas and Samish (1974) reported that SLW and net photosynthesis were not correlated. Hence efforts to reduce leaf weight and increase leaf area at later stages of crop growth assume greater importance.

The study indicated the presence of an inverse relationship between CGR at 60 DAS and at 90 DAS. Moisture stress prevalent between 72 and 99 DAS might be the reason for the negative relationship between CGR at 60 and at 90 DAS. Plants that had produced good growth rate despite the stress produced more pod and kernel weights per plant as indicated by positive and strong correlation with kernel weight. CGR at 90 DAS was also strongly and positively associated with LAR at 90 DAS and LAI at 90 DAS. Hence CGR at 90 DAS emerged to be the most important physiological character in the study. The findings of Williams *et al.* (1975) indicated that kernel growth rate early in the reproductive phase of groundnut was influenced by CGR. The importance of crop growth rate as yield contributing characters had also been established by character association studies of Reddy and Murthy (1994). Similar positive relationship between CGR and yield was observed by Anuradha (1995) and Sanjeev Kumar *et al.* (2000).

LAR and LAI at 90 DAS followed a similar trend of association with all the physiological characters. The correlations among themselves and with SLW at 30 DAS, CGR at 90 DAS, pod and kernel weights per plant were strong and positive. Similar strong association of LAI from 60 DAE with pod, kernel yield was obtained by Madhavi (1988), but it was not significant with SLW at 30 DAS. Patra *et al.* (1995) found that LAI at 70 DAS was the key growth variable positively influencing pod yield. Arjunan *et al.* (1997) observed that LAI had the highest significant positive correlation with pod weight before stress (at 40 DAS) after imposing stress (at 75 DAS) and at final harvest. Sanjeev Kumar *et al.* (2000) reported that LAI and LAR significantly affected pod yields in Virginia groundnuts. Nautiyal *et al.* (2002) observed that LAI decreased during stress and increased after the relief producing more new leaves.

SCMR at 30 DAS expressed positive association with SLW at 60 and at 90 DAS but negative with SLA at 60 DAS and at 90 DAS. It can be inferred that leaf weight rather than leaf area is related with higher chlorophyll content. SLW in the studies of Arjunan *et al.* (1999) exhibited negative correlation with transpiration rate indicating the reduced transpiration due to increased leaf thickness (SLW). SCMR, which was strongly linked with mesophyll efficiency controlling transpiration, was also proved to be linked with transpiration efficiency in correlation studies of Bindu Madhava *et al.* (2002). An inverse relationship as observed in the present study between SLA and SCMR indicated that SCMR was a potential physiological trait to employ as a surrogate for transpiration efficiency (Reddy *et al.*, 2004).

Harvest index had a direct bearing on pod and kernel weights per plant as indicated by strong positive correlations. Its correlation was also strong and positive with SLW at 90 DAS but was strongly and negatively associated with SLA at 90 DAS, CGR at 60 DAS, LAR and LAI at 90 DAS. Wright *et al.* (1991) identified harvest index as a major factor in improving pod yield. Similar positive correlations were observed by Venkateswarlu *et al.* (1991), Suresh Kumar (1993), Arunachalam (1993), Reddy and Murthy (1994), Mishra (1995), Sharma and Varshney (1995), Anuradha (1995), Jayalakshmi (1997) and Nigam *et al.* (2001). Negative correlation of harvest index with pod weight, SLW and LAI was also reported (Madhavi, 1988). Whereas Jayalakshmi (1997) reported positive association of harvest index with SLA both in parents and F_1s.

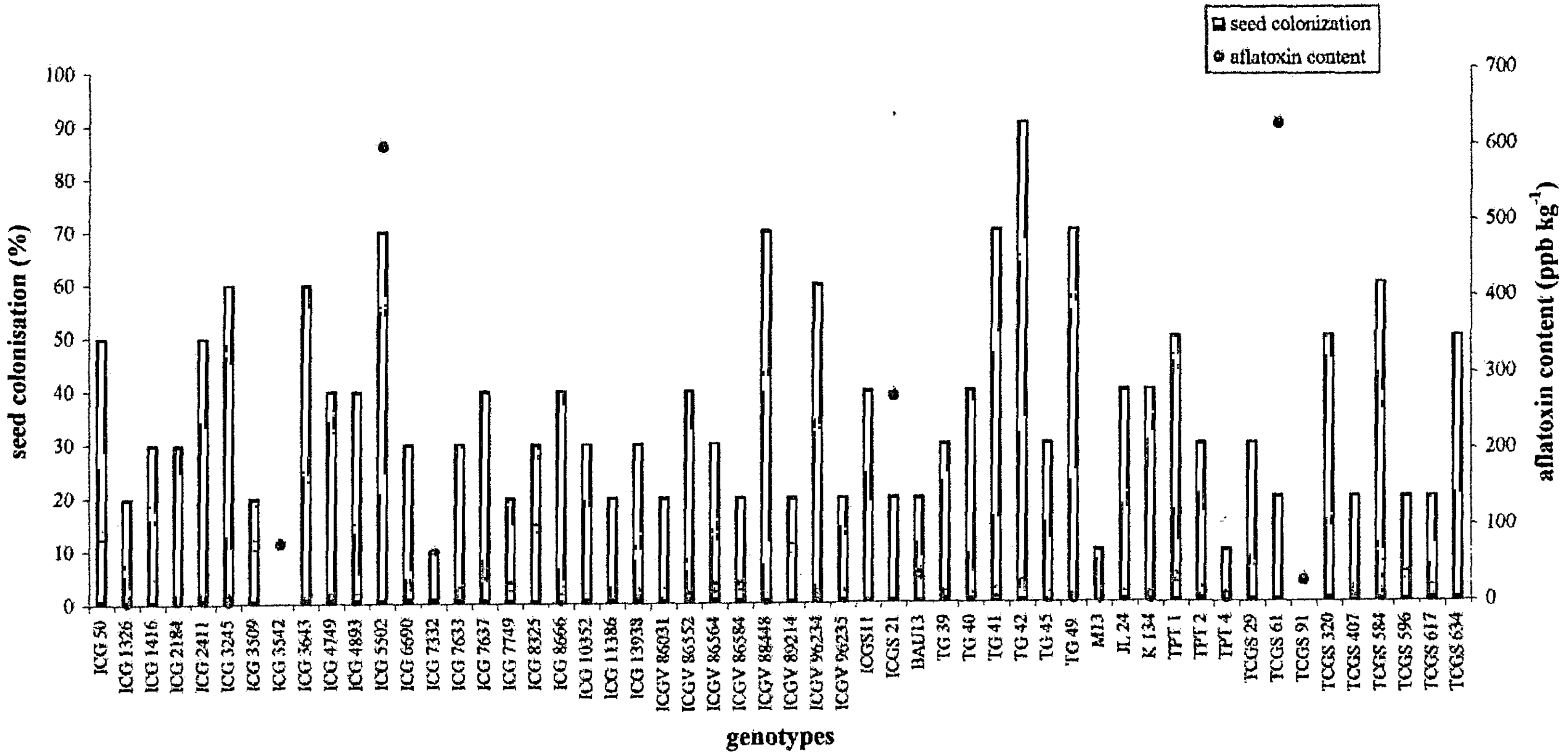
Pod weight per plant, as presumed, was associated with kernel weight per plant. Several reports corroborated these findings (Anuradha, 1995; Vindhiya Varman and Raveendran, 1996; Cherian Mathews *et al*, 2000; Singh *et al.* 2000; Venkataravana *et al.*, 2000 a; and Dhaliwal *et al.*, 2003). The positive and strong association was due to the similar strong association with SLA at 90 DAS, CGR at 90 DAS, LAR at 90 DAS, LAI at 90 DAS and harvest index. SLW at 90 DAS also had positive correlation with pod and kernel weights per plant.

5.2.1.5 Relationship between aflatoxin content and seed colonization percentage.

Healthy sound mature seeds with intact seed coat and free from any damage were selected from each genotype for *in vitro* inoculation by *A. flavus* to observe seed colonization percentage. The data on seed colonization percentage presented in annexure A revealed that the genotypes ICG 3542 and TCGS 91 were least infected with the pathogen (0%). ICG 1326, ICG 7332, M 13 and TPT 4 closely followed them with 10% seed colonization. Higher percentage of seed colonization (> 70%) was observed in ICG 5502, ICGV 88448, TG 41 and TG 42.

The genotypes ICG 1326, M 13 and TPT 4 also recorded low aflatoxin content in their seed. However when all genotypes were taken into consideration there was no

Fig.2: Relationship between aflatoxin content and seed colonization percentage



relationship between seed colonization percentage and aflatoxin production ($R^2 = -0.0322$) (fig. 2). The results were in agreement with earlier findings of Ghewande (1993), Davidson *et al.* (1982) and Reddy *et al.* (2003). This might be primarily due to the differences in seed sampling. For *in vitro* studies healthy seeds were sampled and for aflatoxin estimation a random sample of seeds was taken. Common sampling could not be followed as the presence of single infected seed in the petridish for *in vitro* studies produced 100 percent seed colonization. Hence, screening the genotypes for aflatoxin resistance (the ultimate concern), instead of screening for *in vitro* resistance was followed and recommended.

5.2.2. PATH COEFFICIENT ANALYSIS

The correlation coefficients measure the relationship between pairs of characters. But a dependent character is an interaction product of many mutually associated component characters and change in any one component disturbs the whole network of cause and effect system. The path coefficient analysis, which takes into account the cause and effect relation between variables, is unique in partitioning the association into direct and indirect effects through other independent variables. This analysis also measures the relative importance of causal factors involved. Hence in the present study path coefficient analyses were worked out not only for kernel weight per plant but also for aflatoxin content.

5.2.2.1 *Path analysis of morphological and biochemical characters on kernel weight per plant.*

Genotypic path analysis of morphological and biochemical characters on kernel weight revealed that the direct effect of mature pods on kernel weight per plant was very high (table 9). The other characters, shell volume, free space in pod, shelling percentage exhibited high direct positive effects. Moderate positive direct effects were recorded for 100 seed weight where as high direct negative effect was observed for carbohydrate content and moderate negative direct effect for oil percentage. However high direct effects of seed yield on oil were reported by Sah *et al.* (2000) and Vidhiya Varman and Raveendran (1996a). The rest of the characters had low to negligible direct effects on kernel weight per plant. Earlier reports directed the path towards pod yield. Suresh Kumar (1993) revealed that number of mature pods, shelling percentage had positive indirect effect on pod yield through kernel yield. Similarly Sah *et al.* (2000) reported that 100 seed weight indirectly through seed yield effected pod yield. The order of importance as indicated by direct effects of characters on kernel weight per plant was for mature pods per plant, shelling percentage, shell volume, free space in pod and 100 seed weight. Selection in positive direction for these characters and against oil percentage might be perceived to improve kernel weight.

5.2.2.2 *Path analysis of morphological and biochemical characters on aflatoxin content.*

When correlations obtained for morphological and biochemical characters were partitioned by genotypic path into direct and indirect effects on aflatoxin content, shell volume exhibited very high direct positive effect on aflatoxin content followed by free space in pod and mature pods per plant (table 10). Whereas, pod volume, shelling percentage and 100 seed weight recorded very high to high negative direct effects.

The characters, shell volume and pod volume were strongly correlated among themselves. However their direct effects were in one direction (positive) on kernel weight and in opposite direction on aflatoxin content. Shell volume expressed positive but pod volume the negative direct effects on aflatoxin content. Both the characters, shell and pod volume expressed a proportional increase with respect to harboring the soil born pathogen, which was reflected by their positive correlations with aflatoxin content. The high negative indirect effects expressed through 100 seed weight, which exhibited high negative direct effect on aflatoxin content, nullified the positive correlation of pod volume on aflatoxin content. The inclusion of genotypes like, ICG 50, ICG 5502, ICG 7633 etc. that possessed 3-4 seeded long pods having thin shell, might have allowed the pathogen to enter the pod, infect the seed and produce more aflatoxin content. A rise in shell volume can be anticipated because of the presence of such material in the study (annexure A). The observations reiterate the importance of shell thickness (Nigam *et al.*, 1991 and Nahdi, 1989), which was not studied in the present investigation. However contradictory results indicating the unimportance of shell thickness were also reported (Venkataramanamma et al., 2004).

Free space in pod is yet another important character which showed high direct positive effects on aflatoxin content. It was reported (Venkataramanamma *et al.*, 2004) that the genotypes, which maintained high pod and kernel moisture during dry spells in the standing crop, had low aflatoxin contamination. The free space in pod estimated in dried pods might have contained moisture in them at the time of harvest. Because the pods in this study were shade dried, and as the moisture in the pods might have served as a medium for the pathogen to find access to the seed and produced aflatoxin. The high positive indirect effects through shell volume, along with low positive indirect effects through carbohydrate content collectively aided free space in pod in establishing a high positive direct effect on aflatoxin content.

Shelling percentage not only registered strong negative correlation but also recorded high negative direct effect on aflatoxin content. The idea of compact seed filling had low aflatoxin content was brooded from the fact that shell volume, pod volume, free space in pod had strong negative correlation with shelling percentage.

Mature pods per plant showed moderate positive direct effect on aflatoxin content. Its indirect effects through most of the morphological and biochemical characters were low to negligible. Aflatoxin content increased with an increase in number of mature pods. Over mature pods seemed to have attracted the pathogen and most of them were observed to be infected by the saprophytic pathogen (Eeden *et al.*, 1994).

Immature pods per plant did not exhibit direct effects on aflatoxin because they were not retained in the stored produce. So the production of immature pods on the plant did not have any effect on aflatoxin production by the pathogen. If they were retained in the stored produce, they could have been attracted by the pathogen because of more pod moisture present in them. This gives an indication that the estimation of pod moisture at the time of harvest might have some relevance to aflatoxin resistance if the pods suffer from improper drying.

The negative very high indirect effects through pod volume might have registered a high negative direct effect of 100 seed weight on aflatoxin content. The larger the seed weight, the lesser was the aflatoxin content. This gives a scope to produce large seeded varieties having low aflatoxin from the breeding material studied.

The importance of seed moisture percentage was found to be low as indicated by its low direct effect on aflatoxin content. Not only the seed moisture percentage but also all of the biochemical characters viz., oil percentage, protein content, carbohydrate content, reducing and non-reducing sugar contents had either low of negligible direct and indirect effects on aflatoxin content except through shell volume and pod volume. The impact of these characters was felt in correlation studies but not in path analysis. A large residual effect of 0.7306 indicated that apart from the characters chosen for the investigation some other characters also might be associated with aflatoxin production, which needs further investigation. A continuation of the work was proposed to analyze the association of component characters of oil, protein, carbohydrate including polyphenols, tannins etc. with aflatoxin production.

5.2.2.3 *Path analysis of physiological characters on kernel weight per plant*

Specific leaf area recorded at 30 DAS and 90 DAS showed negative direct effects on kernel weight per plant (table 1). Where as, the direct effect of SLA at 60 DAS on kernel weight per plant was positive. SLA at 60 DAS was found to be more important character than SLA at 30 or 90 DAS. The moisture stress prevailed between 72 and 99 DAS made the character less important at 90 DAS. Most of the plants might have senesced their leaves at 90 DAS. Similar results on direct effects for SLW at 30, 60 and 90 DAS reiterates the importance of the character, SLW at 60 DAS. The direct effect of SLW recorded by Arjunan *et al.* (1999) on pod yield was negative and high.

Crop growth rate before the stress (at 60 DAS) and during stress (at 90 DAS) did not change their direct effects on kernel weight per plant. Both were positive and very high. Where as the very high positive direct effects of CGR at 90 DAS on kernel weight per plant was due to the cumulative action of the low to moderate positive indirect effects of SLW at 90 DAS, LAR at 90 DAS and pod weight per plant.

Leaf area ratio at 90 DAS established very high positive direct effect on kernel weight. Its indirect effects through CGR at 90 DAS, and pod weight per plant were positive and high. LAR at 90 DAS might be selected to frame selection criteria for increasing higher kernel weight per plant.

On the other hand LAI at 90 DAS exhibited very high negative direct effect on kernel weight. This had no importance in the selection criteria to be formulated for increasing kernel weight per plant.

SCMR at 30 DAS with its negligible direct and indirect effects for most of the traits could not find a place in the selection indices developed for increasing kernel weight per plant. Though harvest index exhibited negligible direct because of its positive high correlation with kernel weight and its indirect contribution to kernel weight through pod weight per plant it assumed importance. Previous studies indicated that harvest index had high positive direct effect on pod yield (Singh and Singh, 2001; Suresh Kumar, 1993; Ursal *et al.*, 1995). Negative direct effect of harvest index on pod yield was also reported (Arjunan *et al.*, 1999).

Pod weight per plant expressed high positive direct effect on kernel weight per plant. Similar high positive effect of pod yield on kernel yield was observed by Suresh Kumar (1993). In most of the earlier studies high positive direct effect of kernel yield was observed on pod yield (Anuradha, 1995; Uddin *et al.*, 1995; Cherian Mathews *et al.*, 2000; Venkataravana *et al.*, 2000 a; Mathews *et al.*, 2000; and Dhaliwal *et al.*, 2003). Its indirect effects through CGR at 90 DAS and LAR at 90 DAS were also positive and high. Consequently more emphasis was laid on these characters for improving kernel weight per plant.

5.2.2.4 Path analysis of physiological characters on aflatoxin content.

In the carly part of the plant growth SLA at 30 DAS and SLW at 30 DAS exhibited very high negative direct effects on aflatoxin content (table 12). But in the later part, LAI at 90 DAS expressed very high negative direct effect on aflatoxin content. The rest of the characters showed low to very high positive direct effects. The direct effects recorded during stress period (at 90 DAS) except by LAI were highly positive. CGR at 90 DAS and LAR at 90 DAS though expressed positive direct effects their indirect effects through LAI at 90 DAS were negative and very high. The indications that the SLA and SLW in the early stage and LAI at later stage of plant growth were related to reduction in aflatoxin content require further probe and analysis to draw a meaningful conclusion.

It can be inferred from the association analysis that selection criteria in positive and negative directions could be formulated with shell volume, pod volume, free space in pod, shelling percentage, mature pods per plant, immature pods per plant, 100 seed weight, protein content, oil percentage, carbohydrate and non-reducing sugar contents, SLA at 60 DAS, SLW at 60 DAS, CGR at 60 DAS, CGR at 90 DAS, LAR at 90 DAS, harvest index, and pod weight per plant for improving kernel weight per plant and at the same time reducing aflatoxin content (table 34).

5.3 VARIABILITY

Varietal improvement work in groundnut indicates that more emphasis was laid on improvement of morphological characters like pod size (Reddy, 1988) and number of pods per plant (Prasad *et al.*, 1984) as selection criteria. However, very little progress has been made in terms of identification and exploitation of variability present in physiological characters. Similar is the case with biochemical characters, which have profound influence on quality of groundnuts. The success of breeding programmes for yield and quality depends not only on mere inclusion of desirable characters identified based on their association analysis but also on the existence of transferable genetic variability for these characters.

The genetic parameters; range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of mean (GAM), estimated for morphological, biochemical and physiological characters are discussed separately to make meaningful relative comparisons between the characters.

Among the morphological characters, high PCV and GCV were present for shell volume, pod volume, free space in pod and immature pods per plant (table 1). Similar high GCV for immature pods per plant was observed by Chaudhary (1993) and moderate values of GCV and PCV by Vasanthi *et al.* (2004). Where as, mature pods per plant, 100 seed weight and kernel weight per plant showed moderate estimates for PCV and GCV. The results were in agreement with that of Ganesan and Sudhakar (1995), Vasanthi *et al.* (2004) and John *et al.* (2004) who had recorded moderate values for mature pods per plant. In contrast high estimates of GCV for mature pods per plant were recorded by Reddy and Gupta (1992) and Amit Vikram *et al.* (2003). Similar high GCV and PCV for 100 seed weight was reported by Mishra and Yadav (1992), Uddin *et al.* (1995), Naik *et al.* (2000) and Vijayasekhar (2002). Low GCV for kernel yield was reported by Nisar Ahmed (1995). Where as Uddin *et al.* (1995) obtained high GCV for seed yield. Moderate estimates of PCV and GCV for kernel yield were observed by John *et al.* (2004). This indicated that the existence of variability in the material studied for these characters and the scope of their exploitation. However, low estimates of GCV and PCV for shelling percentage indicated the limitation in the scope of improvement made for this character. Similar low GCV estimate for shelling percentage was observed by Vindhya Varman and Raveendran (1996a) and Naik *et al.* (2000). However Vijayasekhar (2002) reported high PCV and GCV for shelling percentage. The environmental influence was profound on the expression of the characters viz., aflatoxin content, mature pods per plant, immature pods per plant, kernel weight per plant and free space in pod as indicated by the difference between PCV and GCV.

High estimates for both heritability and GAM for shell volume, pod volume, free space in pod, immature pods per plant and 100 seed weight and high heritability and moderate GAM for mature pods per plant and kernel weight per plant revealed that all these characters were most likely influenced by additive gene action. Reddy and Gupta (1992) and Uddin *et al.* (1995) reported high estimates of heritability and GAM for kernel weight. Mishra and Yadav (1992), Uddin *et al.* (1995), Salara and Gowda (1998), Naik *et al.* (2000) and Vijayasekhar (2002) reported high heritability coupled with high GAM for 100 seed weight. Chaudhary (1993) observed high heritability and GAM for immature pods per plant. Reddy and Gupta (1992) reported high estimates of heritability and GAM for mature pods per plant. Where as low GAM for kernel weight was reported by Nisar Ahmed (1995). Ganesan and Sudhakar (1995), Vasanthi *et al.* (2004) and John *et al.* (2004) recorded moderate values of heritability in broad sense and GAM for mature pods per plant.

High heritability with low GAM was recorded for shelling percentage. This indicated the presence of non-additive gene action and simple selection to improve this character might not be possible. This observation on shelling percentage was similar to that of Vindhiya Varman and Raveendran (1996). Shelling percentage as observed by Reddy and Murthy (1994) in most of the studies recorded low to medium heritability. However reports of moderate to high genetic advance (Uddin *et al.*, 1995), high heritability and high genetic advance (Vijayasekhar, 2002) were not uncommon.

Both GCV and PCV were high in magnitude for some of the biochemical characters; reducing sugar content, non-reducing sugar content and aflatoxin content which indicated ample scope for improvement. Where as the GCV and PCV values for oil percentage, protein, and carbohydrate content revealed low variability and the response to selection for these characters would be less. Misra *et al.* (2000) reported high variability for reducing sugar content, moderate for protein content and least in oil content. Pattee *et al.* (2000) observed that high genotypic variation in carbohydrate components was similar to the high genotypic variation observed for sweetness. Low estimates of GCV for oil content were also reported by Nadaf and Habib (1987), Reddy and Murthy (1994) and Vindhiya varman and Raveendran (1996a). Where as the variability reported for protein content was high (Dwivedi *et al.* 1990). High heritability and GAM for reducing sugar content, non-reducing sugar content and aflatoxin content indicated the preponderance of additive gene action and simple selection would be effective in the improvement of these characters. The heritability estimates for resistance to aflatoxin production were reported to be low to moderate (Utomo *et al.*, 1990). The characters; oil percent, protein content, carbohydrate content had high heritability and low GAM which indicated the influence of non additive genes in the expression of these characters. Low estimates of heritability and GAM for oil content were reported by Nadaf and Habib (1987). High heritability (Basu *et al.*, 1988), low to medium heritability (Reddy and Murthy, 1994), high heritability coupled with low GAM (Vindhiya Varman and Raveendran, 1996a), moderate heritability (Jayalakshmi, 1997) and low heritability (Parmar *et al.*, 2002) were reported for oil content. Moderate to high heritability for protein content (Parmar *et al.*, 2001 a) and high heritability for protein in F_1 and F_2 generations of groundnut crosses (Parmar *et al.*, 2002) were also reported. Where as for carbohydrate components heritability was reported to be high (Pattee *et al.*, 2000).

Relative comparisons made between physiological characters for genetic parameters revealed that moderate to high variability as indicated by GCV and PCV was observed for all the physiological characters except for SLA at 90 DAS, SLW at 90 DAS and SCMR at 30 DAS (table 14). SLA at 90 DAS and SLW at 90 DAS recorded low GCV and moderate PCV indicating low genetic variability and the low influence of the environment. Where as SCMR at 30 DAS showed low GCV and PCV estimates indicating the presence of low magnitude of variability. High genotypic variation for harvest index was reported by Qadri and Khunti (1982), Reddy and Gupta (1992), Sharma and Varshney (1995) and Jayalakshmi (1997). High variability for SLW (Madhavi, 1988) was also reported. The environmental influence in the expression of character was more on pod weight per plant, SLA at 90 DAS and SLW at 90 DAS. Similar high differences between PCV and GCV were reported for pod yield by Hari Singh *et al.* (1982). High heritability was recorded for all the characters excepting those two characters (SLA at 90 DAS and SLW at 90 DAS), which showed less variability. GAM was high for CGR at 60 DAS, CGR at 90 DAS, moderate for SLA at 30 DAS, SLW at 30 DAS, LAI at 90 DAS, LAR at 90 DAS, SLW at 60 DAS, SLA at 60 DAS and harvest index. High heritability coupled with high GAM for the characters; CGR at 60 and at 90 DAS indicated the involvement of additive gene action and simple selection would be rewarding for improvement of these characters. SLA at 90 DAS and SLW at 90 DAS recorded low heritability and GAM, which indicated non-additive gene action. For harvest index high heritability (Hari Singh *et al.*, 1982; Qadri and Khunti, 1982; Jayalakshmi, 1997 and Vaddoria and Patel, 1990), low heritability (Chauhan and Shukla, 1985), high GAM (Reddy and Gupta, 1992), high heritability and GAM (Sharma and Varshney, 1995) and moderate to high GAM (Vasanthi and Raja Reddy, 2002) were reported. Anuradha (1995) reported low heritability and GAM for SLA at 90 DAS and moderate heritability for LAI at 30 DAS. Where as Jayalakshmi (1997) recorded high heritability for SLA and SLW despite low GAM. Though SCMR at 30 DAS recorded high heritability the scope of improvement was restricted due to low variability and GAM. Where as Vasanthi *et al.* (2004) in their studies observed moderate values of heritability and GAM along with GCV and PCV for SCMR.

When variability, heritability and GAM were considered together, shell volume, pod volume, free space in pod, immature pods per plant, mature pods per plant and 100 seed weight among morphological characters; reducing sugar content and non-reducing

Fig. 3a : Contribution (%) of morphological and biochemical characters towards divergence

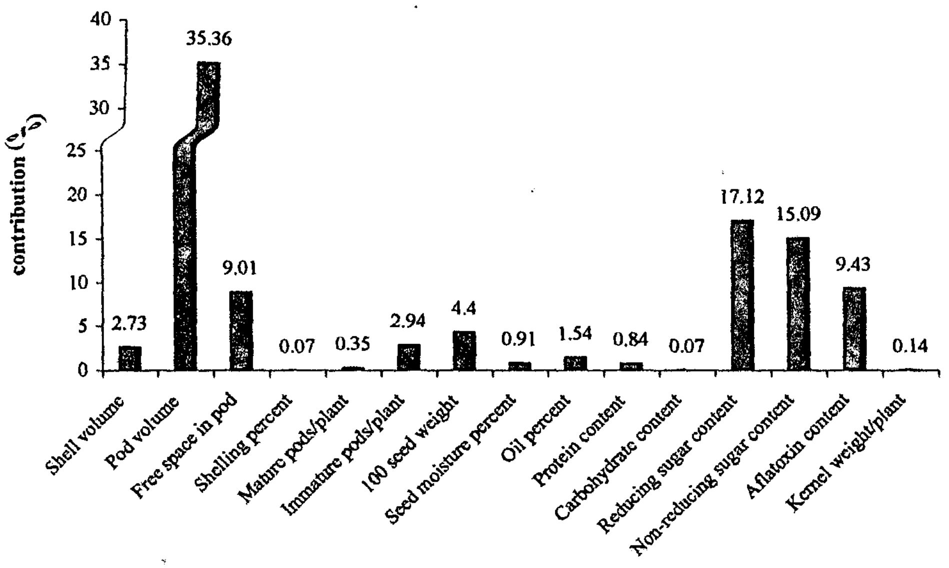
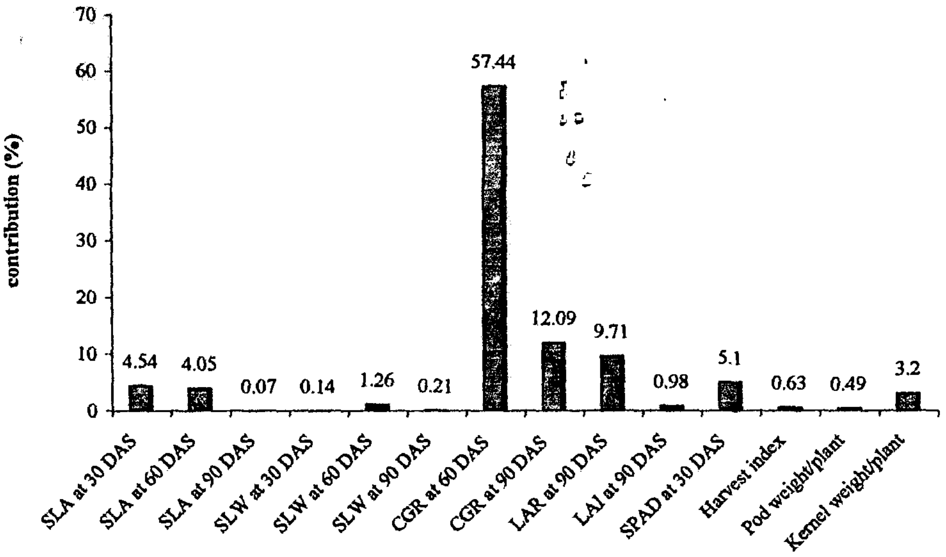


Fig. 3b : Contribution (%) of pysiological characters towards divergence



sugar content among biochemical characters and CGR at 60 and at 90 DAS among physiological characters were found to be a better choice of characters. Improvement either in positive or negative direction is possible with the available quantum of variability for all these characters (table 36).

5.4 GENETIC DIVERGENCE

Genetic divergence studies are the tools for the evaluation of germplasm lines and selection of parents for breeding programme (Arunachalam, 1981). The multivariate analysis using Mahalanobi's D^2 statistic provides a useful statistical tool for measuring the magnitude of genetic diversity available in a given population in respect of the characters considered together. It also discriminates the characters based on their contribution to total diversity. In the present investigation, it was observed that pod volume, free space in pod and100 seed weight among morphological characters; reducing sugar content, aflatoxin content and non-reducing sugar content among biochemical characters and SLA at 30 and at 60 DAS, CGR at 60 and at 90 DAS, LAR at 90 DAS and SCMR at 30 DAS among physiological characters had contributed more to diversity (figure 3a and 3b). The characters harvest index (Rajkumar, 1991; Anuradha, 1995; Vijayasekhar, 2002), shelling percentage (Rajkumar, 1991; and Vijayasekhar, 2002), pod and kernel yields (Anuradha, 1995) and 100 seed weight (Vijayasekhar, 2002) were observed to have contributed towards genetic divergence in the previous reports. The information thus generated on the importance of the characters through genetic divergence studies can be effectively utilized, along with character association, variability, heritability and GAM in formulating selection indices.

The data on 28 characters grouped into two, one group with morphological and biochemical characters and the other with physiological characters including pod and kernel weight per plant were collected from 54 groundnut genotypes, were subjected to multivariate analyses and the genetic diversity was estimated separately for the two groups of characters. Test with Wilk's 'V' criterion was highly significant when all the characters were considered simultaneously for both groups of characters. The magnitude of D^2 values for both the groups of characters suggested that there was considerable diversity in the material studied. This range of variation allowed for grouping of 54 genotypes into 11 clusters for morphological and biochemical characters and into 17 clusters for physiological characters which in turn substantiated maximum diversity for both the groups of characters. Nayak and Patra (1997) studied 18 characters and grouped 128 genotypes belonging to all botanical groups into 15 clusters using D^2 statistic. Where as John Joel and Mylsamy (1998) reported moderate genetic diversity among the genotypes studied for nine aggregate characters as they were grouped into three clusters only.

The clusters framed for morphological and biochemical characters had a minimum of two genotypes (cluster X) and a maximum of 33 genotypes (cluster I). The formation of largest cluster I comprising 33 genotypes might be due to the free flow or exchange of breeding material from one place to another or /and the unidirectional selection practiced by breeders of different locations. Seven genotypes could not be clubbed with any other clusters as they maintained separate identify from all others. They were grouped in the clusters, III, IV, V, VII, VIII, IX and XI each exhibiting high genetic diversity with most of the clusters.

Similarly the range in D^2 values allowed the constellation of 54 genotypes in 17 clusters for physiological characters. The minimum and maximum number of genotypes were present in the clusters III (2) and I (22) respectively. The clusters with solitary position were from V to XVIII and each genotype in these clusters was distinctly different with other cluster.

Constellation of genotypes into different clusters for morphological, biochemical and physiological characters was at random and independent of each other. When clustering pattern was related to geographical origin, no regular demarcation was discernible in the pattern of constellation of genotypes into various clusters. For instance the genotypes developed from one center i.e., Tirupati had fallen in different clusters in both the analyses carried for both the groups of characters. Similar lack of relationship between geographical origin and genetic diversity of genotypes was also reported by Nayak and Patra (1997), Venkataramana *et al.* (2000) and Vijayasekhar (2002).

Inter cluster distances were greater in magnitude for both the groups of characters confirming the presence of diversity among clusters. Moll and Stuber (1971) opined that crosses between divergent parents usually produced greater heterosis than those between closely related ones. Where as Arunachalam (1981) pointed out that extreme divergence may not produce the highest frequency of heterotic crosses. The maximum inter cluster distance for morphological and biochemical characters was observed between clusters II and XI suggesting wide diversity between these two groups. On the other hand the minimum intercluster distance between IV and V indicated that most of the characters had similar magnitude for these two clusters. The presence of only one genotype in the clusters like III, IV, V, VII, VIII, X and XI was the reason of obtaining 0 values for their intra cluster distance. Maximum intra cluster distance was found in clusters X, VI and I as selection of genotypes from cluster I having maximum number of genotypes (33) might be fruitful to produce good recombinants.

Most of the intracluster distances for physiological characters were at par. This could be implicated to the common origin of genotypes (John Joel and Mylsamy, 1998). Maximum intra cluster distance was observed in clusters I, II and IV. As the clusters I and II comprised maximum number of genotypes (2 and 11 respectively), parents for hybridization can be selected from these clusters. Maximum intercluster distance between cluster III and XV and between VI and XVII indicated greater diversity between these clusters. In contrast the minimum intercluster distance between IX and XI and X and XII indicated the close relationship between the clusters.

As the material consisted of high diverse forms belonging to all botanical groups, unforeseen crossing barriers were contemplated and some of the parents were chosen within the clusters, which were having high intra cluster distances. However major emphasis was made on cluster means and scores (explained in materials and methods) for selecting the best parents for crossing program.

Means for morphological and biochemical characters in clusters, I, II, IV, V, VI, IX were higher than their overall means. Two genotypes from clusters I and II and one each from clusters, IV, V, VI and IX were selected based on overall scoring for morphological and biochemical characters (table 36). Similarly for physiological characters, four genotypes from cluster I, three from cluster II and one each from clusters VII and XI were selected based on the same criterion followed for selecting genotypes for morphological and biochemical characters. The common genotypes selected for their efficiency in both groups of characters were finalised as nine (table 23). Bold seeded genotypes (ICGV 86564, TG 42, TG 49, M 13 and TPT 4) were used as testers for easy identification of F_1s as the large seed size was reported to be dominant (Murthy and Reddy, 1996). The remaining four genotypes, ICG 1326, ICG 3245, ICG 3542 and ICG 7633 were used as lines. The four lines and the five testers were crossed in line X tester fashion to obtain 20 crosses.

SELECTION CRITERION

A) Selection of important characters

As per the methodology described under 3.5.5.6 six morphological (shell volume, pod volume, free space in pod, shelling percentage, 100 seed weight and mature pods per plant), three each among physiological characters (CGR at 60 DAS, CGR at 90 DAS, harvest index) and biochemical characters (protein content, reducing sugar content and non-reducing sugar content) were considered to formulate a selection criterion (table 36). Though the importance of protein content was observed only in correlation studies, it was selected because of its relevance to quality and its negative correlation with aflatoxin content. Similarly harvest index exhibited strong positive correlation with kernel weight. And its significance in other biometrical analyses was not observed. Because of its universal acceptability as an important yield contributing character it was also included as an additional character. As all the analyses in the present investigation were directed towards reduction of aflatoxin content and improvement of kernel weight these two characters were included in formulating the selection criteria.

b) Selection of genotypes

The genotypes with high overall scoring were ICG 1326, ICG 3245, ICG 3542, ICG 7633, ICG 11386, ICGV 86564 and TG 49 (table 37). Among these nine genotypes M 13 and ICG 11386 had spreading habit. The habit of the rest of the genotypes was erect and they are of short duration with an exception to ICGV 86564, which was erect, and of *long duration.* *The genotypes, which were significant for aflatoxin resistance and kernel* yield, were selected unconditionally even if their overall score was less than the selection criterion. Accordingly, M 13 along with TPT 4 was selected as one of the parents for hybridization. The superiority of ICGV 86564 was also observed for pod yield per plant,

Table 36: Selection of important characters related to high kernel yield and low aflatoxin content

S. No.	Characters showing				Characters with high		Characters contributed more to diversity	Characters selected	Breeding strategy
	Significant correlation with		High direct effects on		Variability	Heritability and genetic advance			
	Kernel yield	Aflatoxin content	Kernel yield	Aflatoxin content					
1	Pod volume (+)	Shell volume (+)	Shell volume (+)	Shell volume (+)	Pod volume	Shell volume	Pod volume	Shell volume	Reduce
2	Free space in pod (+)	Pod volume (+)	Pod volume (+)	Pod volume (-)	Free space in pod	Pod volume	Free space in pod	Pod volume	Improve
3	Mature pods per plant (+)	Shelling percent (-)	Free space in pod (+)	Free space in pod (+)	Reducing sugar content	Free space in pod	100 seed weight	Free space in pod	Reduce
4	Immature pods per plant (+)	Oil percent (-)	Shelling percent (+)	Shelling percent (-)	Non-reducing sugar content	Mature pods per plant	Reducing sugar content	Shelling percent	Improve
5	100 seed weight (+)	Protein content (-)	Mature pods per plant (+)	Mature pods per plant (+)	Immature pods per plant	Immature pods per plant	Non-reducing sugar content	100 seed weight	Improve
6	Protein content (-)	Carbohydrate content (+)	100 seed weight (+)	100 seed weight (-)	Shell volume	100 seed weight	SLA at 30 DAS	Mature pods per plant	Improve
7	Carbohydrate content (+)		Oil percent (-)		CGR at 60 DAS	Reducing sugar content	SLA at 60 DAS	Protein content	Improve
8	Non-reducing sugar content (+)		Carbohydrate content (-)		CGR at 90 DAS	Non-reducing sugar content	CGR at 60 DAS	Reducing sugar content	Improve
9	SLA at 90 DAS (+)		SLA at 60 DAS (+)		LAI at 90 DAS	CGR at 60 DAS	CGR at 90 DAS	Non-reducing sugar content	Improve
10	CGR at 90 DAS (+)		SLW at 60 DAS (+)			CGR at 90 DAS	LAR at 90 DAS	CGR at 60 DAS	Improve
11	LAR at 90 DAS (+)		CGR at 60 DAS (+)				SCMR at 30 DAS	CGR at 90 DAS	Improve
12	LAI at 90 DAS (+)		CGR at 90 DAS (+)					Harvest index	Improve
13	Harvest index (+)		LAR at 90 DAS (+)					Aflatoxin content	Reduce
14	Pod weight per plant (+)		LAI at 90 DAS (-)					Kernel weight plant	Improve
15	----		Pod weight per plant (+)						

- Negative association/effect + Postitive association/effect

Table 37: Selection of genotypes for crossing in L X T design based on significant mean values

Genotype	Shell *volume*	Pod *volume*	Free space *in shell*	Shelling *percent*	Mature *pods/plant*	100 seed *weight*	Protein *content*	Reducing *sugar* content	Non-*reducing* sugar content	CGR at *60 DAS*	CGR at *90 DAS*	Harvest *index*	Aflatoxin *content*	Kernel *yield* per plant	Overall *score*
Weightage	1	1	1	1	1	1	1	1	1	1	1	1	3	2	17
ICG 50	-		-												2
ICG 1326	-		-	+				+	+				-		8
ICG 1416			-				+			+					3
ICG 2184	-		-					+					-		6
ICG 2411	-		-	+					+						4
ICG 3245	-		-	+				+	+	+			-		9
ICG 3509		+					+		+						3
ICG 3542	-		-	+	+			+	+		+			+	9
ICG 3643	-		-				+								3
ICG 4749	-			+			+				+		-		7
ICG 4893	-			+											2
ICG 5502		+						+		+					3
ICG 6690		+						+							2
ICG 7332			-			+	+	+			+				5
ICG 7633		+		+				+	+		+	+		+	8
ICG 7637								+	+	+					3
ICG 7749									+	+					2
ICG 8325		+													1
ICG 8666											+		-		4
ICG 10352	-		-	+				+							4
ICG 11386	-		-		+	+	+			+				+	8
ICG 13938	-							+	+		+				4
ICGV86031															0
ICGV 86552			-					+			+				3
ICGV 86564		+			+	+		+	+		+			+	8
ICGV 86584	-			+	+		+							+	6
ICGV 88448	-		-									+	-		6
ICGV 89214		+				+					+			+	5
ICGV 96234	-		-	+	+					+					5
ICGV 96235		+				+				+					3
ICGS11	-		-		+							+			4
ICGS 21	-									+	+				3
BAU13		+				+					+				3
TG 39	-					+	+					+			4
TG 40		+				+						+	-		4
TG 41		+				+	+								3
TG 42		+				+		+		+		+			5
TG 45		+				+							-		3
TG 49		+				+			+	+		+	-		8
M13		+				+							-	+	7
JL 24			-										-		4
K 134	-		-	+							+		-		7
TPT 1	-		-				+	+			+				5
TPT 2			-							+					2
TPT 4	-						+			+			-	+	8
TCGS 29		+			+					+				+	5
TCGS 61		+				+			+	+				+	6
TCGS 91	-		-					+	+	+	+				6
TCGS 320										+					1
TCGS 407	-		-							+					3
TCGS 584		+					+								2
TCGS 596		+								+					2
TCGS 617		+				+		+	+	+				+	7
TCGS 634	-		-												2

- Negative selection + Positive selection shelling percentage, 100 kernel weight, SMK weight, kernel weight per plant, harvest index and oil percentage and oil yield per plant among 144 genotypes studied by Venkataravana *et al.* (2000). Although M 13 and ICG 11386 were long duration and spreading genotypes, ICG 11386 was dropped and M 13 was only selected, as it possessed low aflatoxin content and high kernel weight per plant as well. M 13 was also found to be superior for most of the traits in an earlier report (Vindhiya Varman and Senthil, 1998). A biased selection was made for TG 42 (overall score was 5) as it had high harvest index, bold seeds and short duration. As a matter of fact early duration is related to escape from end-of-season drought, which in turn related to escape from *A. flavus* infection.

5.5 COMBINING ABILITY ANALYSIS

The choice of parents in the hybridization programme is of immense importance for getting better seggregants in a crop like groundnut where hybridization followed by pedigree method of breeding is the most commonly used breeding method. The information generated through genetic divergence analysis on parents can be utilized for further analysis to find out their combining ability for selected characters and also the gene action involved. Among the different methods adopted to generate the aforesaid information, the line X tester analysis has been recommended for early evaluation of parents because of its simplicity in both experimentation and analysis (Dhillon, 1975).

The knowledge on the association of kernel weight and aflatoxin resistance with the morphological, biochemical and physiological characters, their variability and diversity would be of paramount importance not only in identifying the better parents and their crosses but also the best high yielding aflatoxin resistant seggregants. Accordingly 14 out of 28 morphological, biochemical and physiological characters were selected (explained in 3.5.5.6) for combining ability and heterosis analyses. Hence, the discussion is restricted to 14 characters viz., shell volume, pod volume, free space in pod, shelling percentage, mature pods per plant, 100 seed weight, protein content, reducing sugar content, non-reducing sugar content, CGR at 60 DAS, CGR at 90 DAS, harvest index, aflatoxin content and kernel weight per plant.

It was with this background, nine genotypes out of 54 were selected based on the aforesaid analyses. Bold seeded genotypes (ICGV 86564, TG 42, TG 49, M 13 and TPT 4) were used as testers for easy identification of F_1 s as the character was reported to be dominant (Murthy and Reddy, 1996). The remaining four genotypes, ICG 1326, ICG 3245, ICG 3542 and ICG 7633 were used as lines. The four lines and the five testers were crossed in line X tester fashion to obtain 20 crosses. The results thus obtained are briefly discussed hereunder.

5.5.1 Analysis of variance

The mean sum of squares due to females (lines) and males (testers) provide a measure of their general combining ability while the interaction of L X T provide a measure of specific combining ability. In the present study, simple randomized block design analysis indicated that for all the 14 characters studied, the crosses differed significantly. This information facilitated to subject the material to combining ability analysis. The analysis of variance for combining ability revealed significant difference among parents (lines + testers), line and tester *per se* for all the characters thus justifying the selection of parents for the study. This has further resulted in substantial variability among the crosses also as evident from significance of mean squares due to crosses. This was also reflected through the presence of average heterosis in the crosses as evident from significance of single degree of freedom comparison (parent *vs* crosses) except for aflatoxin and harvest index. The significance of variance due to lines was found for the

Fig.4: Proportional contribution of lines, testers and line x tester interaction towards variation

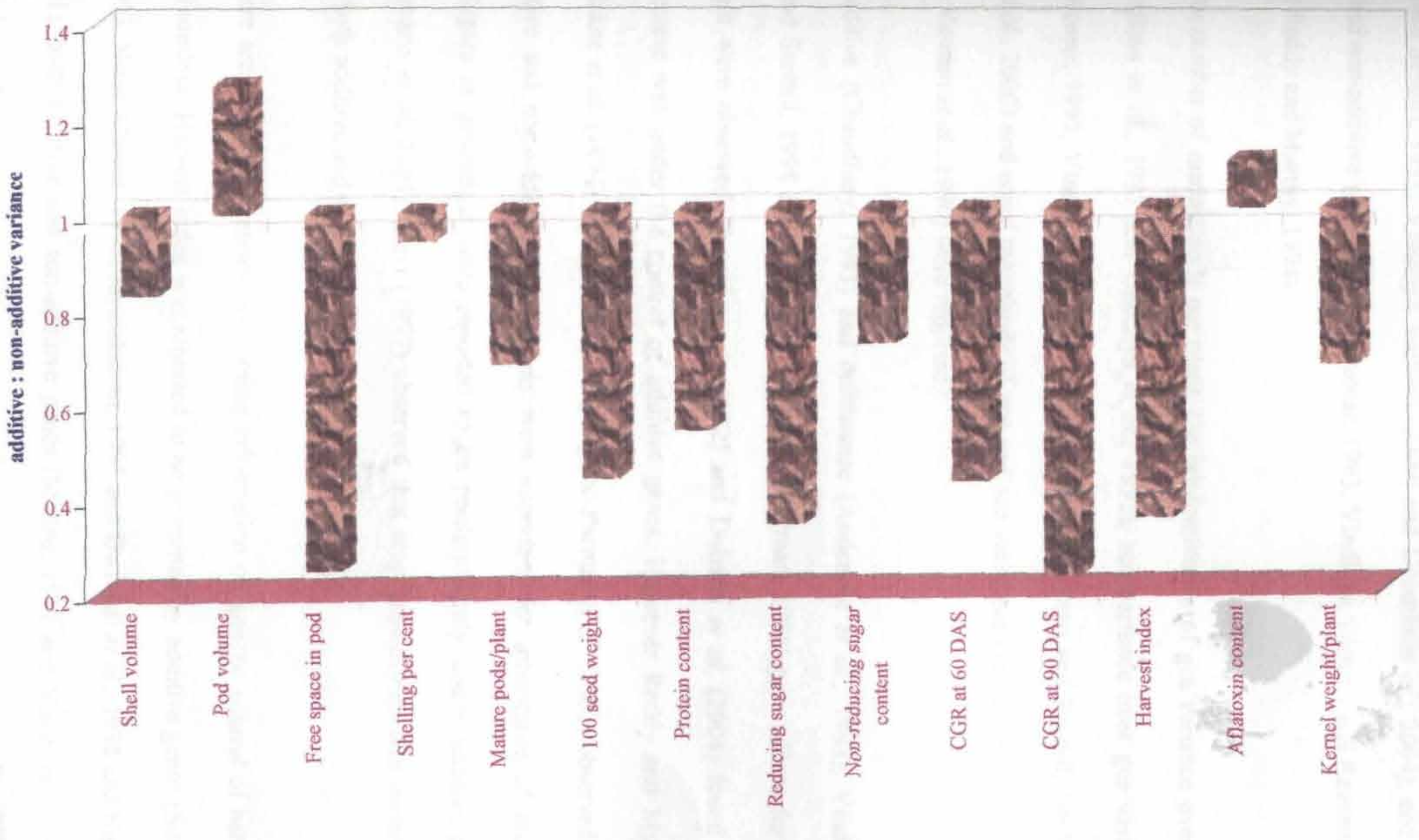
pod volume and that due to testers for shelling percentage. The non-significant variances for the others characters indicated that there were no differences among lines and testers. However, the line X tester interaction for all the characters indicated that the lines did not appeared to behave consistently over different testers and vice versa.

Relative contribution percentage of lines, testers and line x tester interaction towards variation illustrated in fig. 4 revealed that more than 50 per cent of variation in crosses for pod volume was contributed by lines, and the testers for shelling percentage. Relatively, lines had contributed more than testers for morphological and physiological characters whereas the reverse was true for biochemical characters. However, the line x tester interaction component apportioned greater percentage of the total variation for majority of the characters.

5.5.2 Gene action

An overall understanding of the gene action for different characters is possible by making comparison of variances due to GCA and SCA. The breeding methods might be decided based on the relative importance of general and specific combining ability variances. In groundnut, a self pollinated crop, high SCA effects of a particular cross combination will be useful if it is accompanied by high GCA effects of respective parents. In the present study, partitioning of combining ability variances into fixable additive genetic variance and non fixable dominance variances revealed that non additive genetic variance was higher in magnitude for majority of the characters indicating the preponderance of dominance gene action in controlling the expression of these traits figure 5). They were; shell volume, free space in pod, shelling percentage, mature pods per plant, 100 seed weight, protein content, reducing sugar content, non-reducing content, CGR at 60 DAS, CGR at 90 DAS, harvest index and kernel weight per plant. Most of

Fig.5: Magnitude of genetic variance for morphological, physiological and biochemical characters



studies on inheritance pattern of these characters reported varying results. Shelling percentage was reported to exhibit preponderance effects of additive genes (Manoharan *et al.* 1985; Basu *et al.*, 1987 and Kumar and Patel, 1999), non-additive genes (Vindhiya Varman and Senthil, 1998; Vindhiya Varman, 2000; and Dobaria *et al.*, 2004), and both additive and non-additive genes (Suresh Kumar, 1993, Vindhiya Varman and Raveendran, 1994 and Reddy and Murthy, 1994).

For number of mature pods per plant, the predominance of gca variance over sca variance (Basu *et al.*, 1987 and Upadhyaya *et al.*, 1992), sca variance over gca variance (Suresh Kumar, 1993, Vindhiya Varman, 2000; Vindhiya Varman and Senthil, 1998 and Mathur *et al.*, 2000) and equal magnitude of gca and sca variances (Jayalakshmi 1997 and Vindhiya Varman *et al.*, 1990) were reported.

Additive (Chaudhary, 1993) and dominance (Anderson *et al.*, 1993); Vindhiya Varman and Senthil, 1998 and Senthil and Vindhiya Varman, 1998) gene effects for 100 seed weight were observed. Bansal *et al.* (1992) and Dobaria *et al.* (2004) found that protein content was under the control of additive genes. However Reddy and Murthy (1994), Makne *et al.* (1994), Parmar *et al.* (2001 a) and Parmar *et al.* (2002) observed that both additive and non-additive gene effects were important for inheritance of protein content. Sugars in groundnut were reported to be predominantly under additive gene action (Dobaria *et al*, 2004). Devi (1997) observed that crop growth rate was under the control of both additive and non-additive genes.

There are conflicting reports concerning information on genctic control of harvest index in groundnut. Harvest index was reported to be governed by additive genes (Suresh Kumar, 1993, Nisar Ahmed, 1995; Jayalakshmi, 1997 and Dwivedi *et al.*, 1998 and Nigam *et al.*, 2001), both additive and non-additive genes (Makne, 1992 and Vindhiya Varman and Raveendran, 1994) and non-additive genes (Makne, 1992).

All the three types of gene action were reported for kernel yield. Preponderant additive gene effects (Hariprasad, 1990 and Vindhiya Varman, 2000), dominant gene effects (Suresh Kumar, 1993, Nisar Ahmed, 1995 and Jayalakshmi, 1997) and both additive and dominant gene effects (Reddy and Reddy, 1988) were found to be important in the inheritance of kernel yield.

Non-additive gene action for majority of the characters indicated that the improvement of these characters was possible through exploitation of heterosis breeding. But groundnut being a self-pollinated crop, heterosis breeding is not advisable due to the constraints involved in the synthesis of commercial hybrids. Therefore, to get better genotypes by way of recombination breeding hybridization followed by selection in later generations was suggested for exploitation of dominance gene action. GCA variance was greater in proportion than SCA variance for the characters pod volume and aflatoxin content. As such, these traits can be improved by employing breeding methods, which xploit additive gene action.

5.5.3 EVALUATION OF PARENTS

The parents with high order *per se* performance would be of greater importance in breeding program (Singh *et al.*, 1983). The potentiality of a genotype participating in a cross is best judged by its *per se* performance and gca effects (Singh *et al.*, 1985). Hence, parents were evaluated based on their *per se* performance and gca effects. Based on the results of association analysis, positive or negative direction of selection was applied to the characters. Parents that had positive and significant values were considered as desirable ones for pod volume, shelling percentage, mature pods per plant, 100 seed weight, protein content, reducing sugar content, non-reducing sugar content, CGR at 60 DAS, CGR at 90 DAS, harvest index and kernel weight per plant. While for other characters, viz., shell volume, free space in pod and aflatoxin content, parents with negative and significant values were taken in to consideration.

5.5.3.1 *Per se* performance

Four parents viz., L_1, L_2, T_3 and T_5 were identified with significantly lower shell volume. High *per se* performance for pod volume was recorded by L_3, L_4, T_1 and T_2. Where as significantly low free space was observed in L_2, L_3, T_3, T_4 and T_5. The lines; L_2, L_3 and the testers; T_3 and T_5 had high *per se* performance of shelling percentage. Likewise for mature pods; L_1, T_1, T_4 and T5, for 100 seed weight; L_2, T_1, T_2, T_3 and T_4, for protein content; L_2, L_3, T_1, T_2 and T_5, for reducing sugar content; L_3, T_2 and T_4, for non-reducing sugar content; L_3, L_4, T_2 and T_3 for CGR at 60 DAS; L_1, L_3 and T_4, for CGR at 90 DAS; L_1, T_1 and T_5; for harvest index; L_2, L_4, T_2 and T_3 and for kernel weight; L_1, L_4, T_1 and T_3 exhibited high *per se* performance. For aflatoxin content, L_1, L_2, T_2, T_3 and T_5 were observed to show low *per se* performance.

Several parents had significant mean performance for more than one character. The parents that exhibited significant *per se* performance for more than six characters which accounted for 50 per cent of total characters, were considered as the best ones. They were L_1 (ICG 1326), L_2 (ICG 3245), L_3 (ICG 3542), T_2 (TG 42), T_3 (TG 49) and T_5 (TPT 4). The line L_1 showed significance for shell volume, mature pods per plant, CGR at 60 DAS, CGR at 90 DAS, aflatoxin content and kernel weight per plant. Like wise, the line, L_2 for shell volume, free space in pod, shelling percentage, 100 seed weight per plant, protein content, harvest index and aflatoxin content, and the line L_3 for pod volume, free space in pod, shelling percentage, protein content, reducing sugar content, non-reducing content and CGR at 60 DAS. Similarly the tester T_3 expressed significant *per se* performance for shell volume, free space in pod, shelling percentage, 100 seed weight, non-reducing sugar content, harvest index, aflatoxin content and kernel weight. T_5 showed significance for shell volume, free space in pod, shelling percentage, mature pods per plant, protein content, CGR at 90 DAS and aflatoxin content. While T_2 had significant mean values for pod volume, 100 seed weight, protein content, reducing sugar content, non-reducing sugar content, harvest index and aflatoxin content. Hence, these parents were considered desirable for developing high yield groundnut varieties with aflatoxin resistance. The line, L_1 (ICG 1326), a small seeded genotype and the tester, T_3 (TG 49) a bold seeded genotype expressed significance for aflatoxin content and kernel weight per plant as well. The resistance of ICG 1326 to aflatoxin production was a proven fact since it served as donor parent for aflatoxin resistance in many breeding programmes. With respect to TG 49 also the same level resistance was observed in both the seasons of the study. Infact TG 49 recorded lower infection than the resistant genotype, ICG 1326 (J 11) in earlier report (Harish Babu *et al.*, 2003). But yield of the two genotypes seemed to be fluctuating in the two seasons. They did not significantly out yielded the general mean during *kharif*, 2002. However they can be directly recommended as aflatoxin resistant varieties to the problem prone areas for immediate use and can be utilized in the breeding programmes for later use to enhance yield and reduce aflatoxin content levels.

5.3.2 General combining ability effect

The gca effects of parents were estimated to evaluate the ability of parents to transmit desirable characters to their offspring. The combining ability of parents gives useful information on the choice of parents in terms of expected performance of their progenies (Dhillon, 1975). Tiwari *et al.* (1993) suggested that parents having high gca effects could produce transgressive segregants in the segregating generations. The gca effects of parents had been attributed to additive genetic effects. Hence, if additive gene

Fig.6: General combining ability (gca) effects of nine parents for aflatoxin content

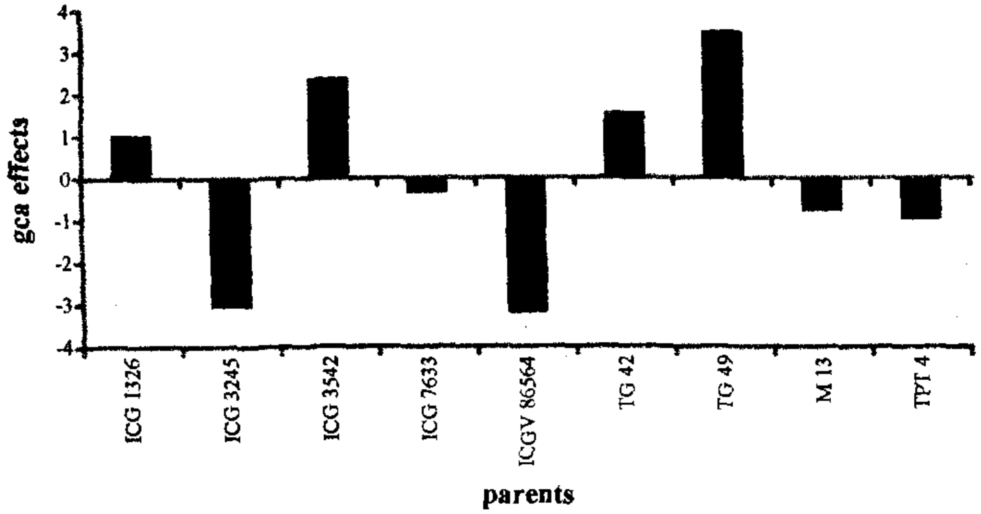
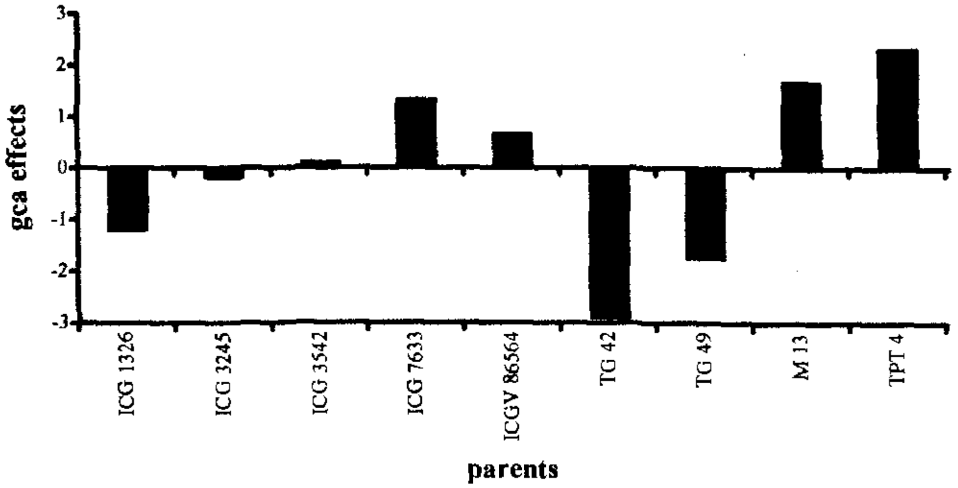


Fig.7: General combining ability (gca) effects of nine parents for kernel weight per plant



action is predominant in self-pollinated species, the breeder can effectively select at various levels of inbreeding because additive genetic effects are readily transmissible from one generation to another.

The gca effects indicated that the number of testers with good gca were either equal or more than the lines for all the characters under study. Among them the tester, T_4 (M 13) was adjudged as the best general combiner. Since it expressed good gca effects for nine characters (free space in pod, shelling percentage, mature pods per plant, 100 seed weight, protein content, reducing sugar content, CGR at 60 DAS, harvest index and kernel weight per plant). This was followed by T_1 (ICGV 86564) and T_5 (TPT 4) both were better for eight characters each. T_1 was a good combiner for pod volume, shell volume, free space in pod, shelling percentage, mature pods per plant, reducing sugar content, CGR at 90 DAS, aflatoxin content and kernel weight per plant (figure 6 and 7). Where as T_5 was good for shell volume, shelling percentage, mature pods per plant, 100 seed weight, protein content, non-reducing sugar content, harvest index and kernel weight per plant.

Among the lines, L_1 (ICG 1326) was proved to be the best with good gca for eight characters (shell volume, free space in pod, shelling percentage, mature pods per plant, protein content, reducing sugar content, non-reducing sugar content and CGR at 60 DAS. The other line, L_4 (ICG 7633) was good combiner for seven characters viz., pod volume, protein content, reducing sugar content, non-reducing sugar content, CGR at 60 DAS, CGR at 90 DAS, harvest index and kernel weight per plant. It was observed that T_1 (ICGV 86564) was the only parent with good gca for both aflatoxin content and kernel weight per plant.

5.5.3.3 *Per se* performance and gca effects

Per se performance of parents was not always associated with high gca effects. For example L_1 and T_3 performed better in mean values for kernel weight per plant but were not good general combiners. Similarly T_1 possessed good gca despite its poor *per se* performance for aflatoxin content. So, it was felt that evaluation of parents based on *per se* performance and gca effects separately might lead to contradiction in selection of promising parents. Instead, combination of both *per se* performance and gca effects will result in the selection of parents with good reservoir of superior genes. So the parents were evaluated for significant *per se* performance coupled with good gca effects (table38). The direction (positive or negative) of selection was observed to identify parents with good *per se* performance and good gca.

The parents, L_2 (ICG 3245), T_4 (M 13) and T_5 (TPT 4) emerged as the best parents with significant mean values coupled with good gca effects for five characters each. L_2 had significant *per se* performance and good gca effects for free space in pod, shelling percentage, 100 seed weight, harvest index and aflatoxin content. Like wise, T_4 was better for free space in pod, mature pods per plant, 100 seed weight, reducing sugar content and CGR at 60 DAS. Another tester, T_5 (TPT 4) was adjudged the next best parent since it howed significant mean and gca values for four characters viz., shell volume, shelling percentage, mature pods per plant and protein content.

Ranking of parents based on *per se* performance and gca effects showed that parallelism between *per se* performance and gca effects did not always existed. It was eflected in the performance of the line, L_1, L_3 and L_4 and the testers, T_1, T_2, T_3 and T_4. For nstance, L_3 and T_2 showed significant mean values for six characters but their gca was

Table 38: Desirable parents selected based on mean and gca effects

S. No.	Characters	Mean	gca effects	Mean and gca effects
1	Shell volume	L_1, L_2, T_3, T_5	L_1, L_3, T_1, T_5	L_1, T_5
2	Pod volume	L_3, L_4 T_1, T_2	L_4 T_1, T_2, T3	L_4 T_1, T_2
3	Free space in pod	L_2, L_3, T_3, T_4, T_5	L_1, L_2, T_1, T_3, T_4	L_2, T_3, T_4
4	Shelling percentage	L_2, L_3, T_3, T_5	L_1, L_2, T_1, T_4, T_5	L_2, T_5
5	Mature pods per plant	L_1, T_1, T_4, T_5	L_1, L_3, T_1, T_4, T_5	L_1, T_4, T_5
6	100 seed weight	L_2, T_1, T_2, T_3, T_4	L_2, T_4, T_5	L_2, T_4
7	Protein content	L_2, L_3, T_1, T_2, T_5	L_1, L_3, L_4, T_3, T_4, T_5	L_3, T_5
8	Reducing sugar content	L_3, T_2, T_4	L_1, L_3, L_4, T_1, T_3, T_4	L_3, T_4
9	Non-reducing sugar content	L_3, L_4, T_2, T_3	L_1, L_4, T_2, T_5	L_4
10	CGR at 60 DAS	L_1, L_3, T_4	L_1, L_4, T_3, T_4	L_1, T_4
11	CGR at 90 DAS	L_1, T_1, T_5	L_3, L_4, T_1, T_3	T_1
12	Harvest index	L_2, T_2, T_3	L_2, L_4, T_4, T_5	L_2
13	Aflatoxin content	L_1, L_2, T_2, T_3, T_5	L_2, T_1	L_2
14	Kernel weight per plant	L_1, L_4, T_1, T_3	L_3, L_4, T_1, T4, T_5	L_4, T_1
	OVER ALL	**L_1, L_2, L_3, T_2, T_3, T_5**	**L_1, L_4, T_1, T_4, T_5**	**L_2, T_4, T_5**

good for two characters only. On the other hand, L_4 expressed good gca for seven characters where as its *per se* performance was significant only in three characters,

Results on the combination of both *per se* performance and gca effects revealed hat identification of superior segregants in the crosses involving L_2 (ICG 3245), T_4 (M 13) and T_5 (TPT 4) might be possible for most of the characters studied. The parents L_4 (ICG 7633) and T_1 (ICGV 86564) though had significant gca effects for seven and eight characters including kernel weight and aflatoxin content (T_1), failed to show significant *per se* performance for more than 50 % of the characters. The significant gca effects of these two parents for more than six characters indicated that the characters were under the control of additive genes and therefore they can be utilized in the hybridization programme and the segregants can be screened for superior genotypes. The importance of the parents, L_2 (ICG 3245), L_4 (ICG 7633) and T_1 (ICGV 86564) which expressed significant mean and gca values for aflatoxin content and kernel weight per plant respectively could not be elucidated in the present study. However their recombinants cannot be ignored in the present context of developing aflatoxin resistant high yielding groundnut varieties.

5.5.4 EVALUATION OF CROSSES

Combination of favorable genes present in the parents is the main aim of hybridization. The hybrids thus developed can be utilized either as commercial hybrids which is a remote possibility in groundnut or selecting superior segregants from the crosses in the subsequent generations and realizing best recombinants.

ICG 7633 ICG 7633 X M 13 M 13

Plate 7: F_1 cross suitable for high kernel yield through recombination breeding

5.5.4.1 *Evaluation of crosses for recombination breeding*

Recombination breeding has been the major avenue in groundnut improvement programmes over decades. The crosses selected for this purpose should satisfy the criteria that they should possess non-significant sca effects with their parents showing significant gca effects. The basic principle involved in this concept is that the segregation of these crosses is likely to throw more recombinants possessing favorable additive genes from both the parents. Therefore the information on the parents with significant gca effects and their crosses with non significant sca effects were pooled into the table 39 for valid comparison.

The number of crosses with non-significant sca effects for each character was very less. For characters like shell volume, pod volume, shelling percentage, mature pods per plant, 100 seed weight, protein content, non-reducing sugar content, CGR at 90 DAS, harvest index and aflatoxin content, none of the crosses, whose parents had significant gca effects, showed non significant sca effects. Hence no cross could be suggested for recombination breeding for these characters. One cross each for the characters, free space in pod (L_1 X T_1), CGR at 60 DAS (L_1 X T_4) and kernel weight per plant (L_4 X T_4) exhibited non-significant sca with significant gca for their parents. They can be persuaded for obtaining superior segregants. Reducing sugar content was the only character that had two crosses, L_1 X T_3 (ICG 1326 X TG 49) and L_4 X T_3 (ICG 7633 X TG 49) showing non-significant sca with high gca of their parents, these two crosses can be recommended for recombination breeding. It was very fortunate to obtain a cross, L_4 X T_4 (ICG 7633 X M 13) that showed promise for recombination breeding with its non-significant sca and significant gca of its parents for kernel weight per plant (plate 7).

Table 39: Crosses chosen for recombination breeding

S. No.	Characters	Parents with significant gca effects	Crosses chosen based on non-significant sca effects
1	Shell volume	L_1, L_3, T_1, T_5	--
2	Pod volume	L_4, T_1, T_2, T_3	--
3	Free space in pod	L_1, L_2, T_1, T_3, T_4	L_1 X T_1
4	Shelling percentage	L_1, L_2, T_1, T_4, T_5	--
5	Mature pods per plant	L_1, L_3, T_4, T_5	--
6	100 seed weight	L_2, T_4, T_5	--
7	Protein content	L_1, L_3, L_4, T_3, T_4, T_5	--
8	Reducing sugar content	L_1, L_3, L_4, T_1, T_3, T_4	L_1 X T_3, L_4 X T_3
9	Non-reducing sugar content	L_1, L_4, T_2, T_5	--
10	CGR at 60 DAS	L_1, L_4, T_3, T_4	L_1 X T_4.
11	CGR at 90 DAS	L_3, L_4, T_1, T_3	--
12	Harvest index	L_2, L_4, T_4, T_5	--
13	Aflatoxin content	L_2, T_1	--
14	*Kernel weight per plant*	*L_3, L_4, T_4, T_5*	*L_4 X T_4*

5.5.4.2 *Evaluation of crosses for heterosis breeding*

As there were only a few crosses available and as there was no single cross showing significance for more than two characters for recombination breeding, focus was made on the exploitation of non-additive gene action. Heterosis breeding offers an opportunity to accomplish this endeavor. Heterosis breeding has three bases of selection criteria. The primary criterion is to evaluate the crosses on their mean performance. The second important criterion is the significance of sca effects. And high heterosis forms the third basic criterion. Any single criterion alone in the present investigation had little importance in the selection of the best heterotic crosses across more number of characters.

In the present study, the cross L_1 X T_1 recorded significant mean values for all the characters except 100 seed weight and CGR at 90 DAS. It was followed by L_4 X T_5 which showed significant mean values for nine characters viz., shell volume, pod volume, shelling percentage, 100 seed weight, protein content, non-reducing sugar content, harvest index, aflatoxin content and kernel weight per plant. Next in line were L_2 X T_5, L_3 X T_4 and L_4 X T_4 with significant mean values for eight characters each. The common characters having significant mean values for the three crosses were shell volume, harvest index and kernel weight per plant. They were differing for other characters for their mean values. The other cross combinations; L_1 X T_3, L_2 X T_4 and L_3 X T_1 had shown significant mean performance for more than 50 % of the characters.

A character wise analysis revealed that there were 16 out of 20 crosses, which showed significantly lower shell volume. Significant low mean values were recorded for free space in pod by nine crosses. More than six crosses were identified for each character with significant mean performance. Where as, only four crosses were identified for reducing aflatoxin content.

Therefore, the crosses; L_1 X T_1 (ICG 1326 X ICGV 86564), L_4 X T_5 (ICG 7633 X TPT 4), L_4 X T_4 (ICG 7633 X M 13), L_2 X T_5 (ICG 3245 X TPT 4), L_3 X T_4 (ICG 3542 X M 13), L_2 X T_4 (ICG 3245 X M 13), L_1 X T_3 (ICG 1326 X TG 49) and L_3 X T_1 (ICG 3542 X ICGV 86564) were considered as outstanding ones for improving kernel weight per plant with aflatoxin resistance based on *per se* performance.

5.4.3 sca effects

The index to determine the usefulness of a particular cross combination for exploitation of heterosis is the sca effect. The sca effects are due to non-additive and epistatic gene action (Sprague and Tatum, 1942) and have also been attributed to the combination of positive favorable genes from different parents, which might be due to the presence of linkage in repulsion phase (Sarsar *et al.*, 1986). Hence, sca effects were considered as the second important criterion for evaluation of crosses.

Significantly higher sca effects were recorded in a reasonable number of crosses for each character. There were more than six crosses for each cross with an exception for aflatoxin content. Protein content had the highest number of crosses at its disposal for it s improvement (11 crosses). It was followed by free space in pod, CGR at 90 DAS and harvest index with nine crosses each. Where as kernel weight had seven crosses with significant sca effects (fig 8 and 9).

A cross wise analysis indicated that the cross L_1 X T_1 with significant sca effects for ten character values (pod volume, shelling percentage, mature pods per plant, protein content, reducing sugar content, non-reducing sugar content, CGR at 60 DAS, harvest index, aflatoxin content and kernel weight per plant) was adjudged as the best cross combination. The crosses L_3 X T_4 and L_4 X T_5 were the next best specific combiners for

Fig.8: Specific combining ability (sca) effects of 20 F_1 crosses for aflatoxin content

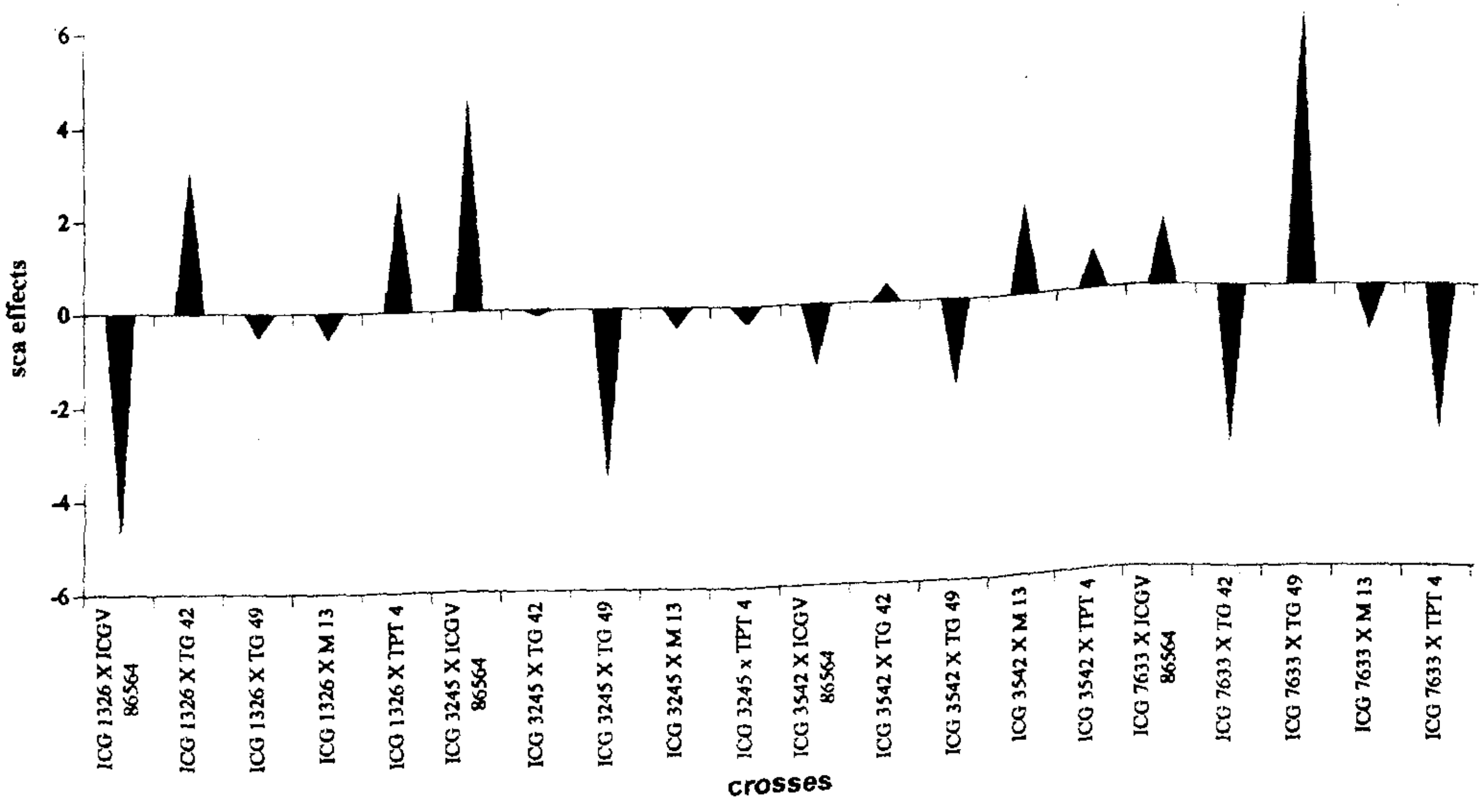
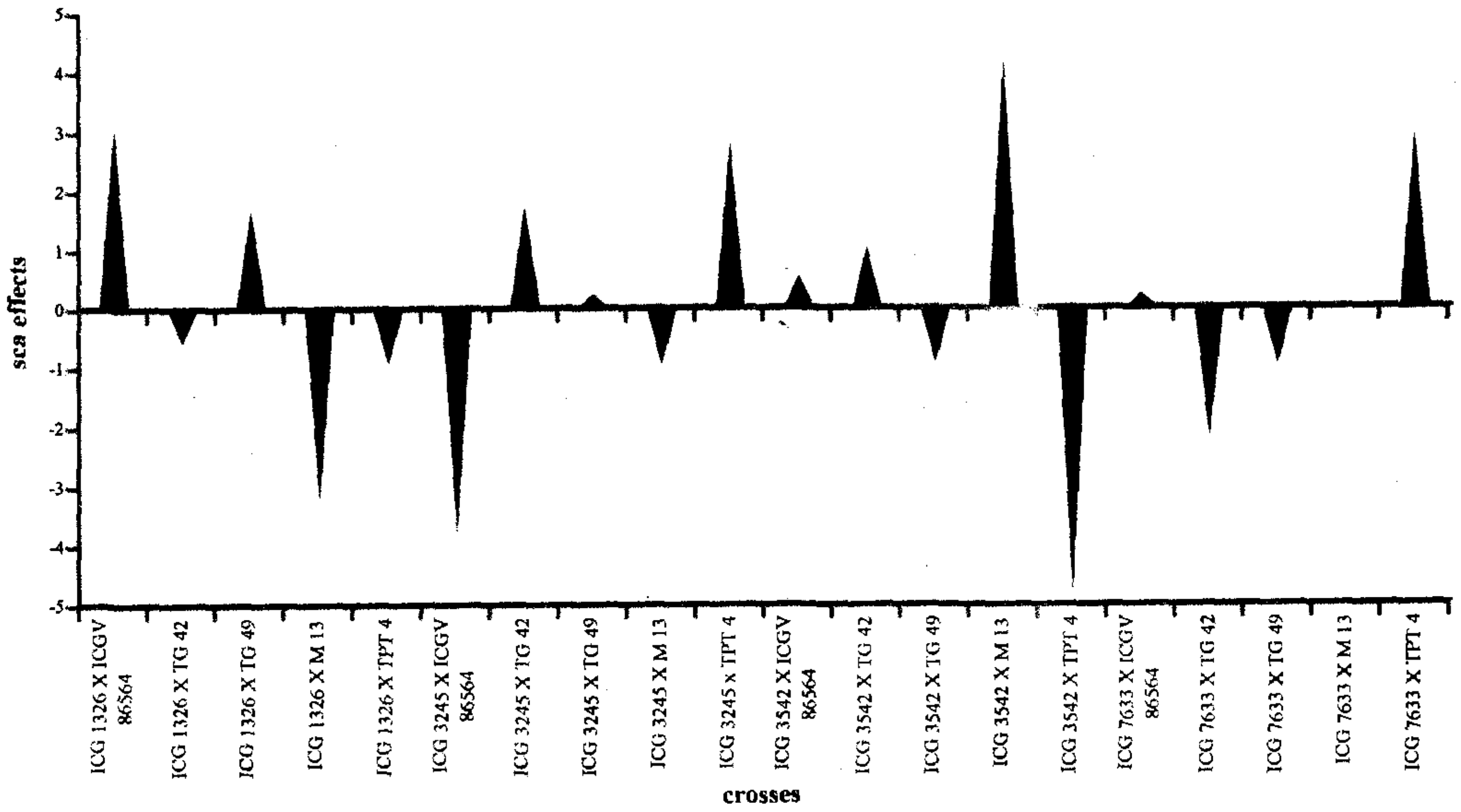


Fig.9: Specific combining ability (sca) effects of 20 F_1 crosses for kernel weight per plant



eight characters each. The former recorded high sca effects for shell volume, shelling percentage, mature pods per plant, protein content, reducing sugar content, non-reducing sugar content, CGR at 90 DAS, harvest index and kernel weight per plant. Where as in the latter cross, high sca effects were noticed in the characters; shell volume, shelling percentage, 100 seed weight, protein content, non-reducing sugar content, harvest index, aflatoxin content and kernel weight per plant. The other cross that had high sca effects for more than 50 % of characters (seven) was L_2 X T_5. It had significant sca effects for free space in pod, shelling percentage, mature pods per plant, 100 seed weight, reducing sugar content, harvest index and kernel weight per plant.

Hence, from the above discussion, it could be concluded that the crosses, L_1 X T_1 (ICG 1326 X ICGV 86564), L_3 X T_4 (ICG 3542 X M 13), L_4 X T_5 (ICG 7633 X TPT 4) and L_2 X T_5 (ICG 3245 X TPT 4) were considered as good specific combiners for majority of the characters.

5.4.4.4 *Heterosis*

Manifestation of heterosis, which depends on directional dominance, must invariably result in favorable direction for crop improvement. Shull (1948) emphasized the importance of heterosis to result always in desired direction for economic gains but should not be negative and said that reporting of negative heterosis should be avoided. Hence, the desired direction of a trait should be defined before hand. Accordingly, negative direction was followed for the characters; shell volume, free space in pod and aflatoxin content and positive direction for rest of the characters.

Among the three types of heterosis, relative heterosis is of limited importance since it is only the deviation of F_1 from mid- parental value (Grakh and Chaudhary, 1985).

Table 40: Crosses chosen for heterosis breeding

S. No	Characters	Mean	sca effects	Standard heterosis/Heterobeltiosis	Combination of three criteria
1	Shell volume	$L_1 X T_1, L_1 X T_2, L_1 X T_3, L_1 X T_4, L_1 X T_5, L_2 X T_1, L_2 X T_2, L_2 X T_3, L_2 X T_5, L_3 X T_1, L_3 X T_2, L_3 X T_3, L_3 X T_4, L_3 X T_5, L_4 X T_4, L_4 X T_5$	$L_1 X T_5, L_2 X T_1, L_2 X T_2, L_3 X T_3, L_3 X T_4, L_3 X T_1, L_4 X T_4, L_4 X T_5$	$L_1 X T_1, L_1 X T_2, L_1 X T_4, L_1 X T_5, L_2 X T_1, L_2 X T_2, L_2 X T_5, L_3 X T_1, L_3 X T_2, L_3 X T_3, L_3 X T_4, L_3 X T_5, L_4 X T_5$	$L_1 X T_5, L_2 X T_1, L_2 X T_2, L_3 X T_3, L_3 X T_4, L_4 X T_5$
2	Pod volume	$L_1 X T_1, L_1 X T_2, L_2 X T_3, L_2 X T_4, L_3 X T_5, L_4 X T_1, L_4 X T_2, L_4 X T_3, L_4 X T_4, L_4 X T_5$	$L_1 X T_1, L_1 X T_2, L_2 X T_3, L_2 X T_4, L_3 X T_5, L_4 X T_1, L_4 X T_2, L_4 X T_3$	$L_1 X T_1, L_4 X T_1, L_4 X T_2, L_4 X T_3$	$L_1 X T_1, L_4 X T_1, L_4 X T_2, L_4 X T_3$
3	Free space in pod	$L_1 X T_1, L_1 X T_3, L_1 X T_4, L_2 X T_4, L_2 X T_5, L_3 X T_1, L_3 X T_2, L_4 X T_1, L_4 X T_4$	$L_1 X T_3, L_1 X T_4, L_2 X T_4, L_2 X T_5, L_3 X T_1, L_3 X T_2, L_3 X T_5, L_4 X T_1, L_4 X T_4$	$L_1 X T_3, L_1 X T_4, L_2 X T_4, L_2 X T_5, L_3 X T_2, L_4 X T_4$	$L_1 X T_3, L_1 X T_4, L_2 X T_4, L_2 X T_5, L_3 X T_2, L_4 X T_4$
4	Shelling percentage	$L_1 X T_1, L_1 X T_3, L_2 X T_3, L_2 X T_4, L_2 X T_5, L_3 X T_4, L_4 X T_1, L_4 X T_5$	$L_1 X T_1, L_1 X T_3, L_2 X T_4, L_2 X T_5, L_3 X T_4, L_4 X T_1, L_4 X T_2, L_4 X T_5$	$L_1 X T_1, L_1 X T_2, L_1 X T_3, L_1 X T_4, L_1 X T_5, L_2 X T_1, L_2 X T_2, L_2 X T_3, L_2 X T_4, L_2 X T_5, L_3 X T_1, L_3 X T_3, L_3 X T_4, L_3 X T_5, L_4 X T_1, L_4 X T_2, L_4 X T_4, L_4 X T_5$	$L_1 X T_1, L_1 X T_3, L_2 X T_4, L_2 X T_5, L_3 X T_4, L_4 X T_1, L_4 X T_5$
5	Mature pods per plant	$L_1 X T_1, L_1 X T_4, L_1 X T_5, L_3 X T_2, L_3 X T_4, L_4 X T_4$	$L_1 X T_1, L_2 X T_3, L_2 X T_5, L_3 X T_2, L_3 X T_4, L_4 X T_3, L_4 X T_4$	$L_1 X T_1, L_1 X T_2, L_1 X T_3, L_1 X T_4, L_1 X T_5, L_2 X T_3, L_2 X T_4, L_2 X T_5, L_3 X T_1, L_3 X T_2, L_3 X T_3, L_3 X T_4, L_3 X T_5, L_4 X T_1, L_4 X T_3, L_4 X T_4, L_4 X T_5$	$L_1 X T_1, L_3 X T_2, L_3 X T_4, L_4 X T_4$
6	100 seed weight	$L_1 X T_2, L_1 X T_4, L_2 X T_1, L_2 X T_4, L_2 X T_5, L_3 X T_1, L_4 X T_4, L_4 X T_5$	$L_1 X T_2, L_2 X T_4, L_2 X T_5, L_3 X T_1, L_3 X T_3, L_4 X T_3, L_4 X T_5$	-	-
7	Protein content	$L_1 X T_1, L_1 X T_3, L_1 X T_5, L_2 X T_4, L_3 X T_1, L_3 X T_3, L_3 X T_4, L_4 X T_4, L_4 X T_5$	$L_1 X T_1, L_1 X T_3, L_2 X T_2, L_2 X T_3, L_2 X T_4, L_3 X T_1, L_3 X T_2, L_3 X T_3, L_3 X T_4, L_4 X T_4, L_4 X T_5$	$L_1 X T_1, L_1 X T_3, L_1 X T_5, L_3 X T_1, L_3 X T_3, L_3 X T_4, L_4 X T_4, L_4 X T_5$	$L_1 X T_1, L_1 X T_3, L_3 X T_1, L_3 X T_3, L_3 X T_4, L_4 X T_4, L_4 X T_5$
8	Reducing sugar content	$L_1 X T_1, L_1 X T_3, L_3 X T_1, L_3 X T_4, L_4 X T_2, L_4 X T_3$	$L_1 X T_1, L_2 X T_3, L_2 X T_5, L_3 X T_1, L_3 X T_4, L_4 X T_2$	$L_1 X T_1, L_1 X T_2, L_1 X T_3, L_1 X T_4, L_1 X T_5, L_2 X T_1, L_2 X T_2, L_2 X T_3, L_2 X T_4, L_2 X T_5, L_3 X T_1, L_3 X T_3, L_3 X T_4, L_3 X T_5, L_4 X T_1, L_4 X T_2, L_4 X T_3, L_4 X T_4, L_4 X T_5$	$L_1 X T_1, L_3 X T_1, L_3 X T_4, L_4 X T_2$

Table 40 (cont.)

S. No	Characters	Mean	sca effects	Standard heterosis/Heterobeltiosis	Combination of three criteria
9	Non-reducing sugar content	$L_1 X T_1$, $L_1 X T_2$, $L_3 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_1 X T_2$, $L_2 X T_1$, $L_2 X T_3$, $L_3 X T_3$, $L_3 X T_4$, $L_4 X T_5$	$L_1 X T_2$, $L_4 X T_5$	$L_1 X T_2$, $L_4 X T_5$
10	CGR at 60 DAS	$L_1 X T_1$, $L_1 X T_3$, $L_1 X T_4$, $L_2 X T_4$, $L_3 X T_3$, $L_3 X T_5$, $L_4 X T_1$, $L_4 X T_2$	$L_1 X T_1$, $L_1 X T_3$, $L_2 X T_2$, $L_2 X T_4$, $L_3 X T_3$, $L_3 X T_5$, $L_4 X T_1$, $L_4 X T_2$	$L_1 X T_1$, $L_2 X T_1$, $L_3 X T_1$, $L_4 X T_1$, $L_1 X T_2$, $L_2 X T_2$, $L_3 X T_2$, $L_4 X T_2$, $L_1 X T_3$, $L_2 X T_3$, $L_3 X T_3$, $L_4 X T_3$, $L_1 X T_4$, $L_2 X T_4$, $L_3 X T_4$, $L_4 X T_4$, $L_1 X T_5$, $L_2 X T_5$, $L_3 X T_5$, $L_4 X T_5$	$L_1 X T1$, $L_1 X T_3$, $L_2 X T_4$, $L_3 X T_3$, $L_3 X T_5$, $L_4 X T_1$, $L_4 X T_2$
11	CGR at 90 DAS	$L_1 X T_1$, $L_1 X T_3$, $L_2 X T_1$, $L_3 X T_2$, $L_3 X T_5$, $L_4 X T_1$, $L_4 X T_3$	$L_1 X T_2$, $L_1 X T_3$, $L_1 X T_4$, $L_2 X T_1$, $L_3 X T_2$, $L_3 X T_4$, $L_3 X T_5$, $L_4 X T_1$, $L_4 X T_3$	$L_2 X T_1$, $L_4 X T_1$, $L_4 X T_3$	$L_2 X T_1$, $L_4 X T_1$, $L_4 X T_3$
12	Harvest index	$L_1 X T_1$, $L_2 X T_2$, $L_2 X T_3$, $L_2 X T_5$, $L_3 X T_1$, $L_3 X T_2$, $L_3 X T_4$, $L_4 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_2 X T_2$, $L_2 X T_3$, $L_2 X T_5$, $L_3 X T_1$, $L_3 X T_2$, $L_3 X T_4$, $L_4 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_1 X T_4$, $L_2 X T_2$, $L_2 X T_3$, $L_2 X T_4$, $L_2 X T_5$, $L_3 X T_1$, $L_3 X T_2$, $L_3 X T_4$, $L_4 X T_1$, $L_4 X T_2$, $L_4 X T_3$, $L_4 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_2 X T_2$, $L_2 X T_3$, $L_2 X T_5$, $L_3 X T_1$, $L_3 X T_2$, $L_3 X T_4$, $L_4 X T_4$, $L_4 X T_5$
13	Aflatoxin content*	$L_1 X T_1$, $L_2 X T_4$, $L_2 X T_5$, $L_4 X T_5$	$L_1 X T_1$, $L_2 X T_3$, $L_4 X T_2$, $L_4 X T_5$	$L_1 X T_1$, $L_1 X T_4$, $L_2 X T_1$, $L_2 X T_4$, $L_3 X T_1$, $L_3 X T_2$, $L_3 X T_3$, $L_3 X T_4$, $L_3 X T_5$, $L_4 X T_1$, $L_4 X T_2$, $L_4 X T_4$, $L_4 X T_5$	$L_4 X T_1$, $L_4 X T_5$
14	Kernel weight/plant	$L_1 X T_1$, $L_2 X T_5$, $L_3 X T_1$, $L_3 X T_4$, $L_4 X T_1$, $L_4 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_1 X T_3$, $L_2 X T_2$, $L_2 X T_5$, $L_3 X T_2$, $L_3 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_1 X T_3$, $L_1 X T_4$, $L_1 X T_5$, $L_2 X T_1$, $L_2 X T_2$, $L_2 X T_3$, $L_2 X T_4$, $L_2 X T_5$, $L_3 X T_1$, $L_3 X T_2$, $L_3 X T_3$, $L_3 X T_4$, $L_3 X T_5$, $L_4 X T_1$, $L_4 X T_2$, $L_4 X T_3$, $L_4 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_2 X T_5$, $L_3 X T_4$, $L_4 X T_5$
	OVER ALL	$L_1 X T_1$, $L_1 X T_3$, $L_2 X T_4$, $L_2 X T_5$, $L_3 X T_1$, $L_3 X T_4$, $L_4 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_2 X T_5$, $L_3 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_1 X T_3$, $L_1 X T_4$, $L_1 X T_5$, $L_2 X T_1$, $L_2 X T_4$, $L_2 X T_5$, $L_3 X T_1$, $L_3 X T_2$, $L_3 X T_3$, $L_3 X T_4$, $L_3 X T_5$, $L_4 X T_1$, $L_4 X T_2$, $L_4 X T_3$, $L_4 X T_4$, $L_4 X T_5$	$L_1 X T_1$, $L_3 X T_4$, $L_4 X T_5$

* Heterobeltiosis instead of standard heterosis was furnished.

Fig.10: Relative heterosis (di), heterobeltiosis (dii) and standard heterosis (diii) of 20 F_1 crosses for aflatoxin content

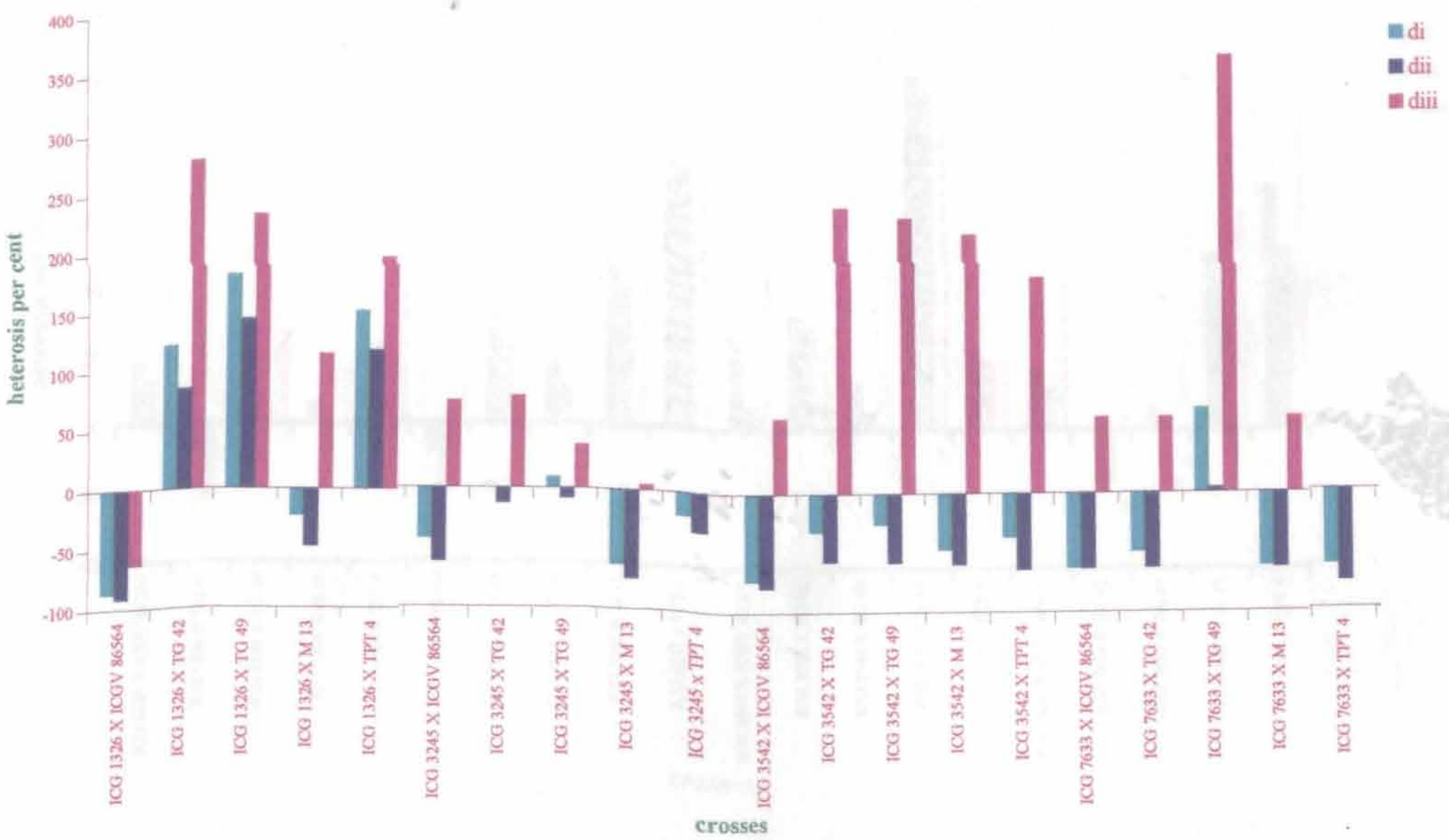
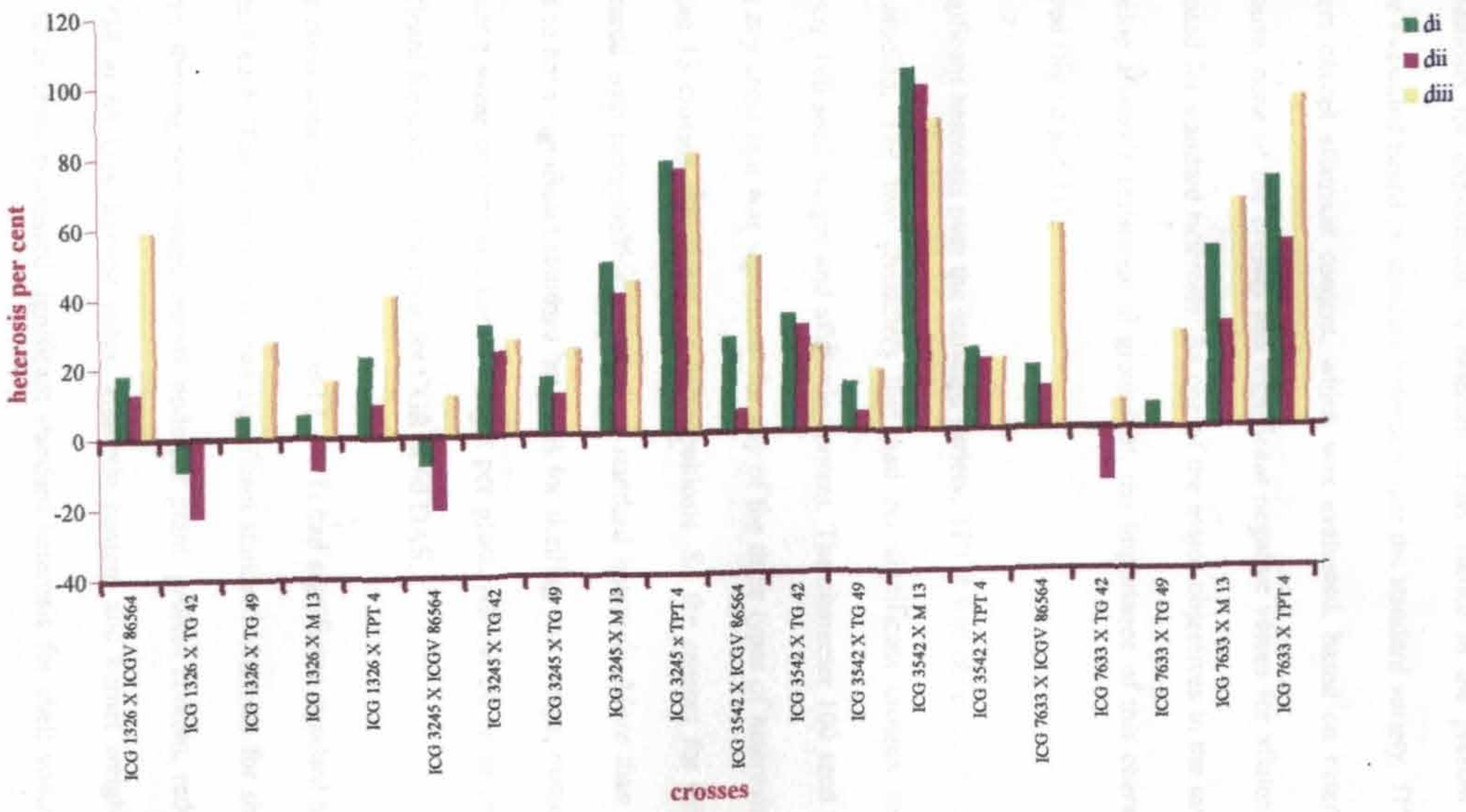


Fig.11: Relative heterosis (di), heterobeltiosis (dii) and standard heterosis (diii) of 20 F$_1$ crosses for kernel weight/plant



Further, the need of computing standard heterosis for commercial exploitation of hybrid vigour has been stressed by Swaminathan *et al.* (1972), Kadambavanasundaram (1983) and Siddiq (1987). Where as, Bhandari (1978) insisted the importance of standard heterosis and heterobeltiosis for exploitation of heterotic cross. Hence in the present study the crosses were evaluated based on standard heterosis over the standard variety, TPT 4 for all the characters except aflatoxin content, which was evaluated, based on heterobeltiosis. This is because, none of the crosses had significant negative values for aflatoxin content when evaluated for standard heterosis. As one of the major objectives in the investigation was to develop aflatoxin resistance in groundnut, the importance of this character could not be ignored (fig.10 and 11).

Significant heterosis over the standard variety, TPT 4 was observed in 12 out of 14 characters studied. The two characters that had no significant crosses for standard heterosis were 100 seed weight and aflatoxin content. The character 100 seed weight did not possess any cross that was significant for any of the three types of heterosis. However aflatoxin had 13 crosses significant for heterobeltiosis. So the crosses for this character were compared with heterobeltiosis instead of standard heterosis. More than 17 crosses were found to have significant standard heterosis for shelling percentage, mature pods per plant, reducing sugar content and kernel weight per plant. All the 20 cross combinations were significant for standard heterosis for CGR at 60 DAS.

The cross combinations L_1 X T_1 and L_4 X T_5 had significant standard heterosis for ten characters each. The former cross had significant standard heterosis for shell volume, pod volume, shelling percentage, mature pods per plant, protein content, reducing sugar content, CGR at 60 Das, harvest index, aflatoxin content and kernel weight per plant. While the latter cross possessed significant standard heterosis for shell volume, shelling percentage, mature pods per plant, protein content, reducing sugar content, non-reducing sugar content, harvest index, aflatoxin content and kernel weight per plant. All the crosses except; L_1 X T_2, L_2 X T_2 and L_2 X T_3 recorded significant heterotic values for more than 50 % of the characters (more than six).

High positive (Siva Kumar, 1984) and mid parental (Garet, 1976) heterosis were reported for shelling percentage. Bansal *et al.* (1993) recorded postive and significant heterosis for mature pods. High average heterosis (Jayalakshmi, 1997) and high heterobeltiosis for mature pods were also reported. For 100 seed weight positive (Sridharan and Marappan, 1980 and Siva Kumar, 1984) heterosis were reported. Where as, Senthil and Vindhiya Varman (1998) recorded high mid parental heterosis for 100 seed weight. Prasad (1996) observed high heterosis for protein content. Where as, low mid parental heterosis was recorded by Parmar *et al.* (2001) for protein content. Reports of both positive (Nisar Ahmed, 1995) and negative (Swe and Branch, 1986) heterosis for harvest index were observed. Most of the earlier reports indicated high positive heterosis for kernel yield (Wynne *et al.*, 1970; Reddi *et al.*, 1989; Vanisree, 1992) in groundnut, which also included reports on average heterosis (Jayalakshmi, 1997) and heterobeltiosis (Senthil and Vindhiya Varman, 1998).

Combining standard heterosis for majority of the traits with heterobeltiosis for aflatoxin content, L_1 X T_1 (ICG 1326 X ICGV 86564) and L_4 X T_5 (ICG 7633 X TPT 4) were observed to be the best heterotic crosses.

5.5.4.5 *Evaluation of crosses for exploiting hybrid vigour*

Instead of analyzing the crosses and interpreting individually, the classification of crosses based on mean, sca and heterosis for all the characters would reward perfect estimates to draw sound conclusions. The crosses with desirable mean, sca effects and heterosis percentage (standard heterosis/heterobeltiosis) were presented in table 40. Based

Table 41 : Significance of three types of heterosis (di,dii and diii) for 20 F_1 crosses in groundnut

Crosses	Shell volume	Pod volume	Free space in pod	Shelling %	Mature pods per plant	100 seed weight.	Protein content	Reducing sugar content	Non-reducing sugar content	CGR at 60 DAS	CGR at 90 DAS	Harvest index	Aflatoxin content	Kernel weight per plant	Overall
$L_1 X T_1$	*			*	*		*	*		*		*		*	8
$L_1 X T_2$	*		*						*						3
$L_1 X T_3$			*	*			*	*		*					5
$L_1 X T_4$	*		*							*		*			4
$L_1 X T_5$	*						*	*						*	4
$L_2 X T_1$	*							*			*				3
$L_2 X T_2$	*									*				*	3
$L_2 X T_3$					*			*						*	3
$L_2 X T_4$			*	*						*				*	4
$L_2 X T_5$					*			*		*		*		*	6
$L_3 X T_1$	*				*			*				*		*	5
$L_3 X T_2$	*				*									*	4
$L_3 X T_3$	*				*		*	*		*					5
$L_3 X T_4$	*		*	*	*			*				*		*	6
$L_3 X T_5$	*				*					*				*	4
$L_4 X T_1$			*	*	*			*		*	*			*	6
$L_4 X T_2$								*		*					2
$L_4 X T_3$					*			*		*	*				4
$L_4 X T_4$			*	*	*		*			*		*		*	7
$L_4 X T_5$	*		*	*	*		*	*	*	*				*	8
Overall	12	0	7	7	12	0	6	13	2	13	3	6	0	13	

Fig.12: Comparison of F_1 crosses with corresponding parents for aflatoxin content

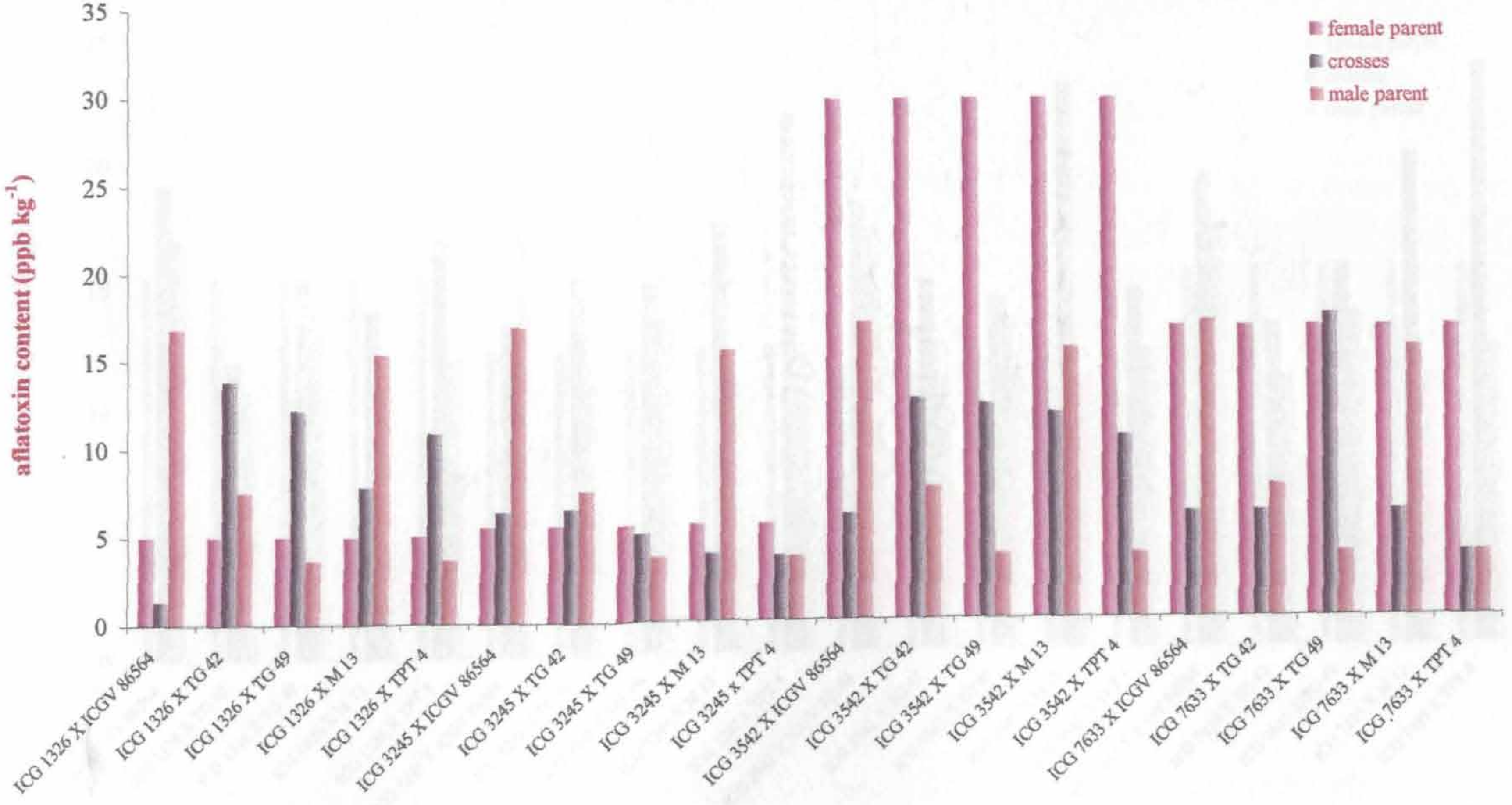
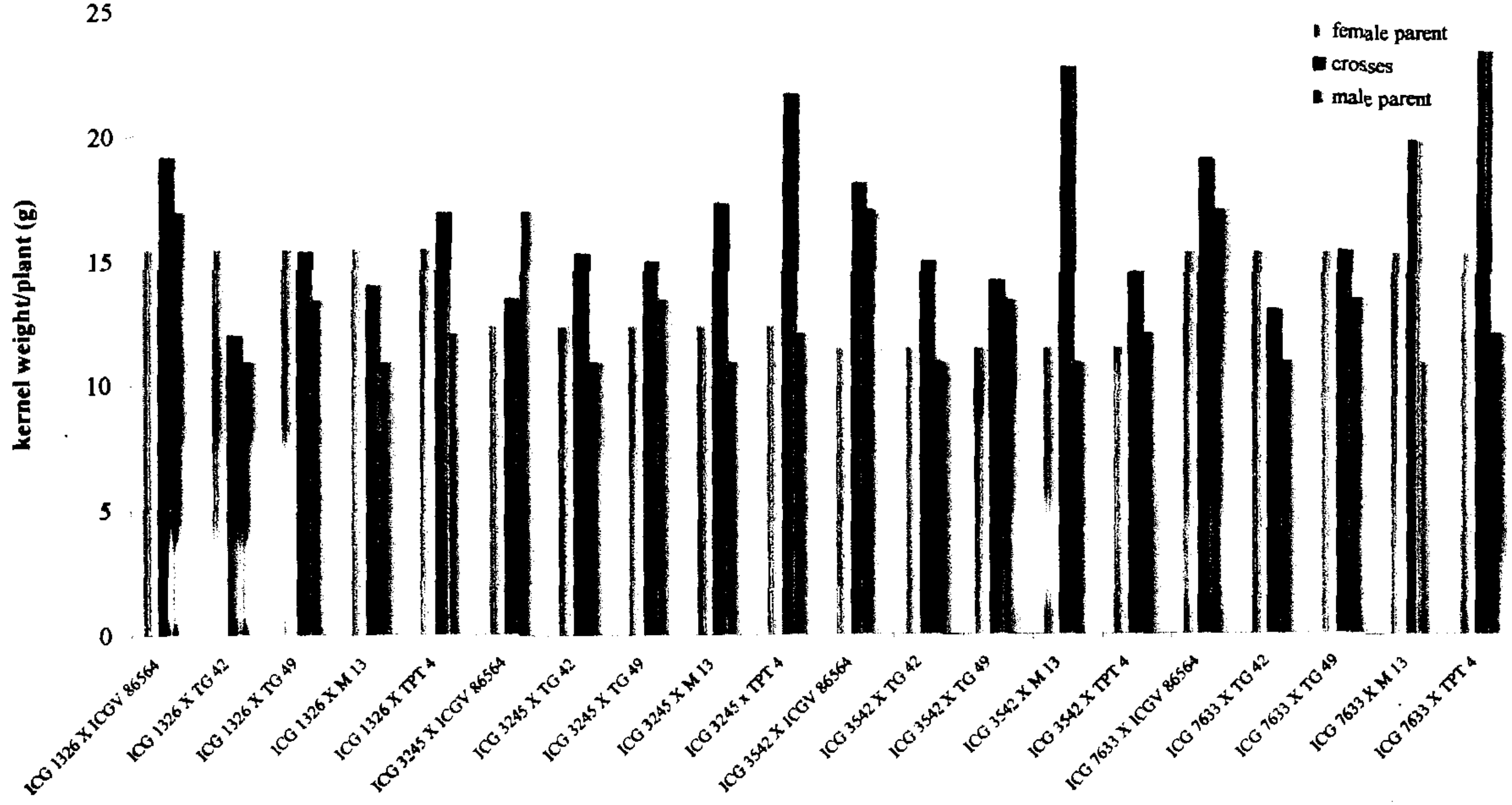


Fig.13: Comparison of F_1 crosses with corresponding parents for kernel weight/plant



ICG 1326 | ICG 1326 X ICGV 86564 | ICGV 86564

Plate 8: F_1 crosses suitable for high kernel yield with aflatoxin resistance by exploiting hybrid vigour

Plate 8 (cont.)

ICG 7633

ICG 7633 X TPT 4

TPT 4

on these three selection criteria, the crosses L_1 X T_1 (ICG 1326 X ICGV 86564), L_3 X T_4 (ICG 3245 X M 13) and L_4 X T_5 (ICG 7633 X TPT 4) were found to be suitable for heterosis breeding since they expressed high values for more than 50 % of the characters, viz., pod volume, shelling percentage, mature pods per plant, protein content, reducing sugar content, CGR at 60 DAS, CGR at 90 DAS, harvest index, aflatoxin content and kernel weight per plant. The other crosses L_3 X T_4 and L_4 X T_5 expressed significance at the three levels for seven characters each. The common characters for which they were significant were; shell volume, shelling percentage, protein content, harvest index and kernel weight per plant.

The cross combinations, L_1 X T_1 (ICG 1326 X ICGV 86564), and L_4 X T_5 (ICG 7633 X TPT 4) have shown significance for aflatoxin content and kernel weight at all the three selection criteria (plate 8) (fig. 12 and 13). When the three types of heterosis were considered together (table 41), the same combinations proved to be the best for eight characters each. Further more, their parental gca effects were highly significant for more than 50 % of the characters which means that these crosses possess double advantage and can be cultivated either as commercial F_1 hybrids or can be persuaded to develop recombinant genotypes through transgressive segregation. As groundnut being a self pollinated crop and commercial feasibility of F_1 hybrid is of remote possibility, transgressive segregants can be developed into out standing genotypes with high yield coupled with aflatoxin resistance by adopting simple breeding methods like pedigree method and selecting both in early as well as in advanced stages of segregation to exploit both additive and non-additive gene effects.

HIGHLIGHTS:

- A comprehensive evaluation of the 54 genotypes for morphological and biochemical characters related to quality indicated that the genotypes, TPT 4, M 13 and ICGV 86564 can be straight away recommended for cultivation for their higher yield and quality.
- The study could not elucidate common varieties for yield, quality and drought tolerance. However, ICGV 86552 can be grown successfully in environments characterized with end-of-season moisture stress.
- *Aspergillus flavus* seemed to prefer carbohydrates to protein and oil in producing aflatoxin in the seed.
- Large poded varieties not only produced high kernel weight per plant but also possessed higher quantities of carbohydrates relative to protein.
- As higher test weight is negatively associated with aflatoxin content it gives a scope to produce large seeded varieties having low aflatoxin from the material studied.
- More number of mature pods were produced in small seeded genotypes rather than in large seeded genotypes.
- Compact filling (high shelling percentage, and low free space in pod) was not favoured by the pathogen to produce aflatoxin. Selection for the character may reduce the aflatoxin risk in groundnut.
- Protein content exhibited an increasing tendency with oil content but it was at the cost of carbohydrate accumulation in the seed.
- Increase in crop growth rate despite acute moisture stress during pod filling stage has a direct bearing on enhanced pod and kernel yields.
- SCMR, a potential physiological character can be employed as a surrogate for transpiration efficiency.
- A selection criteria with shell volume, pod volume, free space in pod, shelling percentage, 100 seed weight, mature pods per plant, CGR at 60 and at 90 DAS, harvest index, protein content, reducing sugar content, non-reducing content may be formulated for selecting high yielding aflatoxin resistant genotypes.
- The genotype ICGV 86564 expressed significant gca for both aflatoxin content and kernel weight.

- When *perse* performance, sca and heterosis were considered together the crosses, ICG 1326 X ICGV 86564 and ICG 7633 X TPT 4 emerged as the best combinations for persuasion and selection for transgressive segregants.

FUTURE LINE OF WORK:

- The relationship of pod moisture at harvest and shell thickness with aflatoxin resistance may be worked out as they gave some indications in the present study.
- The negative association of aflatoxin content with total protein and oil contents may be further analysed for their components, which may enable to alter the composition of amino acids and fatty acids for developing resistance to aflatoxin at cotyledonary stage.
- Although some of the physiological characters like SLA and SLW in early stage and LAI at later stage of plant growth expressed positive association with aflatoxin resistance, the possible reasons require a deeper probe and analysis.
- The insignificant relationship between seed colonization and aflatoxin production observed not only in the present study but also in the literature surveyed might be due to the difference in seed sampling methods. To overcome this difficulty, seeds may be powdered and the same powder may be used for both the screening techniques.
- Inclusion of ICG 11386 with high score and ICGV 86552 with physiological efficiency in the crossing programme may throw some useful segregants for drought tolerance.
- The crosses, ICG 1326 X ICGV 86564 and ICG 7633 X TPT 4, identified for high yield and aflatoxin resistance may be persuaded to develop varieties to solve the problem envisaged in the present investigation which may in turn boost groundnut exports.

CHAPTER VI

SUMMARY

CHAPTER VI

SUMMARY

Groundnut is grown primarily for edible oil in developing countries and for edible protein, in the form of value added products, in developed nations. The crop is grown in an area of 26.46 m.ha. world wide with an estimated total production of 35.65 m.t. and an average productivity of 1.35 t ha^{-1} (FAO, 2003). Developing countries contribute about 60 % to the total world groundnut production. In India it is cultivated in 8 m.ha. with a total production of 7.5 m.t. and productivity of 0.94 t ha^{-1} (FAO, 2003). Besides low productivity, which ranges from 0.7 to 0.8 t ha^{-1} in these regions, drought particularly the one which occurs at the end of season, predisposes the crop with invasion by the aflatoxin producing fungus, *Aspergillus flavus*, which impairs the quality of the produce, though not yield. The marketability of the produce coming from these areas where aflatoxin management practices are difficult to adopt is not possible in the international market due to stringent standards of permissible limits on aflatoxin contamination set by the importing countries. Enhancement of yield and quality levels in groundnut assumes importance in the changed global trading system with the advent of WTO regime.

Aspergillus flavus can invade groundnut seed in the field before harvest, during post harvest drying and curing, and in storage and transportation. Therefore the right strategy is the development of resistance to pre harvest infection by the pathogen at the entry stage itself by developing resistant lines. Development of groundnut varieties with resistance to pre harvest infection and aflatoxin contamination requires a reliable screening technique to estimate genetic variance for resistance. The theory that cereal based inoculum would serve as a carrier for the fungus and result in more stable pathogen load in the pod zone, and that water deficit during pod development was conducive for the fungus to infect the pods, was utilized in the present study to screen the 54 groundnut genotypes for aflatoxin resistance. The drought that prevailed during end of season in the two years of experimentation was utilized to impose moisture stress by with holding irrigations for 20 days. In the first year (*kharif*, 2002) of experimentation 54 genotypes were evaluated for 31 morphological, biochemical and physiological characters along with aflatoxin resistance to select parents. While in the second year (*kharif*, 2003), 20 F_1 crosses obtained by mating the selected nine parents in L X T fashion were evaluated for 14 selected characters. The study did not depend on screening the genotypes for resistance to seed colonization as it did not establish significant correlation (-0.0322) with aflatoxin content, the ultimate concern.

The 54 genotypes were evaluated during *kharif*, 2002 for 10 morphological and biochemical characters related to quality. For morphological characters like high kernel yield, high shelling percentage, high 100 seed weight, desirable testa colour and elongated shape, TPT 4 along with ICGV 86564, TG 40, M 13 and ICG 7633 were adjudged as the best genotypes. Whereas, TPT 4 along with TCGS 584, ICG 1326 and ICG 3643 were identified as superior genotypes for biochemical characters like low aflatoxin content, low oil percentage, high protein and high non-reducing sugar content. Though combination of kernel yield with quality was difficult to find, in view of the relative desirability of quality characters vis-à-vis kernel yield the genotypes; TPT 4, M 13 and ICG 86564 were identified as the best genotypes suitable for cultivation and trading as HPS varieties.

The performance of the genotypes for their physiological efficiency was observed for end-of-season soil moisture stress. Data recorded at 90 DAS on most of the physiological characters made it possible to screen the genotypes for terminal drought. TPT 4 was the only genotype that showed significant and consistent performance over general mean during entire crop growth period for specific leaf area. TPT 4, ICG 8325 and

ICG 10352 maintained steady increase in leaf area at 30, 60 and 90 DAS. The genotypes, ICGV 86031 and ICGV 88448 recorded significant values for SLW and exhibited increasing trend in all the three stages of crop growth. Two genotypes, ICGS 21 and TCGS 91 showing higher values for CGR at 60 and 90 DAS might be utilized in improving CGR in groundnut. The genotypes, TCGS 634 and ICGV 86552 were adjudged as the best genotypes that maintained photosynthesizing surface even during water deficits as indicated by high LAI. ICGV 86552 recorded significant values not only for LAR at 90 DAS but also for all the growth parameters at one or the other stage. ICGV 86031 was found to be the best for SCMR at 30 DAS while TG 40, TG 42 and TG 49 for harvest index. Based on the mean values of physiological characters, ICGV 86552 was identified as the most efficient genotype as it recorded significant values during stress (at 90 DAS) for most of the growth parameters.

Association analysis of 28 morphological, biochemical and physiological characters with aflatoxin and kernel weight provided information on these characters to identify indirect selection tools for improving yield and quality in groundnut. They might also be used to surrogate the costly selection procedure for low aflatoxin contamination. Correlation studies of morphological and biochemical characters revealed that the characters in order of strong and positive correlation with kernel weight per plant were pod volume, mature pods per plant, immature pods per plant, 100 seed weight, free space in pod, seed moisture percentage, carbohydrate and non-reducing sugar contents. Kernel weight exhibited high negative correlation with protein content. The rest of the associations were negligible. The correlation of shell volume and pod volume with other characters indicated that large seeded varieties not only produced high kernel weight having high test weight but also possess higher quantities of carbohydrates. Mature pods per plant was the most important character that can be indirectly selected to improve kernel weight. It was indicated in the correlation studies that more the number of pods ere mature, more was the accumulation of carbohydrate and its components (reducing and non-reducing sugar contents) and that mature pods were produced more in small eeded varieties rather than in large seeded varieties. The relationship of mature pods with arbohydrate content and immature pods with oil percentage indicated that oil percentage declined after maturity with a corresponding increase in carbohydrate content and its omponents. While oil percentage expressed negative association with carbohydrate, its association with protein content was positive and strong. It indicated that protein content exhibited an increasing tendency with oil percentage but it was at the cost of carbohydrate accumulation. The negative correlation between protein and kernel weight might be implicated to be a function of the fact that an increase in kernel weight was associated with a disproportionately large deposition of carbohydrates relative to protein. The difficulty in simultaneous selection for both high yield and protein content might be solved by making selection initially for high yield and later in the selected families, plants having the highest percentage of protein should be identified for further selection and inter mating.

The order of importance as indicated by direct effects of characters on kernel weight was for mature pods per plant, shelling percentage, shell volume, free space and 100 seed weight. Selection in positive direction for these characters and against oil percentage might be perceived to improve kernel weight per plant.

Aflatoxin content exhibited negative and strong correlation with shelling percentage, protein content, oil percentage and strong positive correlation with shell volume and pod volume and carbohydrate content and non-significant correlation with reducing and non-reducing sugar contents. The positive inter correlation between protein content and oil percentage and their negative inter correlation with carbohydrate content might have led to the negative association of aflatoxin content with protein content and oil.

The fungus might have preferred carbohydrate to protein and oil percentage in producing aflatoxin in seeds. Positive correlation with shell and pod volume indicated that aflatoxin was produced more in large seeded varieties.

When these correlations were partitioned by genotypic path into direct and indirect effects on aflatoxin content, shell volume followed by free space in pod and mature pods per plant exhibited very high direct positive effects on aflatoxin content. Whereas pod volume, shelling percentage and 100 seed weight recorded high negative direct effects. The character free space in pod recorded high positive direct effect on aflatoxin content. Losing pod moisture during drying process creates free space in pod. Because the pods were shade dried, and as the moisture in pods might have served as a medium for the pathogen to find access to the seed and produced aflatoxin. The high positive indirect effects through shell volume, along with low positive indirect effects through carbohydrate content might have collectively aided free space in pod in establishing high positive direct effect on aflatoxin content. The idea of compact seed filling is related to low aflatoxin content was brooded from the fact that shelling percentage not only registered strong negative correlation but also recorded high negative direct effect on aflatoxin content. Mature pods per plant rather than immature pods recorded positive direct effect on aflatoxin content. Over mature pods seemed to have attracted the pathogen. The positive correlation of pod volume with aflatoxin content when further analyzed to understand the cause and effect relationship showed that the moderate negative indirect effects expressed through 100 seed weight which exhibited high negative direct effect on aflatoxin content nullified the positive correlation of pod volume on aflatoxin content. This gives a scope to produce large seeded varieties having low aflatoxin content. The indications that SLA and SLW in the early and LAI in the later stage of plant growth were related to low aflatoxin require further probe to draw a meaningful conclusion.

An examination of the correlation coefficient between physiological characters and kernel weight revealed that LAI at 90 DAS, LAR at 90 DAS, harvest index, SLA at 90 DAS, CGR at 90 DAS in that order including pod weight per plant were positively and strongly associated with kernel weight plant. However SLW at 90 DAS expressed negative association. The crop experienced moisture stress at 90 DAS. Hence, the significance of most of the growth parameters at 90 DAS was observed. SLA and SLW at 60 DAS was found to be more important than at 30 or 90 DAS as indicated by their high positive direct effects on kernel weight per plant. Crop growth rate before the stress (at 60 DAS) and during stress (at 90 DAS) did not change their direct effects on kernel weight per plant. LAR at 90 DAS also established very high positive direct effect on kernel weight per plant. On the other hand LAI at 90 DAS exhibited very high negative indirect effect. SCMR at 30 DAS did not show any association with kernel weight per plant. Its association with SLA was negative and with SLW was positive. This relationship indicated that SCMR was potential physiological trait to employ as a surrogate for transpiration efficiency. Pod weight showed both positive correlation and high positive direct effect on kernel weight per plant.

Mere inclusion of these characters based on association analysis will not suffice but the existence of transferable genetic variability is required for characters' improvement. Among the morphological characters high PCV and GCV were present for shell volume, pod volume, free space in pod and immature pods per plant. Where as, mature pods per plant, 100 seed weight and kernel weight per plant showed moderate estimates for PCV and GCV. This indicated the existence of variability in the material studied for these characters and the scope of their exploitation. However, low estimates of GCV and PCV for shelling percentage indicated the limitations in the scope of improvement made for this character. High estimates for both heritability and GAM for shell volume, pod volume, free space in pod, immature pods per plant, 100 seed weight and high heritability and moderate GAM for mature pods and kernel weight per plant revealed that all these characters were most likely influenced by additive gene action. High heritability and low GAM for shelling percentage indicated the presence of non-additive gene action and simple selection to improve these characters might not be possible.

The magnitude of GCV and PCV were high for the biochemical characters viz., reducing sugar content, non-reducing content and aflatoxin content which indicated ample scope for improvement. Whereas, the variation as indicated by GCV and PCV values for oil percentage, protein and carbohydrate contents was low and the response to selection for these characters would be less. High heritability and GAM for reducing sugar content, non-reducing content and aflatoxin content indicated the preponderance of additive gene action and simple selection procedures would be effective in the improvement of these characters.

Moderate to high variability as indicated by GCV and PCV was observed for all the physiological characters except for SLA at 90 DAS, SLW at 90 DAS and SCMR at 30 DAS. Whereas, SLA at 90 DAS and SLW at 90 DAS recorded low GCV and moderate PCV indicating low genetic variability. Low values of GCV and PCV for SCMR at 30 DAS revealed low magnitude of variability. High heritability was recorded for all the characters excepting those two characters (SLA at 90 DAS and SLW at 90 DAS), which showed less variability. High heritability coupled with high GAM for the characters; CGR at 60 and at 90 DAS indicated the involvement of additive genes in the expression of these characters and simple selection would be rewarding for improvement of these characters. Whereas SLA at 90 DAS and SLW at 90 DAS recorded low heritability and GAM which indicated non-additive gene action and simple selection would not bring out improvement.

Due importance was given to the discrimination of characters based on their contribution to total diversity in divergence analysis. It was observed that pod volume, free space in pod, 100 seed weight among morphological characters, reducing sugar, aflatoxin and non-reducing sugar contents among biochemical characters and SLA at 30 DAS and at 60 DAS, CGR at 60 DAS and at 90 DAS, LAR at 90 DAS and SCMR at 30 DAS among physiological characters contributed more to diversity.

Based on all the biometrical analyses carried out so far, shell volume, pod volume, free space in pod, shelling percentage, 100 seed weight, mature pods per plant among morphological characters, CGR at 60 DAS, CGR at 90 DAS and harvest index among physiological characters and protein, reducing sugar and non-reducing sugar contents among biochemical characters were selected for further analysis. The 14 characters thus selected formed the basis of selection for developing high yielding aflatoxin resistant groundnut genotypes.

The information generated through genetic divergence analysis, carried out separately for two groups of characters; one group with morphological and biochemical characters and the other with physiological characters along with mean values for the 14 selected characters, was utilized for selecting parents for hybridization. The magnitude of D^2 values for both the groups of characters suggested that there was considerable diversity in the material studied. This range of variation allowed for grouping of 54 genotypes into 11 clusters for morphological and biochemical characters and into 17 clusters for physiological characters and substantiated maximum diversity for both the groups of characters. The formation of largest cluster I for morphological and biochemical characters comprising 33 genotypes and for physiological characters comprising 22 genotypes might be due to the free flow or exchange of breeding material from one place to another or /and the unidirectional selection practiced by breeders of different locations.

Constellation of genotypes into different cluster for all the characters was at random and independent of each other. When clustering pattern was related to geographical origin, no regular demarcation was discernible in the pattern of constellation of genotypes into various clusters.

Maximum inter cluster distance between cluster II and XI and maximum intra cluster distance in cluster, X, VI and I was observed for morphological and biochemical characters. Where as for physiological characters maximum inter cluster distance between cluster III and XV and between VI and XVII indicates greater diversity between these clusters. Cluster means for majority of morphological and biochemical characters in clusters, I, II, IV, V, VI and IX were higher than their overall means. Similarly higher cluster means for more physiological characters were observed in clusters I, II, V, VI, VII, VIII, IX, XI, XIV, XV, XVI and XVII. Major emphasis was made on cluster means and scores rather than cluster distances for selecting the best parents for crossing programme. Two genotypes from clusters; I and II and one each from clusters; IV, V, VI and IX were selected based on overall scoring for selected morphological and biochemical characters. While four genotypes from cluster I, three from II, and one each from VII and XI were selected based on the important physiological characters. A total of nine genotypes were selected from the divergence analysis. Five bold seeded genotypes (ICGV 86564, TG 42, TG 49, M 13 and TPT 4) were used as testers and the remaining four genotypes, ICG 1326, ICG 3245, ICG 3542 and ICG 7633 were used as lines and crossed in line x tester fashion to obtain 20 F_1 crosses during *rabi*, 2002.

The 20 F_1 crosses thus generated were evaluated along with their parents in a RBD design during *kharif*, 2003 to find out gene action and heterosis for 14 selected characters. The analysis of variance for combining ability revealed significant differences among parents and crosses thus justifying the selection of parents for the study. Relatively contribution of lines x testers interaction apportioned greater percentage of the total variation for majority of the characters.

Partitioning of combining ability variances into fixable additive genetic variance and non fixable dominance variances revealed that non additive genetic variance was higher in magnitude for majority of the characters indicating the preponderance of dominance gene action in controlling the expression of these traits. They were; shell volume, free space in pod, shelling percentage, mature pods per plant, 100 seed weight, protein content, reducing sugar content, non-reducing sugar content, CGR at 60 DAS, CGR at 90 DAS, harvest index and kernel weight per plant. Non-additive gene action for majority of the characters indicated that the improvement of these characters was possible through exploitation of heterosis breeding. But groundnut being a self-pollinated crop, heterosis breeding is not advisable due to the constraints involved in the synthesis of commercial hybrids. Therefore, to get better genotypes by way of recombination breeding, hybridization followed by selection in late generation was suggested for exploitation of dominance gene action. GCA variance was greater in proportion than SCA variance for the characters pod volume and aflatoxin content. As such, these traits can be improved by employing breeding methods, which exploit additive gene action.

Mean performance of parents indicated that the line, L_1 (ICG 1326), a small seeded genotype and the tester, T_3 (TG 49) bold seeded genotype expressed significance for aflatoxin content and kernel weight per plant as well. However they can be directly recommended as aflatoxin resistant varieties to the problem prone areas for immediate use and can be utilized in the breeding programmes for later use to enhance yield and reduce aflatoxin content levels.

Among the lines, L_1 (ICG 1326) was proved to be the best with good gca for eight characters (shell volume, free space in pod, shelling percentage, mature pods per plant, protein content, reducing sugar content, non-reducing sugar content and CGR at 60 DAS). The other line, L_4 (ICG 7633) was a good combiner for seven characters viz., pod volume, protein content, reducing sugar content, non-reducing sugar content, CGR at 60 DAS, CGR at 90 DAS, harvest index and kernel weight per plant. It was observed that T_1 (ICGV 86564) was the only parent with good gca for both aflatoxin content and kernel weight per plant.

Results on the combination of both *per se* performance and gca effects revealed that identification of superior segregants in the crosses involving L_2 (ICG 3245), T_4 (M 13) and T_5 (TPT 4) might be possible for most of the characters studied.

The crosses selected for recombination breeding should satisfy the criteria that they should possess non-significant sca effects with their parents showing significant gca effects. It was very fortunate to obtain a cross, L_4 X T_4 (ICG 7633 X M 13) that showed promise for recombination breeding with its non-significant sca and significant gca of its parents for kernel weight per plant.

As there were only a few crosses available and as there was no single cross showing significance for more than two characters for recombination breeding, focus was made on the exploitation of non-additive gene action through heterosis breeding. The crosses; L_1 X T_1 (ICG 1326 X ICGV 86564), L_4 X T_5 (ICG 7633 X TPT 4), L_4 X T_4 (ICG 7633 X M 13), L_2 X T_5 (ICG 3245 X TPT 4), L_3 X T_4 (ICG 3542 X M 13), L_2 X T_4 (ICG 3245 X M 13), L_1 X T_3 (ICG 1326 X TG 49) and L_3 X T_1 (ICG 3542 X ICGV 86564) were considered as outstanding ones for improving kernel weight per plant with aflatoxin resistance based on *per se* performance. While, the crosses, L_1 X T_1 (ICG 1326 X ICGV 86564), L_3 X T_4 (ICG 3542 X M 13), L_4 X T_5 (ICG 7633 X TPT 4) and L_2 X T_5 (ICG 3245 X TPT 4) were considered as good specific combiners for majority of the characters.

Combining standard heterosis for majority of the traits with heterobeltiosis for aflatoxin content, L_1 X T_1 (ICG 1326 X ICGV 86564) and L_4 X T_5 (ICG 7633 X TPT 4) were observed to be the best heterotic crosses.

Instead of analyzing the crosses and interpreting individually, the classification of crosses based on mean, sca and heterosis for all the characters would reward perfect estimates to draw sound conclusions. The cross combinations, L_1 X T_1 (ICG 1326 X ICGV 86564), and L_4 X T_5 (ICG 7633 X TPT 4) have shown significance for aflatoxin content and kernel weight at all the three selection criteria. When the three types of heterosis were considered together, the same combinations proved to be the best for eight characters each. Furthermore, their parental gca effects were highly significant for more than 50 % of the characters which means that these crosses possess double advantage and can be cultivated either as commercial F_1 hybrids or can be persuaded to develop recombinant genotypes through transgressive segregation. As groundnut being a self pollinated crop and commercial feasibility of F_1 hybrid is of remote possibility, transgressive segregants can be developed into out standing genotypes with high yield coupled with aflatoxin resistance by adopting simple breeding methods like pedigree method and selecting both in early as well as advanced stages of segregation to exploit both additive and non-additive gene effects.

LITERATURE CITED

LITERATURE CITED

Adams J Whitaker T B Barug D Egmond H P van Lopez Garcia R Osenbruggen W A van and Visconti A 2004 Peanuts, aflatoxin, and the U S origin certification program. Meeting the mycotoxin menace pp. 183-196 **In** Proceedings of the 2nd World Mycotoxin Forum 17-18 Feb Nordwijk, The Netherlands.

*Ahmed E M and Young C T 1982 Composition, quality and flavour of peanuts. pp. 655-88 **In** Peanut Science and Technology (ed Pattee H E and Young C T). American Peanut Research and Education Society, Yoakum, Texas, USA.

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 J. of Botany 26(1): 75-82.

Ali N Nawaz M S and Bashir K 1996 Genetic variability, heritability and correlation studies in groundnut (*Arachis hypogaea* L.). pp. 201 Abstracts of poster session; 2nd International Crop Science Congress, 17-24 November, 1996 New Delhi, India.

Allard R W 1960 Principles of Plant Breeding. John Wiley and Sons Inc., New York.

Amit Vikram, Roy D Vikram A 2003 Selection of characters for constructing selection index in groundnut (*A. hypogaea* L.). Legume Research 26(2): 137-139.

Anderson W F Holbrook C C and Wilson D M 1996 Development of greenhouse screening for resistance to *Aspergillus parasiticus* infection and preharvest aflatoxin contamination in peanut. Mycopathologia 135(2): 115-118.

Anderson W P Fitznca M M Isleib T G Cerfune J C and Phillips T D 1993 Combining ability for large pod and seed traits in peanut. Peanut Science 20: 49-52.

Anuradha V 1995 Studies on genetic diversity in thirty genotypes of groundnut (*Arachis hypogaea* L.) M.Sc (Ag) Thesis Andhra Pradesh Agricultural University, Hyderabad.

Arjunan A Manahoran V and Senthil N 1999 Path analysis of characters contributing to drought resistance in groundnut. Madras Agricultural Journal 86(1-3): 36-39.

Arjunan A Senthil N and Dharmalingam V 1997 Correlation between physiological traits contributing to drought tolerance in groundnut at three development stages. Madras Agricultural Journal 84(8): 518-519.

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

Arunachalam V 1993 Seed nitrogen and fatty acids reflecting yield variation in groundnut (*Arachis hypogaea*) Indian Journal of Agricultural Science 63(5): 289-291.

Arunachalam V and Bandyopadhyay A 1986 Limits to genetic divergence for occurrence of heterosis – experimental evidence from crop plants. Indian Journal of Genetics 44 (3): 548-554.

Arunachalam V Bandyopadhyay A Nigam S N and Gibbons R W 1984 Heterosis in relation to genetic divergence and specific combining ability in groundnut (*Arachis hypogaea* L.) Euphytica 33(1): 33-39.

*Arunachalam V Bandyopadhyay A Nigam SN and Gibbons R .W 1982 Heterotic potential of single crosses in groundnut (*Arachis hypogaea* L.) Oleagineux 37: 416-418.

Arunachalam V. and Bandyopadhyay A 1984 Character association among components of genetic variation in F_1 generation in *Arachis hypogaea* L. Madras Agricultural Journal 71(7): 431-438.

Azer M and Cooper C 1991 Determination of aflatoxins in food stuffs by HPLC and immuno sorbent assay system. Journal of Food Protection 54(4): 291-294.

Bandyopadhyay A Arunachalam V and Venkaiah K 1985 Efficient selection intensity in early generation index selection in groundnut (*Arachis hypogaea* L.). Theoretical and Applied Genetics 71(2): 300-304.

Bansal V K Satija D R Gupta V P Sanjha A S and Verma M M 1993 Heterosis in relation to plant type in groundnut for yield. pp 6-7 **In** Heterosis Breeding in Crop Plants – Theory and Application, Symposium, 23-24 February, Ludhiana, India.

Bansal V K Satijia D R and Ahuja K L 1992 Combining ability in inter and intra growth habit crosses for quality traits in groundnut (*Arachis hypogaea* L.). SABRAO Journal 24: 1-6.

Basu M S Nagaraj G and Reddy P S 1988 Genetics of oil and other major biochemical components in groundnut (*Arachis hypogaea* L). International Journal of Tropical Agriculture 6: 106-110.

Basu M S Vaddoria M A Singh N P and Reddy P S 1987 Combining ability for yield and its components in a diallel cross of groundnut. Indian Journal of Agricultural Science 57: 82-84.

Bera S K and Das P K 1998 Oil yield and fatty acid profile of some promising groundnut (*Arachis hypogaea* L.) genotypes. Madras Agricultual Journal 85(10-12): 668-670.

Bhagat N R Lalwani H B Ahmed T Dhapwal G S and Nagraj G 1984 Evaluation of groundnut collection from Zambia. Indian Journal of Genetics 44(3): 406-410.

Bhandari D K 1978 Line X Tester analysis and its interaction with environment in American cotton (*Gossypium hirsutum* L.). Madras Agricultural Journal 65: 218-225.

Bhat R V 1989 Risk to human health associated with consumption of groundnuts contaminated with aflatoxins. **In** Aflatoxin contamination of groundnut. Proceedings of the International Workshop ICRISAT, India.

Bindu Madhava H Sheshshayee M S Shankar A G Prasad T G and Udayakumar M 2002 Use of SPAD Chlorophyll Meter to assess transpiration efficiency of peanut. pp. 3-9 **In** Breeding of drought resistant peanuts (ed Cruickshank A W Rachaputi N C Wright G C and Nigam S N 2003) Proceedings of a collaborative review meeting held on 25-27 February, 2002 at Hyderabad, India.

Borate D N Dumbre A D and Bhingarde M T 1993 Effect of seed size on growth, yield and seed quality of groundnut (*Arachis hypogaea* L.) under summer conditions. Seed Research 21: 107-109.

Brim C A and Burton G W 1979 Recurrent selection in soybean II Selection for increased per cent protein seeds. Crop Science 19: 494-498.

*Burton G W 1952 Quantitative inheritance in grasses. Proceedings of sixth international grassland congress 1: 277-283.

Carter J B H 1973 The influence of the testa damage and seed dressing on the emergence of groundnut. Annals of Applied Biology 74: 315-323.

Chandrasekhar G 1991 Groundnut quality requirements for the export market – Present status, constraints and future needs in India. pp: 287-292 **In** Uses of tropical grain legumes: Proceedings of a consultants' meeting 27-30 Mar 1989 ICRISAT Patancheru.

Chauhan R M and Shukla P T 1985 Variability, heritability and genetic advance in bunch and spreading types of groundnut. Indian Journal of Agricultural Science 55: 71-74.

Chavan A A and Dhoble M V 1994 Studies on genetic variations in groundnut (*Arachis hypogaea* L.) under water stress and natural condition. Journal of Oilseeds Research 11: 9-14.

Cherian Mathews, Nagada A K and Sharma U C 2000 A study of path analysis in groundnut. Madras Agricultural Journal 87(7-9): 480-481.

Chaudhary S K 1993 Variability, heritability and genetic advance in groundnut under mid altitude condition. Indian Journal of Hill Farming 6(2): 171-174.

Clavel D Sarr B Marone E and Ortiz R 2004. Potential agronomic and physiological traits of Spanish groundnut varieties (*Arachis hypogaea* L.) as selection criteria under end-of-cycle drought conditions. Agronomie 24(2): 101-111.

*Cole R J 1989 Preharvest aflatoxin in peanuts. Int. Biodeterior 25: 253-257.

Cole R J Dorner J W and Holl Brook C C 1995 Advances in mycotoxin elimination and resistance. 13: 456-474 **In** Advances in Peanut Science, American Peanut Research and Education Society.

Cole R J Sobolev V S and Dorner J W 1993 Potentially important sources of resistance to prevention of pre harvest aflatoxin contamination in peanuts. **In** Proceedings of American Research and Education Society 78.

Cooper M and Hammer G L 1996 Plant adaptation and crop improvement. CAB International, Wallingford, UK.

Damodaram T and Hegde D M 2000 Oilseed situation: A statistical compendium 2000 Directorate of Oilseeds Research, Hyderabad.

Davidson J I Hill R A Cole R A Mixon A C and Henning R J 1982 Field performance of two peanut cultivars relative to resistance to invasion by *A. flavus* and subsequent aflatoxin contamination. **In** Proceedings of the American Peanut Research and Education Society 14(1): 74-78.

Dayanatha Jha 2002 Priorities in oil seeds research. pp 446-451 **In** Oilseeds and Oils: Research and Development Needs (ed Rai Mangala Singh Harvir and Hegde D M) Indian Socicty of Oil seeds Research, Hyderabad.

Deodhar A D Sharma Y and Kadshankar K 1973 Mass selection by specific gravity for oil and protein in groundnut. SABRAO News letter 4: 129-132.

Desai B B Kotecha P M and Salunkhe D K 1999 Science and technology of groundnut: Biology, Production, Processing and Utilization, Naya Prokash Culcutta pp. 498-523.

Deshmukh S N Basu M S and Reddy P S 1986 Genetic variability character association and path co-efficient of quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Science 56: 816-821.

Devi K L 1997 genetic analysis in F2 generation of a 6 x 6 diallel set of groundnut (*Arachis hypogaea* L.) crosses. M.Sc.(Ag.) Thesis ANGRAU, Hyderabad.

Dewey J R and Lu K H 1959 Correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal 51: 515-518.

Dhaliwal G P S Nagda A K and Abhay Dashara 2003 Genetic variability, correlation and path analysis in groundnut (*Arachis hypogaea* L.) **In** National seminar on advances in genetics and plant breeding – Impact of DNA revolution, Oct. 2003.

Dhillion B S 1975 The application of partial diallel crosses in plant breeding – A review. Crop Improvement 2: 1-7.

Diehl A L Johnson V A and Mattern P J 1978 Inheritance of protein and lysine in three wheat crosses. Crop Science. 18: 391-95.

Dobaria J R Rathnakumar A L and Bharodia P S 2004 Genetic analysis of yield components and confectionery traits in crosses involving large seeded genotypes of groundnut (*Arachis hypogaea* L.). Journal of Oil Seeds Research 21(1): 11-16.

*Dowell F E Tsai Y J Dorner J W Cole R J and Davidson J I 1992 Performance of visual and chemical methods in identifying aflatoxin contamination in farmers stock peanuts. Oleagineux Paris 47(10): 583-586.

Dube H C 1990 An introduction to fungi. Vikas Pub. House Pvt. Ltd. New Delhi pp. 540-541.

Duncan, W G Mc Cloud D E Mc Graw R L and Boote K J 1978 Physiological aspects of peanut yield improvement. Crop Science 18: 1015-1020.

Dwivedi S L Jambunathan R Nigam SN Raghunath K Shankar K R and Nagabhushanam G V S 1990 Relationship of seed mass to oil and protein contents in peanut (*Arachis hypogeae*). Peanut Science 17: 48-52.

Dwivedi S L Nagabhushanam G V S Nigam S N Raghunath K and Jambunathan R 1994 Germplasm enhancement for seed quality traits in groundnut. International Arachis Newsletter 14: 14-15.

Dwivedi S L Nigam S N, Chandra S Ramjau V M 1998 Combining ability of biomass and harvest index under short and long-day conditions in groundnut. Annals of Applied Biology 133: 237-244.

Dwivedi S L Tendapani K and Nigam S N 1989 Heterosis and combining ability studies and relationship among fruit and seed characters in peanut. Peanut Science 16: 14-20.

Eeden C F Van rensburg J B J Van Linde T C K and Vander 1994 The role of insect damage in the colonization of groundnut (*Arachis hypogaea* L.) pods by fungi. South African Journal of Plant and Soil 11: 159-162.

Enyi B A C 1977 Physiology of grain yield in groundnuts (*Arachis hypogaea*). Experimental Agriculture 13: 101-110.

Falconer D S 1964 Introduction to quantitative genetics. Oliver and Boy London pp.340.

FAO Bulletin 2003.

Fisher R A and Yates F 1963 Statistical tables for Biological, Agricultural and Medical research. Oliver and Boyd, London 46-63.

Fonseca S and Patterson F L 1968 Hybrid vigour in seven parent diallel cross in common wheat (*Triticum aestivum* L.). Crop Science 2: 85-88.

Ganesan K and Sudhakar D 1995 Variability studies in spanish bunch groundnut. Madras Agricultural Journal 82: 395-397.

*Garet B 1976 Heterosis and combining ability in groundnut (*Arachis hypogaea* L.) Oleagineux 31: 435-442.

Ghewande M P 1997 Aflatoxin contamination of groundnut and its management in India. Aflatoxin contamination problems in groundnut in Asia: Proceedings of the first Asia working group meeting, 27-29 May 1996; Ministry of Agricultural and Rural Development Hanoi Vietnam (ed. Mehan V K and Gowde C L L) ICRISAT, Patancheru, India.

Ghewande M P Nagaraj G Desai S and Narayana P 1993 Screening of groundnut bold-seeded genotypes for resistance to *Aspergillus flavus* seed colonization and less aflatoxin production. Seed Science and Technology 21(1): 45-51.

Ghewande M P and Nagaraj G and Reddy P S 1987 Aflatoxin research at the Indian National Research Center for Groundnut. Pp. 21 **In** Summary and recommendations of the international workshop on aflatoxin contamination of groundnut. ICRISAT, India.

Ghewande M P and Nagaraj G and Reddy P S 1989 Aflatoxin research at the Indian National Research Center for Groundnut. Pp. 237-243 **In** Proceedings of international workshop 6-9th Oct 1987 ICRISAT. India.

*Graham J 1982 Aflatoxins in peanuts: Occurrence and control. Queensland Agricultural Journal 103(3): 119-122.

Grakh S S and Chaudhary M S 1985 Heterosis for early maturity and high yield in *Gossypium arboreum* Indian Journal of Agricultural Science 55(1): 10-13.

Gulati A and Sharma A 1997. Freeing trade in agriculture: Implications for resource use efficiency and cropping pattern changes. Eco. and political weekly 32 (52): 154 – 164.

Gupta U S 2000 Crop improvement Vol 3 Quality charaters. Oxford and IBH Pub. Co. Pvt. Ltd. New Delhi pp. 1-19.

Hanson W D Probst A H and Caldwell B E 1967 Evaluation of a population of soybean genotypes with implication for improving self-pollinated crops. Crop Science 7: 99-103.

Hari Singh, Yadav A K Yadava T P and Chhabra M L 1982 Genetic variability and heritability for morpho-physiological attributes in groundnut. Indian Journal of Agricultural Sciences 52: 432-434.

Hariprasad A S 1990 Genetic analysis of combining ability, heritability and correlation in groundnut (*Arachis hypogaea* L.). M.Sc.(Ag) Thesis Andhra Pradesh Agricultural University, Hyderabad.

Harish babu B N Gowda M V C Rudra Naik Salimath D M and Raju S G 2003 Resistance to *A. flavus* in large seeded confectionary groundnuts. **In** National seminar on advances in genetics and plant breeding – Impact of DNA revolution, Oct. 2003.

*Hays J D and Foster C A 1974 Heterosis in self pollinating crops with particular reference to barley **In** Heterosis in Plant Breeding. Proceedings XII Congress of Eucarpia, Budapest.

Hiremath S M Janardhan K V Habib A F and Panchal Y C 1984 Varietal differences in leaf photosynthetic rate and its relationship with certain leaf characters. Journal of Nuclear Agriculture and Biology. 13(4): 103-105.

Holbrook C C Kvien C K Rucker K S Wilson D M Hook J E and Matheron M M 2000 Pre-harvest aflatoxin contamination in drought tolerant and drought intolerant peanut genotypes. Peanut Science 27: 45-48.

Holbrook C C Hunter J E Knauft D A Wilson D M and Matheron M E 1994 Fatty acid composition as a possible mechanism for resistance to preharvest aflatoxin contamination of peanut **In** Proceeding American Peanut Res. Edu. Soc. Inc. 26.

ICAR 1987 Aflatoxins in groundnut. Technologies for better crop. Bulletin No. 33. Indian Council of Agricultural Research, New Delhi.

Isleib T G and Wynne J C 1983 Heterosis in test crosses of 27 exotic peanut cultivars. Crop Science 23 (5): 832-841.

Isleib T G Pattee H E and Glesbrecht F G 2004 Oil, sugar, and starch characteristics in peanut breeding lines selected for low and high oil content and their combining ability. Journal of Agricultural Food Chemistry. 52(10): 3165-8.

Isleib T G Wynne J C and Nigam S N 1994 Groundnut breeding **In** The groundnut crop: A scientific basis for improvement. Chapman and Hall, London. pp. 552-623

Isleib T G Wynne J C 1983 Heterosis in test crosses of 27 exotic peanut cultivars. Crop Science 23: 832-841.

Jain D K Nagda A K and Mahawar R K 2003 Genetic divergence in Spanish bunch groundnut (*Arachis hypogaea* L). pp. 30-31 **In** National seminar on advances in genetics and plant breeding – Impact of DNA revolution, Oct. 2003.

Jambunathan R Sridhar R Rashunath K Dwivedi S L and Nigam S N 1993 Oil quality characteristics and head space volatiles of newly released groundnut (*Arachis hypogaea* L.) cultivars. Journal of Science Food and Agriculture. 61: 23-30.

Jayalakshmi V 1997 Genetic analysis of certain morphological and physiological attributes for yield and drought tolerance in a 7 X 7 diallel cross of groundnut (*Arachis hypogaea* L.). Ph.D Thesis. Andhra Pradesh Agricultural University, Hyderabad.

Jayalakshmi V 2003 Correlations in F_2 and F_3 generations of groundnut (*Arachis hypogaea* L.). The Andhra Agricultural Journal 50(3&4): 371-372.

Jayalakshmi V Rajareddy C Reddy P V and Nageswara Rao R C 1999 Genetic analysis of carbon isotope discrimination and specific leaf area in groundnut (*Arachis hypogaea* L.). Journal of Oilseeds Research 16: 1-5.

John Joel A and Mylsamy V 1998 Genetic divergence in groundnut. Madras Agricultural Journal 85(2): 134-135.

John K Vasanthi R P Venkateswarlu O and Sudhakar P 2004 Genetic variability and regression studies for yield and certain physiological attributes in groundnut (*Arachis hypogaea* L.). pp. 110-112 **In** Proceedings of National Seminar on Physiological Interventions for Improved Crop Productivity and Quality: Opportunities and Constraints (ed Reddy P V Rao J S P Reddy K B Sudhakar P Rama Rao G Babitha M Latha P and Jyotsna M K) Plant physiology club (APAU) and Indian society for plant physiology, New Delhi.

Johnson H W Robinson H F and Comstock R E 1955 Estimates of genetic and environmental variability in soybeans. Agronomy Journal 47: 314-318.

Johnson L F and Curl E A 1972 Methods for research on the ecology of soil borne plant pathogen. Burgess Publishing Company, Minnesota. pp. 6-8.

Kadam S S and Chavan J K 1991 Utilization of groundnut in India and scope for novel and alternative uses. pp. 277-285 **In** Uses of tropical grain legumes: Proceedings of a consultants' meeting ICRISAT Patancheru.

Kadambavanasundaram M 1983 Heterotic system in cultivated species of *Gossypium*. An appraisal. Genetic and crop improvement of heterotic systems. pp. 20 **In** Pre-congress scientific meetings of XV international congress of genetics, 7-9 December 1983. TNAU, Coimbatore.

Kale D M Gadgil J D and Murthy G S S 1988 Relationship between seed size, oil and protein contents in groundnut. Journal of Oilseeds Research 5(2): 170-175.

Kannaiyan J and Sithanatham S 1991 Survey on the occurrence of *Aspergillus* contamination of groundnut seeds in Eastern province, Zambia. International Arachis Newsletter 10: 14-16.

Kassam A H Kowal J M and Harkness C 1975 Water use and growth of groundnut at Samaru. Northern Nigeria. Tropical Agriculture (Trinidad) 52: 105-112.

Kempthorne O 1957 An Introduction to Genetic Statistics. John Wiley and Sons Inc., New York.

Kitbite S 1990 Genetic and computer simulation studies of protein yield relationships in wheat. Journal of Genetics and Plant Breeding 44: 179-189.

Knauft D A and Wynne J C 1995 Peanut breeding and genetics. 55: 393-445 **In** Advances in Agronomy.

*Konarev V G 1974 Physiological and biochemical aspects of heterosis. **In** Heterosis in Plant Breeding. Proceedings of VII Congress of Eucarpia, Budapest.

Krishnappa N Narayanaswamy S Balakrishna P Lokesh K Prashant Shankhinamath and Shankhinamath P 2003 Influence of storage mycoflora on seed quality of groundnut (*Arachis hypogaea* L.) varieties stored in different packaging materials. Research on Crops 4(3): 409-417.

Kumar S S and Patel S A 1999 Gene effects for pod characteristics in groundnut (*Arachis hypogaea* L.). Indian Journal of Agricultural Science 69: 111-115.

Layrisse A Wynne J C and Isleib T G 1980 Combining ability for yield, protein and oil of peanut lines from South American centers of diversity. Euphytica 29: 561-570.

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

Li Sinlin Liang Xuanguiang and Li Shaxion 1996 Screening of groundnut germplasm for resistance to *Aspergillus flavus* invasion and colonization in Guangdong, South China. International Arachis Newsletter 16: 24-25.

Lowry O H Rosebrough N J Farr A L and Randall R J 1951 Protein measurement with the folin phenol reagent. Journal of Biological Chemistry. 193: 265-276.

Madhavi K S 1988 Studies on some morphological and physiological characters with specific reference to their inter-relationship and heterosis in *Arachis hypogaea* L. M.Sc.(Ag.) Thesis Andhra Pradesh Agricultural University, Hyderabad.

Madhavilatha K 1998 Genetic analysis of yield and physiological attributes in F_3 generation of 6 x 6 diallel set of mung bean (*Vigna radiata* (L.) Wilczek) crosses. M.Sc.(Ag.) Thesis Acharya N.G. Ranga Agricultural University, Hyderabad.

*Mahalanobis P C 1936 On the generalized distance in statistics. Proceedings of National Institute of Science, India 2: 49-55.

Makhan Lal Roy D Ojha O P and Lal M 2003 Genetic variability and selection response for root and other characters in groundnut (*Arachis hypogaea* L.). Legume Research 26(2): 128-130.

Makne V G 1992 Diallel analysis for studying the inheritance of branches, developed pods and harvest index in groundnut. Journal of Maharashtra Agricultural Universities 17: 153-154.

Makne V G and Bhale N L 1987 Combining ability analysis for yield, protein and oil in groundnut. Indian Journal of Agricultural Science 57: 617-621.

Makne V G and Bhale N L 1991 Heterosis, inbreeding depression and combining ability for oil, protein, pod yield and its components in groundnut (*Arachis hypogaea* L.). pp. 434 **In** Golden Jubilee Symposium on Genetic Research and Education: Current Trends and the Next Fifty Years. February, 12-15, 1991 New Delhi.

Makne V G Khapre P R and Salunke M R 1994 Genetic architecture of protein content in groundnut. Journal of Maharashtra Agriculture University 19(2): 289-290.

Manoharan V Vindhiyavarman P Sundaram N and Thangavelu S 1985 Analysis of combining ability in groundnut. Madras Agricultural Journal 72: 601-605.

Mathews C Nagada A K and Sharma U C 2000 A study of path analysis in groundnut. Madras Agricultural Journal 87: 480-481.

Mathur R K Manivel P and Gor H K 2000 Genetics of reproductive efficiency and yield in groundnut. Annals of Agriculture Research 21(1): 65-68.

Matzinger A K Mann T J Cockerham C C 1962 Diallel cross in *Nicotiana tabacum*. Crop Science 2: 383-435.

Mehan V K 1987 The aflatoxin contamination problem in groundnut - Control with emphasis on host plant resistance. pp: 63-92 **In** Proceedings of the first regional groundnut plant protection group meeting and tour. Harare, Zimbabwe.

Mehan V K 1989 Screening groundnuts for resistance to seed invasion by *A. flavus* and to aflatoxin production. pp: 323-334 **In** Aflatoxin contamination of groundnut: Proceeding of the International workshop, 6-9 October, 1987, ICRISAT, India.

Mehan V K Mc Donald D Haravur L J and Jayanthi S 1991 The groundnut aflatoxin problem – Review and literature data base ICRISAT Patancheru pp. 139.

Mishra C M 1995 Correlation studies in Spanish bunch groundnut (*Arachis hypogaea* L.). Madras Agricultural Journal 82: 65-66.

Mishra I K and Yadav R K 1992 Genetic variability and correlation studies in summer groundnut. Advances in Plant Sciences 5: 106-110.

Misra J B Chauhan S and Mathur R S 1992 Variation in oil and protein contents in groundnut germplasms. Groundnut Newsletter 4(2): 3.

Misra J B Gosh P K Dayal D and Mathur R S 2000 Agronomic, nutritional and physical characteristics of some Indian groundnut cultivars. Indian Journal of Agricultural Sciences 70(11): 741-746.

Mixon A C and Rogers K M 1973 Peanut accessions resistant to seed infection by *Aspergillus flavus*. Agronomy Journal 65: 560-562.

Mohan G Bentur K G Parameshwarappa and Appa Rao 2003 *In vitro* screening of confectionary groundnut genotypes for seed colonization by *A. flavus*. pp: 328-329 **In** ISOR National Seminar: Stress management in oilseeds..

Moll R H and Stuber C W 1971 Comparisons of response to alternative selection procedures initiated with two population of maize (*Zea mays* L.). Crop Science 11: 706-711.

Murthy P S S Reddy P J R and Reddy G H S 1983 Variation in the physiological parameters of popular groundnut varieties. Madras Agriculture Journal 70(9): 603-610.

Murthy T G K and Ghewande M P 1996 Breeding for disease resistance in groundnut (*Arachis hypogeae* L.). pp. 139-169 **In** Genetic Improvement of Oilseed Crops (ed Jafar Nizam, Farook S A and Irfan A Khan). Ukaaz publications, Hyderabad.

Murthy T G K and Reddy P S 1996 Genetics of qualitative traits in groundnut (*Arachis hypogaea* L.) pp. 101-137 **In** Genetic Improvement of Oil Seed crops (ed. Jafar Nizam, Farook S A and Irfan A khan). Ukaaz publication, Hyderabad.

Musingo M N Basha S M Sanders T H Cole R J and Blankenship P D 1989 Effect of drought and temperature stress on peanut (*Arachis hypogaea* L.) seed composition. Journal of Plant Physiology 134(6): 710-715.

Nadaf H C and Habib A F 1987 Studies on genetic variability in bunch groundnut (*Arachis hypogaea* L.). Mysore Journal of Agricultural Sciences 21: 297-301.

Nagabhushanam G V S Subramanyam D and Sreerama Reddy N 1982 Character association and path analysis in erect genotypes of groundnut (*Arachis hypogaea* L.). The Andhra Agricultural Journal 29: 1-5.

Nagaraj G 1996 Composition and quality of oil seeds. pp. 265-313 **In** Genetic improvement of oil seed crops (ed Jafar Nizam, Farook S A and Irfan A khan). Ukaaz publication, Hyderabad.

Nageswara Rao R C Udayakumar M Farquhar G D Talwar H S and Prasad T G 1995 Variation in carbon isotope discrimination and its relationship to specific leaf area and rubulose-1-5-bisphosphate carboxylase content in groundnut genotypes. Australian Journal of Plant Physiology 22: 545-551.

Nageswara Rao R C 1992 Some crop physiological approaches for groundnut improvement. Journal of Oilseeds Research 9: 286-296.

Nageswara Rao R C Graeme W Steven K and Jeff T 2001 Improved agronomic practices to sustain peanut yield and reduce aflatoxin contamination in water limited environments in Southern Queenland. 10th Australian Agronomy Conference 28 Jan – 1 Feb, Hobart, Tasmania.

Nageswara Rao R C Talwar H S and Wright G C 2001a Rapid assessment of specific leaf area and leaf N in peanut (*Arachis hypogaea* L.) using chlorophyll meter. Journal of Agronomy and Crop Science 189: 175-182.

Naguib Kh Naguib M M Daib M M Sahab A F and Amra H 1989 Occurrence of aflatoxins and aflatoxin producing strains of *Aspergillus flavus* in groundnut cultivars in Egypt. pp. 311-317 **In** Aflatoxin contamination of groundnut: Proceedings of international workshop, 6-9th Oct 1987 ICRISAT, India.

Nahdi S 1989 The geocarposphere mycoflora and resistance of groundnut to *A. flavus*. pp 365-378 **In** Aflatoxin contamination of groundnut: Proceedings of the international workshop. ICRISAT, India.

Nahdi S 1996 Drought stress and pre-harvest invasion of selected groundnut genotypes by *Aspergillus flavus* and aflatoxin contamination. Indian Phytopathology 49(1): 52-56.

Naik K S S Reddy P N and Reddy C D R 2000 Variability studies in F_2 populations of some subspecific crosses in groundnut. National Seminar of Oil Seeds and Oil Research and Development needs in the Millennium 2-4: 93.

Natarajaratnam N 1979 Drymatter production and harvest index trends in groundnut (*Arachis hypogaea* L.) Madras Agricultural Journal 66: 218-221.

Nautiyal P C and Joshi Y C 2003 Carbon discrimination and exchange rate, and partitioning of dry matter under natural and simulated drought conditions in groundnut. pp.164 **In** 2nd International Congress of Plant physiology on Sustainable Plant Productivity Under Changing Environment. Jan 18-21 New Delhi, India.

Nautiyal P C Ravindra V and Joshi Y C 2002 Dry matter partitioning and water use efficiency under water-deficit during various growth stages in groundnut. Indian Journal of Plant Physiology. 7(2): 135-139.

Nayak P K and Patra G J 1997 Genetic divergence in a correlation of groundnut germplasm. Environment and Ecology 15(2): 249-254.

*Nelson N 1944 A photometric adaptation of the somogyi method in the determination of glucose. Journal of Biological Chemistry. 153: 375-380.

Newell J A Mason M E and Matlock R S 1967 Precursors of typical and atypical roasted peanut flavour. Journal of Agricultural and Food Chemistry 15: 767-772.

Nigam S N Dwivedi S L and Gibbons R W 1991 Groundnut breeding: Constraints, achievements and future possibilities. Plant Breeding Abstracts 61 (10): 1127-1136.

Nigam S N Dwivedi S L Reddy L J and Vasudeva Rao M J 1989 An update on groundnut breeding activities at ICRISAT center with particular reference to breeding and selection for improved quality. pp. 115-125 **In** Proceedings of the Third Regional Groundnut Workshop 13-18 March 1988 Lilongwe, Malawi.

Nigam S N Giri D Y and Reddy A G S 2004 Groundnut seed production manual. ICRISAT. pp. 27.

Nigam S N Upadhyaya H D Chandra S Nageswara Rao R C Wright G C and Reddy A G S 2001 Gene effects for specific leaf area and harvest index in three crosses of groundnut (*Arachis hypogaea*). Association of Applied Biologists 139: 301-306.

Nisar Ahmed 1995 Heterosis, combining ability and interrelationships among yield and yield attributes in groundnut (*Arachis hypogaea* L.). MSc.(Ag) Thesis Andhra Pradesh Agricultural University, Hyderabad, India.

*Obraztsov A S 1983 Some biological aspects of the problem of breeding for earliness. Skokhozyaistrennaya Biologiya 10: 3-11.

*Olorunju S A S Olorunju P E and Ntare B R 2003 Classification of early maturing groundnut varieties using multivariate method. Agricultura Tropica et Subtropica 36: 27-31.

Palanisami A Manickam A and Neelakantan S 1990 Fungal flora and aflatoxin production in relation to post-harvest practices in groundnut. Madras Agricultural Journal 77: 26-31.

Pallas, J. E. Jr. and Samish Y. B. 1974 Photosynthetic response of peanut. Crop Science 14: 478-482.

Panse V G and Sukhatme P V 1979 Statistical methods for agricultural workers ICAR, New Delhi.

Parmar D L Rathnakumar A L and Bharodia P S 2002 Genetics and inter-relationships of oil and protein content in crosses involving confectionery genotypes of groundnut (*Arachis hypogaea* L.). Journal of Oil Seeds Research 19(1): 32-34.

Parmar D L Rathnakumar A L and Bharodia P S 2001 Heterosis for oil and protein in crosses involving bold seeded groundnut. pp. 60 **In** National symposium on pulses and oil seeds for sustainable agriculture 29-31 July TNAU, Coimbatore.

Parmar D L Rathnakumar A L and Bharodia P S 2001a Genetic implications in breeding for confectionery groundnut. pp. 60 **In** National symposium on pulses and oil seeds for sustainable agriculture 29-31 July TNAU, Coimbatore.

Paroda R S 2002 Towards sustainable agricultural exports – New paradigms pp. 30-57 **In** Indian Agriculture – Current status, prospects and challenges – Commemorative volume. Proceedings of 27th Convention of Indian Agricultural Universities Association – conducted by Indian Agricultural Universities Association and ANGRAU at Hyderabad.

Patil R G Radder G D Patil V C and Ramachandrappa A K 1986 Dry matter production and distribution in bunch groundnut varieties as influenced by the time of sowing and foliar application of nitrogen and iron. Madras Agricultural Journal 71(3): 177-181.

Patra A K Tripathy S K and Samui R C 1995 Physiological basis of yield variation in rain fed groundnut. Indian Journal of Plant Physiology XXXVIII(2): 131-134.

Pattee H E Isleib T G Glesbrecht F G and McFeeters R F 2000 Investigations into genotypic variations of peanut carbohydrates. Journal of Agricultural Food Chemistry. 48(3): 750-756.

Penning de Vries F W T Brunsting A H M and van Laar H H 1974 Products, requirements and efficiency of biosynthesis: a quantitative approach. Journal of Theoretical Biology. 45: 339-377.

Pitt J I 1982 An improved medium for the detection of *A. flavus* and *A. parasiticus*. Applied Bacteriology 54: 109-114.

*Pitt J I 2004 Application of the food safety objective concept to the problem of aflatoxins in peanuts. Mitteilungen-aus-Lebensmitteluntersuchung-und-Hygiene 95(1): 52-58.

Prasad M V R 1996 Groundnut pp. 217-247 **In** Genetics, cytogenetics and breeding of crop plants vol (1) pulses and oil seeds (ed. Bahl P N and Salimath P M) Oxford and IBH publishing co. pvt. ltd. New Delhi.

Prasad M V R, Swarnalatha Kaul and Jain H K 1984 Induced mutants of peanut (*Arachis hypogaea* L.) for canopy and pod bearing characters. Indian Journal of Genetics and Plant Breeding 44:25-34.

Prathiba K M and Reddy M U 1994 Nutrient composition of groundnut cultures (*Arachis hypogaea* L.) in relation to their kernel size. Plant Foods for Human Nutrition 45(4): 365-369.

Qadri M I and Khunti V P 1982 Genetic variability in bunch groundnut. Crop improvement 9: 98-100.

Raheja R K Kanchan G Ahuja K L and Labana K S 1986 Correlation among kernel size, lipid constituents and fatty acid composition in groundnut (*Arachis hypogaea*). Annals of Biology 2: 45-50.

Rai Mangala 2002 Oil seeds on a balance. pp.1-36 **In** Oilseeds and Oils: Research and Development Needs (ed Rai Mangala, Singh Harvir and Hegde D M). Indian Society of Oil seeds Research, Hyderabad.

Raj Kumar M 1991 Studies on genetic diversity and interrelationships in groundnut (*Arachis hypogaea* L.). M.Sc(Ag) Thesis Andhra Pradesh Agricultural University, Hyderabad.

Rajgopal K Yadav S K Ghewande M P Bhalodia P K and Bhagat N R 1994 Assessment of large-seeded Virginia groundnut for confectionery characteristics. Groundnut News 6(1): 4.

Rama Reddy Y 1991 Genetic parameters and character association in groundnut (*Arachis hypogaea* L.). The Andhra Agricultural Journal 38: 272-274.

Ramakrishna N and Mehan V K 1993 Direct and indirect competitive monoclonal antibody based ELISA of aflatoxin B_1 in groundnut. Mycotoxin Research 9(1): 53-63.

Rao C R 1952 Advanced Statistical Methods in Biometrical Research. Wiley and Sons, New York.

Rao M J V Nigam S N Mehan V K and Mc Donald D 1989 *Aspergillus flavus* resistance breeding in groundnut. Progress made at ICRISAT center. pp. 345-356 **In** Aflatoxin contamination of groundnut (ed McDonald D and Mehan V K): Proceedings of the international workshop, 6-9 Oct 1987 ICRISAT India.

Rao R C N and Wright G C 1994 Stability of the relationship between specific leaf area and carbon isotope discrimination across environments in peanut. Crop Science 34: 98-103.

Rao R C N Talwar H S and Wright G C 2001 Rapid assessment of SLA and leaf nitrogen in peanut (*Arachis hypogaea* L.) using chlorophyll meter. Journal of Agronomy and Crop Science 186: 175-182.

Reddi M V Reddy K R Reddy K C M Reddy K H P Reddy P R and Reddy G L K 1989 Heterosis and combining ability in a 6 X 6 diallel set of groundnut (*Arachis hypogaea* L.). Journal of Research APAU 17: 378-383.

Reddy K R and Gupta R V S 1992 Variability and interrelationship of yield and its component characters in groundnut. Journal of Maharashtra Agricultural Universities 17: 224-226.

Reddy B J and Reddy C R 1988 Combining ability estimate in groundnut (*Arachis hypogaea* L.). The Andhra Agricultural Journal 35: 26-29.

Reddy D V R Nambiar P T C Rajeswari R Mehan V K Anjaiah V and Mc Donald D 1988 Potential of enzyme linked immunosorbent assay for detecting viruses, fungi, bacteria, mycoplasma like organisms, mycotoxins and hormones. pp. 43-49 **In** Proceedings of international biotechnology workshop, 12-15 January 1987. International crops research institute for the Semi-arid tropics, Patancheru 502324, Andhra Pradesh, India.

Reddy M J Shetty H S Fanelli C and Lacey J 1992 Role of seed lipids on *Aspergillus parasiticus* growth and aflatoxin production. Journal of the Science of Food and Agriculture 59(2): 177-181.

Reddy P S 1988 Genetics, breeding and varieties pp. 200-317 **In** Groundnut (ed Reddy P S), Indian Council of Agricultural Research, New Delhi, India.

Reddy P S and Murthy T G K 1994 Genetic improvement of groundnut in India: Priorities and prospects. pp. 1-16 **In** Sustainability in oil seeds (ed. Prasad M V R Raghavaiah C V Sastry R K and Damodaran T). Indian Society of Oilseeds Research, Hyderabad, India.

Reddy P V Sudhakar P Sujatha D Babitha M and Latha P 2004 Relationship of SPAD chlorophyll meter reading with specific leaf area, leaf total chlorophyll and pod yield in groundnut (*Arachis hypogaea* L.) pp. 24-27. **In** Proceedings of National Seminar on Physiological Interventions for Improved Crop Productivity and Quality: Opportunities and Constraints (ed Reddy P V Rao J S P Reddy K B Sudhakar P Rama Rao G Babitha M Latha P and Jyotsna M K). Plant physiology club (APAU) and Indian society for plant physiology, New Delhi.

Reddy P V Sudhakar P Sujatha D Vijaya Kumar B 2003 Drought tolerance traits related to preharvest aflatoxin contamination in groundnut. pp.261 **In** 2nd International Congress of Plant Physiology on Sustainable Plant Productivity Under Changing Environment Jan 18-21 New Delhi, India..

Sadasivam S and Manickam A 1996 Biochemical methods. Newage International (P) ltd., New Delhi pp. 8-9.

Sadhana Kumari and Snehalatha Reddy 1998 Oil and protein quality of the selected groundnut varieties. Journal of Oil Seeds Research 15(2): 339-342.

Sah J N Kumar R and Varshney S K 2000 Correlation and path analysis in mutant cultures of groundnut. Journal of Oil Seeds Research 17(1): 23-28.

Sahay S S and Rajan K S 1990 Distribution of aflatoxin in oilseeds and their oil cakes. Geobios 17: 47-48.

Sahoo A K Kulkarni and Vyakaranahal B S 1988 Effect of seed size on yield and quality in bunch groundnut. Seed Research 16: 136-142.

Salara B S and Gowda M V C 1998 Variability and correlation studies in segregating generation of inter sub-specific crosses of groundnut (*Arachis hypogaea* L.). Crop Improvement 25(1): 122-123.

Sanjeev Kumar, Arvind Kumar, Kumar S and Kumar A 2000 Growth analysis of Spanish and Virginia groundnut (*Arachis hypogaea* L.) cultivars in North-western Himalayas of Uttar Pradesh. Indian Journal of Hill Farming 13(1-2): 120-123.

Santos R B and Sutton B G 1982 Effect of defoliation on Virginia bunch peanuts at Camden, NS W. Australian Journal of Agriculture Research 33: 1037-1048.

Sarsar S M Patil R A Bhatade S S 1986 Heterosis and combining ability in upland cotton. Indian Journal of Agricultural Science 56(8): 567-573.

Searle S R 1961 Phenotypic, genetic, and environmental correlations. Biometrics 17: 474-480.

Senthil N and Vindhiyavarman P 1998 Combining ability studies in groundnut. Annals of Agricultural Research 19(2): 231-232.

Senthil N and Vindhiyavarman P 1998 a Heterotic combinations in inter sub-specific crosses of groundnut (*Arachis hypogaea* L.). Annals of Agricultural Research 19(4): 404-406.

Sharma V K and Varshney S K 1995 Analysis of harvest index in groundnut. Journal of Oilseeds Research 12(2): 171-175.

Shull G H 1948 What is 'Heterosis'. Genetics 33: 439-446.

Siddiq E A 1987 Hybrid rice research of the Indian Agricultural Research Institute paper at the group meeting on hybrid rice. Directorate of Rice Research, Hyderabad.

Simmonds N W 1995 The relation between yield and protein in cereal grain. Journal of. Science Food and Agriculture. 67: 309-315.

Singh A K and Simpson C E 1994 Biosystematics and genetic resources. pp. 96-137 **In** The groundnut crop: A scientific basis for improvement (ed. Smartt J). Chapman and Hall, London.

Singh J and Singh M 2001 Character association in spring/summer sown groundnut (*Arachis hypogaea* L.) genotypes. Journal of Research Punjab Agricultural University. 38(3-4): 147-152.

Singh M R K Raheja R K Ahuja and Sharma S R 2000 Correlation between pod yield and quality characters in groundnut (*Arachis hypogaea* L.) genotypes. National Seminar on Oil Seeds and Oils, Research and Development needs in the Millennium 2-4.

Singh R K and Choudhary B D 1977 Biometrical methods in quantitative genetic analysis. Kalyani pub., New Delhi pp.50.

Singh R S Choudhary R K and Singh O N 1983 Heterobeltiosis in relation to *per se* performance in *Brassica juncea* (L.) Zern crosses. pp. 1 **In** Importance of heterotic system. Coimbatore, School of genetics, TNAU.

Singh R S Singh O N and Chaudhary R K 1985 Combining ability for yield in Indian mustard. Indian Journal of Agricultural Science 55: 240-242.

Singhal N C Jain H K and Austin A 1977 Induced variability for protein content in bread wheat. Proc. Of two Research Coordination Meetings, Baden, 28 March, 1 April, 1977 and Vienna 26-30 Sept. 1977.

Siva Kumar M V K and Shaw R H 1978 Methods of growth analysis in field grown soybeans. Annals of Botony. 42: 213-222.

Sivakumar P L V 1984 Studies on heterosis, combining ability and character association for certain traits in groundnut (*Arachis hypogaea* L.) M.Sc. (Ag) Thesis Andhra Pradesh Agricultural University, Hyderabad.

Sivasubramanian S and Menon M 1973 Heterosis and inbreeding depression in rice. Madras Agricultural Journal 60: 1139-1144.

Skyes E E and Michaels T E 1986 Combining ability of Ontario grown peanuts (*Arachis hypogeae* L.) for oil, fatty acid and taxonomic characters. Peanut Science 13: 93-97.

Smith O S Smith S C Bowen S L Tenborg R A and Wall S J 1990 Similarities among a group of elite maize inbreds as measured by pedigree, F_1 grain yield, heterosis and RFLP's. Theoretical and Applied Genetics. 80: 833-840.

*Somogyi M 1952 Notes on sugar determination. Journal of Biological Chemistry. 195: 19-24.

*Sprague G F and Tatum L A 1942 General versus specific combining ability in single crosses of corn. Journal of American Society of Agronomy. 34: 923-932.

Sridharan C S and Marappan P V 1980 Biometrical studies on the hybrids of bunch groundnut (*Arachis hypogaea* L.). pp. 39-42 **In** Proceeding National symposium on the application of genetics for groundnut improvement. Tamil Nadu Agricultural University, Coimbatore.

Stansfield W D 1969 Theory and problems of genetics. Mc Graw Hill, New York.

Subramanyam K and Pandey R K 1981 Photosynthetic characteristics in blackgram (*Vigna mungo* L. Hepper). Journal of Nuclear Agriculture and Biology 10: 41-43.

Sudhakar Rao S 1980 Evaluation of productive efficiency in groundnut (*Arachis hypogaea* L.) genotypes of Virginia, Spanish and Valencia. M.Sc. (Ag.) Thesis Andhra Pradesh Agricultural University, Hyderabad.

Sulochana B N Bhargavi K Reddy T Y Basu M S 2000 Culinary preparations with groundnut (Recipe book in English, Hindi, Tamil, Telugu and Gujarati). Agricultural Research Station, Anantapur, AP. Pub. NRCG, UNDP and ANGRAU.

Sumathi R and Ramanathan T 1995 Genetic variability in intra specific crosses of *Arachis hypogaea* L. Karnataka Journal of Agricultural Science 8: 50-55.

Suresh Kumar S 1993 Studies on combining ability, variability and interrelationships in 15 F_3 progenies of 6 X 6 diallel of groundnut (*Arachis hypogaea* L.). M.Sc(Ag) Thesis Andhra Pradesh Agricultural University, Hyderabad, India.

Swaminathan M S Siddiq E A and Sharma S D 1972 Outlook for hybrid rice in India. pp. 609-613 **In** Rice breeding. International Rice Research Institute, Los Banos, Philippines.

Swe S T and Branch W D 1986 Estimates of combining ability and heterosis among peanut cultivators. Peanut Science 13: 70-74.

Thakur R P Rao V P Reddy S V and Ferguson M 2000 Evaluation of wild *Arachis* germplasm accession for *in vitro* seed colonization and aflatoxin production by *Aspergillus flavus*. International Arachis Newsletter, 20: 44-46.

Tiwari D S Singh V Shukla P S and Singh V 1993 Combining ability studies in mung bean (*Vigna radiata* (L.) Wilczek). Indian Journal of Genetics and Plant breeding. 53(4): 395-398.

Turner J H 1953 A study of heterosis in upland cotton. II. Combining ability and inbreeding effects. Agronomy Journal 45: 487-490.

Tushar Tanna 2002 Quality considerations for export of Oilseeds. pp. 347-354 **In** Oilseeds and Oils: Research and Development Needs (ed Rai Mangala, Singh Harvir and Hegde D M) . Indian Society of Oil seeds Research, Hyderabad.

Udayakumar M Sheshashayee M S Nataraj K N Bindu Madhava H Devendra R Aftab Hussain I S and Prasad T G 1998. Why has breeding for water-use efficiency not been successful? An analysis and alternate approach to exploit this trait for crop improvement. Current Science 74: 994-1000.

Uddin M J Chowdhury M A Z Sultan M K Mitra B N 1995 Genetic variability, correlation and path analysis in groundnut (*Arachis hypogaea* Linn.) Bangladesh Journal of Scientific and Industrial Research 30: 2-3.

Upadhyaya H D Gopal K Nadaj H L and Vijayakumar S 1992 Combining ability studies for yield and its components in groundnut. Indian Journal of Genetics and Plant Breeding 52: 1-6.

Upadhyaya H D Nigam S N Mehan V K and Lenne J M 1997 Aflatoxin contamination of groundnut-prospects of a genetic solution through conventional breeding. pp. 81-85 **In** Aflatoxin contamination problems in groundnut in Asia (ed Mehan V K and Gowda C L L): Proceedings of the First Working Group Meeting, 27-29 May 1996, Ministry of Agriculture and Rural Development, Hanoi, Vietnam, and ICRISAT, Patancheru.

Upadhayaya H D Nigam S N Mehan V K Reddy A G S and Yellaiah N 2001 Registration of *Aspergillus flavus* seed infection resistant peanut germplasm ICGV 91278, ICGV 91283, and ICGV 91284. Crop Science 41: 559-600.

Ursal C K Jadhav A S and Bachehhav S M 1995 Correlation and path coefficient analysis in groundnut. Journal of Maharashtra Agricultural University. 20: 120-121.

Utomo S D Anderson W F Wynne J C Beute M K Hagler Jr and Payne G A 1990 Estimates of heritability and correlation among three mechanisms of resistance to *Asperigillus Parasiticus* in peanut. pp. 26 **In** Proceeding of American Peanut Research and Education Society Inc.

Vaddoria M A and Patel V J 1990 Genetic variability in Virginia runner groundnut (*Arachis hypogaea* L.). Journal of Oilseeds Research 7: 130-132.

Van Egmond H P 1989 Current situation on regulations for mycotoxins. Overview of tolerances and Status of standard methods of sampling and analysis. Food additives and contaminants 6(2): 139-188.

Vanisree G 1992 Analysis of breeding potential of certain induced mutants of groundnut (*Arachis hypogaea* L.) for canopy and reproductive attributes. Ph. D Thesis, Andhra Pradesh Agricultural University, Hyderabad, India.

Varisai Muhammad, Ramanathan S and Ramachandran T 1973 Variation in morphological characters of *Arachis hypogaea* L. Madras Argicultural Journal 60 (9/12): 1373-1379.

Vasanthi R P and Raja Reddy C 2002 Variability studies in F_2 populations of five groundnut crosses involving foliar disease resistant genotypes. Journal of Research APAU 30: 137-42.

Vasanthi R P Babitha M Sudhakar P Reddy P V and John K 2004 Heritability studies for water use efficiency traits in groundnut (*Arachis hypogaea* L.). pp.19-23 **In** Proceedings of National Seminar on Physiological Interventions for Improved Crop Productivity and Quality: Opportunities and Constraints (ed Reddy P V Rao J S P Reddy K B Sudhakar P Rama Rao G Babitha M Latha P and Jyotsna M K). Plant physiology club (APAU) and Indian society for plant physiology, New Delhi.

Velu G Gopalakrishnan S 1985 Habitual and varietal variation in yield, harvest index and quality characteristics of groundnut. Madras Agricultural Journal 72(9): 518-521.

Venkataramanamma N P Eswara Reddy N P Sudhakar P Harinath Naidu R and Chalam T V 2004 Screening of groundnut genotypes for low aflatoxin production. pp. 53-56. **In** Proceedings of National Seminar on Physiological Interventions for Improved Crop Productivity and Quality: Opportunities and Constraints (ed Reddy P V Rao J S P Reddy K B Sudhakar P Rama Rao G Babitha M Latha P and Jyotsna M K). Plant physiology club (APAU) and Indian society for plant physiology, New Delhi.

Venkataravana P Sheriff R A Kulkarni R S Shankaranarayana V and Fathima P S 2000 Genetic divergence in groundnut (*Arachis hypogaea* L.). Mysore Journal of Agricultural Science 34: 321-325.

Venkataravana P Sheriff R A Kulkarni R S Shankaranarayana V and Fathima P S 2000a Correlation and path analysis in groundnut (*Arachis hypogaea* L.). Mysore Journal of Agricultural Science 34: 125-129.

Venkateswarlu O, Reddi M V Reddy K R and Reddy G L K 1991 Character association in groundnut (*Arachis hypogaea* L.). The Andhra Agriculture Journal 38: 257-260.

Verma R J Mehta D N Raval P J and Dube H C 1997 Aflatoxin contamination in oil seeds, oil cakes and oil samples. Indian Phytopathology 50: 77-82.

Vijayasekhar C 2002 Genetic divergence studies through D^2 statistic and isozyme analysis in Spanish bunch groundnut (*Arachis hypogaea* L.). Thesis M.Sc.(Ag.) ANGRAU, Hyderabad.

Vindhiya Varman P 2000 Combining ability estimates in groundnut (*Arachis hypogaea* L.). Madras Agricutural Journal 87 (7-9): 462-466.

Vindhiya Varman P and Raveendran T S 1994. Line X Tester analysis of combining ability in groundnut. Madras Agricultual Journal 81: 529-532.

Vindhiya Varman P and Raveendran T S 1996 Analysis of genetic divergence in groundnut cross combinations. Madras Agricultural Journal 83(12): 787-789.

Vindhiya Varman P and Raveendran T S 1996a Genetic variability and causal relationships in groundnut. Madras Agricultural Journal 83(12): 784-786.

Vindhiya Varman P and Senthil N 1998 Combining ability in inter-subspecific crosses in groundnut. Annals of Agricultural Research 19(2): 229-230.

Vindhiya Varman P Manoharan V and Parthasarathy R 1990 Studies on gene action in groundnut (*Arachis hypogaea* L.). Madras Agricultural Journal 77: 571-573.

Waliar F 1997 An over view of research on the management of aflatoxin contamination of groundnut. pp. 13-17 **In** Aflatoxin contamination problems in groundnut in Asia: Proceedings of first Asia working group meeting 27-29th May 1996 ICRISAT, India.

Waliyar F and Bockeiee-Mor Van A 1989 Resistance of groundnut varieties to *A. flavus* infection. pp. 305-310 **In** Aflatoxin contamination of groundnut (ed Mc Donald D and Mehan V K). Proceedings of the international workshop ICRISAT, India.

Waliyar F Ba A Haesn H Bonkoungou S and Bose J P 1994 Sources of resistance to *A. flavus* and aflatoxin contamination in groundnut in West Africa. Plant Disease 78: 704-708.

Wells R Bi T Anderson W F and Wynne J C 1991 Peanut yield as a result of fifty years of breeding. Agronomy Journal 83: 957-961.

*Wilks S S 1932 Certain generalization in the analysis of variance. Biometrics 24: 471.

Will M E Holbrook C C and Wilson D M 1994 Evaluation of field inoculation techniques for screening peanut genotypes for reaction to pre-harvest *A. flavus* group infection and aflatoxin contamination. Peanut Science 21: 122-125.

*Williams J H Wilson J H H and Bate G C 1975 The growth and development of four groundnut (*Arachis hypogaea*) cultivars in Rhodesia. Rhodesian Journal of. Agricultural Research. 13: 131-144.

Wright G C and Hammer G L 1994 Distribution of nitrogen and radiatin use efficiency in peanut canopies. Australian Journal of Agricultural Research 45: 565-574.

Wright G C Nageswara Rao R C and Farquhar G D 1994 Water-use efficiency and carbon isotope discrimination in peanut under water deficit conditions. Crop Science 34: 92-97.

Wright G C, Hubick K T and Farquhar G D 1991 Physiological analysis of peanut cultivar response to timing and duration of drought stress. Australian Journal of Agriculture Research 42: 453-470.

Wright S 1921 Correlation and Causation. Journal of Agricultural Research 20: 557-585.

Wynne J C Emery D A and Rice P W 1970 Combining ability estimates in *Arachis hypogaea* L. II Field performance of F_1 hybrids. Crop Science 10: 713-715.

*ZafarIqbal HamidullahShah SajidaPerveen Habibullah and Saleemullah 2004 Aflatoxin content of cereals and nuts inoculated by *Aspergillus flavus* in response to their proximate composition. Sarhad Journal of Agriculture 20(1): 153-156.

* Original not seen.

APPENDICES

Appendix A: Ancillary data

S.No	Genotypes	No. primary branches per plant	No. secondary branches per plant	Plant height (cm)	Days to maturity	Haulms yield per plant (g)	Seed colonization percentage	Seed volume (cc)	Three or more seeded pods
1	ICG 50	5	0	37.6	111	32.50	50	0.73	P (>50%)
2	ICG 1326	5	7	32.7	110	30.17	20	0.37	A
3	ICG 1416	6	0	37.5	112	30.67	30	0.67	P
4	ICG 2184	5	0	40.7	110	35.00	30	0.47	A
5	ICG 2411	6	11	36.2	110	40.50	50	0.60	A
6	ICG 3245	4	4	35.3	109	30.83	60	0.43	A
7	ICG 3509	8	0	38.5	116	37.17	20	1.23	P
8	ICG 3542	11	3	38.4	110	34.17	0	0.43	P
9	ICG 3643	6	1	39.6	109	33.33	60	0.57	A
10	ICG 4749	7	0	38.1	111	36.67	40	0.63	A
11	ICG 4893	5	3	45.3	111	37.17	40	0.63	A
12	ICG 5502	5	0	31.4	112	35.50	70	0.70	P (>50%)
13	ICG 6690	9	6	32.3	113	37.17	30	0.77	A
14	ICG 7332	4	6	37.4	120	42.17	10	0.60	A
15	ICG 7633	5	0	33.1	109	31.67	30	0.77	P (>50%)
16	ICG 7637	6	5	23.7	123	33.67	40	0.60	P
17	ICG 7749	12	21	26.6	124	47.33	20	0.73	A
18	ICG 8325	9	7	34.6	114	35.50	30	1.50	A
19	ICG 8666	5	4	40.6	110	37.67	40	0.97	P
20	ICG 10352	6	3	34.9	109	30.50	30	0.60	A
21	ICG 11386	9	6	39.4	123	50.33	20	0.87	A
22	ICG 13938	8	9	26.7	113	36.50	30	0.53	A
23	ICGV 86031	10	0	28.1	115	32.33	20	0.63	A
24	ICGV 86552	12	10	32.3	120	37.67	40	0.97	A
25	ICGV 86564	12	20	26.3	122	44.83	30	1.30	P
26	ICGV 86584	7	16	30.4	123	50.83	20	0.90	A
27	ICGV 88448	9	0	29.2	112	33.83	70	0.83	A
28	ICGV 89214	9	11	37.2	123	39.17	20	1.03	A
29	ICGV 96234	7	0	34.4	112	35.17	60	0.60	A
30	ICGV 96235	4	0	30.3	117	36.17	20	1.13	A
31	ICGS 11	6	0	26.9	113	31.83	40	0.67	A
32	ICGS 21	10	0	32.6	115	39.50	20	0.60	A
33	BAU 13	13	10	28.5	125	48.83	20	1.10	A
34	TG 39	5	2	21.8	108	24.83	30	0.77	A
35	TG 40	4	0	19.3	101	25.50	40	0.97	P
36	TG 41	5	0	18.2	95	26.50	70	1.50	P
37	TG 42	5	0	29.4	95	23.67	90	1.20	P
38	TG 45	5	0	20.5	100	22.83	30	1.00	P (25%)
39	TG 49	6	2	22.2	96	24.00	70	0.93	P
40	M 13	6	7	34.6	125	42.67	10	1.10	A
41	JL 24	7	11	36.9	108	39.67	40	1.00	P
42	K 134	6	0	30.6	108	36.33	40	0.63	A
43	TPT 1	4	0	51.8	109	42.50	50	0.77	A
44	TPT 2	4	0	43.6	110	44.67	30	0.87	A
45	TPT 4	5	0	37.4	110	45.67	10	1.10	A
46	TCGS 29	4	0	44.9	109	41.17	30	0.77	A
47	TCGS 61	11	8	36.2	118	45.33	20	0.73	A
48	TCGS 91	12	13	36.2	114	47.33	0	0.67	A
49	TCGS 320	6	0	34.8	111	45.83	50	0.57	A
50	TCGS 407	6	4	24.7	113	37.83	20	0.70	A
51	TCGS 584	4	0	23.9	113	24.17	60	0.87	P
52	TCGS 596	7	0	34.3	112	46.00	20	1.07	A
53	TCGS 617	11	11	29.1	123	50.17	20	1.03	A
54	TCGS 634	9	7	30.1	111	47.67	50	1.03	A

P = Present A = Absent

Appendix B: Rainfall and soil temperatures during crop growth periods

Standard weeks	Rain fall in mm (rainy days)		Soil temperatures (^{o}c)	
	kharif, 2002	kharif, 2003	kharif, 2002	kharif, 2003
35 (27/8 - 2/9)	25.8 (2)	42.4 (3)	32.2	31.1
36 (3/9 -9/9)	32.6 (3)	0	32.1	31.7
37 (10/9 - 16/9)	54.2 (3)	33.5 (2)	32.4	33.0
38 (17/9 - 23/9)	64.4 (4)	40.2 (2)	30.5	31.3
39 (24/9 - 30/9)	0	45.6 (2)	33.3	32.1
40 (1/10 - 7/10)	10.2 (1)	6.5 (1)	34.6	30.4
41 (8/10 - 14/10)	56.0 (4)	0	31.0	33.8
42 (15/10 -21/10)	23.8 (2)	76.2 (2)	31.7	27.3
43 (22/10 - 28/10)	68.9 (3)	34.0 (2)	28.0	29.2
44 (29/10 - 4/11)	33.8 (3)	6.4 (1)	27.0	31.2
45 (5/11 - 11/11)	37.3 (4)	13.0 (1)	27.5	29.9
46 (12/11 - 18/11)	0	1.4	29.0	29.8
47 (19/11 - 25/11)	0	0	28.0	29.7
48 (26/11 - 2/12)	0	0	28.0	28.9
49 (3/12 - 9/12)	11.6 (1)	0	26.9	28.0
50 (10/12 - 16/12)	0	0	25.9	28.1
51 (17/12 - 23/12)	0	0	26.3	29.2
52 (24/12 - 31/12)	0	7.4 (1)	27.1	28.5