PATH ANALYSIS AND GENETIC DIVERSITY IN COWPEA
[*Vigna unguiculata* (L.) Walp.]

A thesis submitted to the

MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI-413 722, DIST: AHMEDNAGAR,
MAHARASHTRA , INDIA

by

UDDARAJU CHAITANYA

in partial fulfillment of the requirements for the degree of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY
(CYTOGENETICS AND PLANT BREEDING)

COLLEGE OF AGRICULTURE,
PUNE 411 005
(MAHARASHTRA)

2002

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I hereby declare that this thesis entitled **"Path analysis and genetic diversity in cowpea (*Vigna unguiculata* (L.) Walp.)"** or part there of has not been submitted by me or any other person to any other University or Institute for Degree or Diploma.

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Dated : 29/06/2002

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CERTIFICATE

This is to certify that the thesis entitled **"Path analysis and genetic diversity in cowpea (*Vigna unguiculata* (L.) Walp.)"**, submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar for the award of degree of MASTER OF SCIENCE (Agriculture) in Agricultural Botany (Cytogenetics and Plant Breeding), embodies the results of a piece of bona fide research work carried out by **Uddaraju Chaitanya** under my guidance and supervision, and that no part of the thesis has been submitted for any other Degree or Diploma.

The assistance and the help received during the course of this investigation have been acknowledged.

Place : Pune

Dated: 29/06/2002

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CERTIFICATE

This is to certify that the thesis entitled **"Path analysis and genetic diversity in cowpea (*Vigna unguiculata* (L.) Walp.)"**, in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE (Agriculture) in Agricultural Botany (Cytogenetics and Plant Breeding), embodies the results of a piece of bona fide research work carried out by Uddaraju Chaitanya under the guidance and supervision of Dr. P. A. Navale, Associate Professor of Agril. Botany, Department of Agricultural Botany, College of Agriculture, Pune-5 and that no part of the thesis has been submitted for any other Degree or Diploma.

The assistance and the help received during the course of this investigation have been acknowledged.

Place : Pune

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04 JUL 2002

(A.S. Jadhav)

ACKNOWLEDGEMENT

Words are inadequate to convey the depth of feelings of gratitude to Dr. P. A. Navale, Associate professor of Botany, College of Agriculture, Pune for the constant scientific guidance, encouragement and valuable suggestions during the tenure of my investigation and in the preparation of the manuscript. During the period of my research he equipped me with the power to observe critically and rationally all aspects of my study.

It is my privilege to record my sincere gratitude to Dr. H. B.Mungse, Professor of Botany, College of Agriculture, Pune for his valuable advice and encouragement during my research. My special thanks to Prof. Nimbalkar for his extensive help during statistical analysis and interpretation. I am also grateful to Prof. D.B.Lad for his valuable suggestions throughout my period of study.

I extend my thanks to all the teaching staff of the Department of Botany, College of Agriculture, Pune especially Prof. N.D.Bangar and Prof. Mukhekar for the kind co-operation rendered during my research work. I also extend my thanks to all the non-teaching staff who have helped me during my research.

I would be failing in my duties if I don't record a deep sense of appreciation for the wholehearted co-operation and assistance provided in the field by Mr. Kawale, Shri.Hari, Shri.Nerke, Shri.Dewede, Shri. Kalamkar, Shri.Sonawane, Shri.Ghole, Shri.Shankar, Shri.Bhira, Shri. Kakde, Shri.Tawekar and Shri.Gaikwad and Smt.Sawant, Smt.Sable, Smt.Shinde and Smt.Pasalkar.

I am grateful to my friends Minakshi, Lilly, Uday, Harshal, Kapil and Karna for the companionship and enthusiasm, which goaded me on to complete my work. I extend my thanks to all my seniors for their timely help and guidance.

I am totally indebted to my parents, without whose support M.Sc. would have been a distant dream.

Place: Pune

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Date : 29/06/2002

(U. Chaitanya)

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ABSTRACT

Path Analysis and Genetic Diversity in Cowpea (*Vigna unguiculata* (L.)Walp.)

by

UDDARAJU CHAITANYA

A candidate for the degree of

MASTER OF SCIENCE (AGRICULTURE)

MAHATMA PHULE KRISHI VIDYAPEETH, RAHURI

2002

RESEARCH GUIDE	:	**Dr. P. A. Navale**
DEPARTMENT	:	**Agricultural Botany**
MAJOR FIELD	:	**Cytogenetics and Plant Breeding**

The present investigation, "Path analysis and genetic diversity in cowpea (*Vigna unguiculata* (L.) Walp.)" was under taken to study the extent of genetic variability, heritability (b.s), genetic advance, correlation, path analysis and genetic divergence in 99 M_3 mutants of cowpea. The material was evaluated in randomized block design with 3 replications during *kharif*, 2001 at Botany farm, College of Agriculture, Pune. Observations were recorded for 12 characters viz., days to 50 per cent flowering, days to maturity, plant height, plant spread, number of branches per plant, pod length, number of pods per plant, number of seeds per plant, fresh and dry biomass, test weight and grain yield per plant at various stages of crop growth.

Significant treatment sum of squares were observed for days to 50 per cent flowering, pod length and test weight indicating substantial variability for these characters in the mutants. The parameters of genetic variability revealed high GCV values for test weight, dry biomass, number

of seeds per plant and fresh biomass. The highest PCV value was observed for dry biomass followed by number of seeds per plant, grain yield per plant and fresh biomass. The PCV values were higher than GCV values for all the traits, while the difference between PCV and GCV magnitudes was minimum for days to 50 per cent flowering.

Apart from the variability studies, the mutants were classified based on variety and doses of gamma irradiation. It revealed that the gamma radiations produced mutants with early flowering, increased number of pods, pod length, number of seeds per plant and grain yield per plant. However, radiations brought about reduced performance for days to maturity and biomass. The estimates of heritability (b.s.) and genetic advance were high for test weight, days to 50 per cent flowering and pod length.

Grain yield per plant exhibited significant positive correlation with test weight, number of seeds per plant, pod length, number of branches per plant and number of pods per plant. Path analysis revealed that number of seeds per plant had the maximum direct effect on grain yield followed by test weight, days to maturity and pod length.

The D^2 values ranged from 0.82 to 88.44 and a total of three clusters were formed with cluster I accommodating maximum 91 mutants followed by cluster II with 10 mutants and one mutant in cluster III. The cluster variances indicated that test weight was the major contributor towards divergence followed by days to 50 per cent flowering, number of pods per plant and pod length. The extent of divergence was not sufficient to suggest potent parents for exploiting heterosis. However, the mutants 231-25, 161-8, 24-1, 120-18, 782-1 and 96-12 were identified as the best performers and are recommended for multi location trials to assess their stability across environments.

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INTRODUCTION

1. INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.), an annual legume, is commonly referred to as Southern pea, Black eye pea, Crowder pea, *Lobia*, *Coupe*, *Frijole*, *Chavali* and *Allasandhalu*. It is chiefly used as a grain crop, as a vegetable, for animal fodder and as green manure crop. It is cultivated throughout the tropics and subtropics, covering Asia, Africa, Central and South America, as well as parts of southern Europe and the United States.

Cowpea belongs to the genus Vigna, family leguminosae, subfamily fabaceae and tribe phaseoleae and comprises of five subspecies. Vavilov (1951) considered Indian subcontinent as the primary center of origin for cultivated cowpea. However, Faris (1965) assembled evidences to show that of the 170 species of cowpea, 120 species are cultivated in Africa, 22 in India and South East Asia and few in America and Australia. These findings indicate that cowpea is of African origin.

Cowpea is a warm season, annual, herbaceous legume. Plant types are often categorized as erect, semi-erect, prostrate (trailing) or climbing. Good amount of variability has been reported in the species. Growth habit ranges from indeterminate to fairly determinate with the non-viny types tending to be more determinate. Cowpea is strongly tap rooted with adequate nodulation for nitrogen fixation. The plant produces trifoliate leaves, which are smooth, dull to shiny and rarely pubescent. Commonly, the terminal leaflet is longer and larger than the lateral leaflets.

Cowpea generally is day neutral and flowers are borne in multiple racemes on 8" to 20" flower stalks (peduncles) that arise from the leaf axils. Two or three pods per peduncle are common and often four or more pods are carried on a single peduncle. The presence of these long peduncles is a distinguishing feature of cowpea and this characteristic facilitates easy harvesting. Cowpea primarily is a self pollinated crop with a diploid chromosome number $2n = 2x = 22$.

Cowpea pods are smooth, 6 to 10" long, cylindrical and generally somewhat curved. Till the grain development stage the immature pods are used as a vegetable. Pod color may be distinctive, most commonly green, yellow or purple. As the seeds dry, pod color of the green and yellow types becomes tan or brown. The seed coat can be either smooth or wrinkled and of various colors including white, cream, green, buff, red, brown and black. Seed may also be speckled, mottled or blotchy. Seed shape is a major characteristic correlated with seed development in the pod. Seeds develop a kidney shape if not restricted within the pod and when restricted the seed becomes progressively more globular.

Cowpea is of major importance for the livelihood of millions of relatively poor people in under developed countries. It can be used at all stages of growth as a vegetable crop. The tender green leaves and pods are an important food source in Africa. The immature snapped pods are often mixed with other foods and consumed. Green cowpea seeds are boiled as a fresh vegetable or may be canned or frozen. Dry mature seeds are suitable for boiling and canning.

Cowpea seed is a nutritious component in the human diet, as well as a nutritious livestock feed. The protein in cowpea seed is rich in the amino acids, lysine and tryptophan, compared to cereal grains. However, it is deficient in methionine and cystine when compared to animal proteins. Therefore, cowpea seed is valued as a nutritional supplement to cereals and an extender of animal proteins. Cowpea may be used as green or dry fodder. It is also used as a green manure crop for its efficient nitrogen fixing ability (70-350 kg/ha/annum) even under stress conditions.

Table 1.1 Nutritive analysis of cowpea
(per 100 g of edible portion)

Moisture	84.6 g	Phosphorus	74 mg
Protein	4.3 g	Iron	2.5 mg
Fat	0.2 g	Vitamin A	941 I.U
Minerals	0.9 g	Riboflavin	0.09 mg
Fiber	2.0 g	Thiamine	0.07 mg
Carbohydrates	8.0 g	Nicotinic acid	0.9 mg
Calcium	80 mg	Vitamin C	13.0 mg

Aykroyd (1963)

In India cowpea is grown in central and peninsular regions. Agronomic measures are to be supplemented with genetic improvements in developing superior genotypes of cowpea with increased productivity and production. Plant breeding essentially involves improvement of existing genotypes, generation of new variability, selection of high yielding genotypes and identification of superior and diverse parents for hybridization. Induced mutations contribute primarily by creating new variability and in combination with hybridization aid in the development of high yielding cultivars.

Knowledge of genetic variability is very valuable in a planned breeding programme, since it helps in the choice of the best yield attributes either for selection or for hybridization. The PCV, GCV, genetic advance and heritability play an important role in improvement of existing cultivars and searching for superior genotypes.

Yield is a quantitative character and is affected by various components that are highly subjected to environmental variations. The knowledge on the association of yield components with yield forms a pre-requisite for making effective selection when two or more characters are simultaneously considered. The estimation of correlation coefficients enables to eliminate the characters with little or no importance during selection.

Correlation studies are helpful in determining the yield components but they don't provide an exact picture of the relative importance of direct and indirect influences of each of the component characters towards yield. Path coefficient analysis suggested by Dewey and Lu (1959) proves helpful, in partitioning the correlation coefficients into measures of direct and indirect effects of a set of independent variables on the dependent variable. If the correlation is due to direct effect it reflects true relationship and for improving yield such characters can be selected.

Genetic diversity in the crop plays an important role in the development of new cultivars. A method suggested by Mahalanobis (1936) known as "Mahalanobis D^2 Statistics" is widely used to estimate genetic diversity in the available germplasm. This technique measures the forces of differentiation at intracluster and intercluster levels and helps in the selection of genetically divergent parents for their exploitation in hybridization programme. The D^2 statistics also measures the degree of diversification and determines the relative proportion of each component character to the total divergence.

The presence of genetic variability is the primary requirement for improvement of existing genotypes and development of new high yielding cultivars. Mutation breeding is the most efficient method for generating new variability, which involves irradiation of seeds/seedlings with different physical mutagens or treatment with chemical mutagens.

Cowpea being a self pollinated crop, the natural variability for yield and its component characters is narrow. Pillai (2001) treated three varieties of cowpea viz., (i) No. 889, (ii) Sangavi local and (iii) GC 10 with gamma radiations of 15, 25 and 35 KR doses at BARC, Mumbai. The M_1

generation was raised during summer 2000 and about 350 single plant selections were evaluated in replicated trials during *kharif,* 2000. In the M_2 generation studies, Pillai (2001) reported presence of good amount of variability for various qualitative and quantitative characters. Therefore, it is felt necessary to study the genetic diversity among the M_3 lines and classify them into definite clusters. Thus to assess the spectrum of variability for various quantitative characters and genetic diversity among the mutants, the present investigation was carried out with the following objectives.

1. To measure the direct and indirect contribution of various characters to yield in M_3 lines of cowpea.

2. To measure the genetic divergence among different M_3 lines.

3. To group these lines into suitable clusters and study the inter and intra cluster variations.

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REVIEW OF
LITERATURE

2. REVIEW OF LITERATURE

In the present chapter attempts have been made to review the relevant and available literature on the variability, heritability, correlation, path analysis and diversity studies in cowpea. The literature collected is reviewed under the following heads.

1. Genetic variability
2. Heritability and genetic advance
3. Correlation and path analysis
4. Genetic diversity

2.1 Genetic variability

Genetic variability is very important as it serves as a basis for crop improvement programmes. Johannsen (1909) was the first to demonstrate the distinction between genotype and phenotype. Nilsson - Ehle (1908) and East (1916) gave the concept of Multiple Factor Hypothesis to prove inheritance of quantitative characters. All these discoveries led to the fact that variability is due to the interaction between genotype and environment (Fisher, 1930). Charles and Smith (1939) and Power *et al.* (1950) partitioned total variance into genotypic and phenotypic variances by using estimates of environmental variance from non-segregating population. The statistical methods employed to calculate the genetic component of variance were given by Frankel (1947), Burton (1952) and Panse and Sukhatme (1985).

Ramchandran *et al.* (1980) while studying ten polygenic characters of eight cowpea varieties reported high GCV values for yield per plot followed by pod number per plant and internode length. Variation in varietal means was reasonably large for number of days to first harvest, internode length, weight of ten pods, seed number per pod, pod number per plant and yield per plant. Pandita *et al.* (1982) while studying yield components in 40 cowpea varieties observed significant variation for yield per plant, days to flowering and plant height. The highest PCV and GCV values were recorded for yield per plant.

Lawhale (1982) induced genetic variability by irradiating cowpea variety C 152 with gamma radiations and studied the quantitative characters in M_3 generation. The plant height increased in 47 per cent of the progenies while number of branches increased in 33 per cent of the progenies.

Chikkadyavaiah (1985) while studying grain yield per plant and other traits in 117 exotic and 207 indigenous genotypes of cowpea observed good amount of variability for plant spread in *kharif* season and for plant height in summer season. Choulwar and Borikar (1986) studied nine traits in M_3 mutants of cowpea and reported adequate variability in the mutants. High estimates of PCV and GCV were observed for yield per plant. The 100 grain weight was less influenced by gamma rays. Patil and Baviskar (1987) reported the highest GCV and PCV values for pod clusters per plant followed by pods per plant, seed yield per plant and 100 seed weight. Sharma *et al.* (1988) while studying 35 genotypes of cowpea observed maximum GCV for dry biomass followed by plant height, green fodder yield, pods per plant and seed weight.

Roquib and Patnaik (1990) while studying 25 cowpea genotypes for fodder yield and other traits reported the highest phenotypic and genotypic variances for plant height followed by green fodder yield and terminal leaf area. The GCV values were higher for plant height, lateral leaflet area, and days to 50 per cent flowering. Sinha and Bharati (1990) during their variability studies in M_3 mutants of urdbean reported high PCV and GCV values for plant height and low for pod length. Sarma and Talukdar (1991) while studying genetic diversity in M_7 mutants of mungbean reported high GCV values for number of primary branches number of pods per cluster, number of clusters per plant and seed yield per plant. The PCV values were high for number of primary branches and seed yield per plant. Thaware *et al.* (1992) evaluated 30 cowpea genotypes for seven yield components and recorded high genotypic and phenotypic variances for plant height, number of leaves per plant, leaf weight and stem weight. The phenotypic coefficients of variation were however higher than genotypic coefficients.

Sawant (1994) evaluated ten varieties and 45 crosses of cowpea for seed yield and reported high PCV and GCV for plant height, seed yield per plant, pods per plant, inflorescence per plant and 100 seed weight. Ariyo (1995) while studying 26 genotypes of cowpea reported the highest PCV and GCV for seed yield and the lowest values for days to 50 per cent flowering.

Sreekumar *et al.* (1996) studied genetic variability in vegetable cowpea and reported high values of GCV and PCV for pod length and number of seeds per pod. Backiyarani and Nadarajan (1996) while studying 34 cowpea genotypes for yield related characters observed high GCV and PCV for leaf area index, number of pods per plant, number of clusters per plant and 100 seed weight. Sharma and Mishra (1997 b) during their studies on genetic variability for biomass accumulation in cowpea observed high GCV values for dry pod weight at 60 and 80 days after sowing.

Kalaiyarasi and Palanisamy (1998) on their variability studies in F_3 and F_4 generations of cowpea reported high PCV and GCV values for number of pods per plant and seed yield per plant. Vardhan and Savithramma (1998 a) reported high genotypic and phenotypic coefficient of variation for plant height, number of primary branches, secondary branches, seed yield per plant and green pod yield in 102 accessions of cowpea. Vardhan and Savithramma (1998 b) while studying, variability among 29 accessions of cowpea observed high PCV and GCV for green pod yield, pods per plant, plant height and number of secondary branches, suggesting that these traits may be improved through individual plant selection.

Khan *et al.* (1999) while studying M_3 mutants in green gram reported high GCV for number of fertile branches, number of pods and total plant yield and suggested further improvement of these quantitative traits in subsequent generations. Sharma (1999) derived data from 42 diverse genotypes of cowpea on eight yield related traits and observed highest genotypic coefficient of variation for plant height. Tyagi *et al.* (2000) observed adequate variability among 24 genotypes of cowpea. High PCV and GCV were observed for plant height, seed yield per plant, days to maturity and days to 50 per cent flowering. Nehru and Manjunath (2001) while studying variability among 14 genotypes of cowpea observed significant differences in all the traits studied. High estimates of PCV and GCV were observed for number of pods per plant, plant height and 100 seed weight. Singh *et al.* (2001) recorded maximum genetic variability by induced mutations in green gram for yield per plant followed by number of pods per plant and seeds per pod. The genetic parameters showed high values for PCV and GCV for number of pods per plant, number of seeds per pod and plant yield.

2.2 Heritability and genetic advance

Heritability is the relative role of heredity in the expression of phenotypes (Falconer, 1989 and Allard, 1961). Heritability is a good index of transmission of quantitative characters from parents to their offspring (Falconer, 1989). More specifically it could also be defined as the proportion of total variability that is due to genetic causes. Lush (1949) classified heritability into broad sense and narrow sense heritability.

Improvement in the mean genotypic value of selected plants over parental population is known as genetic advance. The genetic advance is the product of heritability, phenotypic standard deviation and selection differential (Burton and Devene, 1953). Robinson (1966) classified heritability estimates into 3 categories viz., low (5 to 10%), medium (10 to 30 per cent) and high (30 percent and above). Heritability and genetic advance are important selection parameters in crop improvement programme.

Ramchandran *et al.* (1980) while studying ten polygenic traits in eight varieties of cowpea reported high estimates of heritability for days to flowering and high genetic advance for number of seeds per pod. Radhakrishnan and Jebaraj (1982) while evaluating 16 varieties of cowpea for 9 yield related traits observed high heritability for all the traits studied. Pandita *et al.* (1982) observed high genetic advance coupled with high heritability for yield per plant in cowpea. Jana *et al.* (1983) revealed highest estimates of heritability (b.s.) for 1000 grain weight in cowpea. Chikkadyavaiah (1985) reported high estimates of heritability and genetic advance for plant height in both *kharif* and summer seasons.

Choulwar and Borikar (1986) studied nine traits in M_3 mutants of 3 parental lines and reported high heritability and genetic advance for yield per plant in mutants (10 KR) compared to control. Apte *et al.* (1987) studied ten yield related traits in 50 genotypes of cowpea and observed high estimates of heritability for 100 seed weight, seeds per pod and days to maturity. The genetic gain was the highest for 100 seed weight followed by plant height, branches per plant and seeds per pod. Sharma *et al.* (1988) observed high estimates of heritability in cowpea for green pod yield (46.9 %) and days to maturity (90.0 %).

Dharmalingam and Kadambavanasundaram (1989) in heritability studies for seed yield and other seven yield related characters from 40 genotypes of cowpea revealed high estimates of heritability (b.s.) for pod length (87.37 %), 100 seed weight (85.38 %) and harvest index (69.58 %). Thiyagarajan and Natarajan (1989) reported high estimates of heritability and genetic advance for plant height, number of seeds per pod and 100 seed weight in cowpea.

Roquib and Patnaik (1990) reported high estimates of heritability for plant height, seed number per plant, pods per primary branches, pod length, pod breadth, days to 50 per cent flowering, days to maturity and seed yield per plant. All these traits except pod breadth showed high genetic advance. Sinha and Bharati (1990) studied M_4 mutants of urdbean and revealed high estimates of heritability for plant height while genetic gain was maximum for number of branches per plant followed by plant height and pods per plant.

Sarma and Talukdar (1991) while studying variability in micromutants of green gram reported high estimates of heritability for primary branches, pods per cluster and number of clusters per plant. All these traits also recorded high genetic advance. Thus simple selections for these traits will be rewarding. Thaware *et al.* (1991) obtained high estimates of heritability and genetic advance for green forage, leaf yield and leaves per plant in 80 genotypes of cowpea. Thaware *et al.* (1992) while evaluating 30 genotypes of cowpea for seven yield components reported heritability in the range of 50.2 % (branches per plant) and 77.9 % (stem weight),

Damarany (1994) observed in 15 genotypes of cowpea that broad sense heritability was the highest in seed weight per plant (94.4 %) followed by number of pods per plant (85.9 %) and 100 seed weight (83.3 %). Sawant (1994) while studying ten varieties and 45 crosses in cowpea reported high heritability and high genetic advance for plant height, inflorescence per plant, pods per plant and 100 seed weight.

Rewale *et al.* (1995) observed in 70 diverse cowpea genotypes that estimates of heritability and genetic gain were high for 100 seed weight, plant height and harvest index.

Sreekumar *et al.* (1996) observed high heritability and genetic advance for pod length and seeds per pod. High heritability with low genetic advance was observed for days to flowering and days to harvesting in 18 cowpea cultivars. Backiyarani and Nadarajan (1996) reported in 34 cowpea cultivars that high heritability coupled with high genetic advance was observed for 100 seed weight, harvest index and yield per plant suggesting additive gene effects. Sharma and Mishra (1997 b) while studying biomass accumulation in 42 indigenous and exotic strains of cowpea observed high estimates of heritability and genetic advance for dry pod weight at 60 and 80 days after sowing.

Kalaiyarasi and Palanisamy (1998) observed high heritability coupled with high genetic advance for number of pods per plant, number of seeds per plant, crude fibre content and seed yield per plant in F_3 and F_4 generations. Rangaiah and Nehru (1998) with their studies on genetic variability in F_2 segregating populations of two cowpea crosses revealed the highest broad sense heritability for number of pods per plant, pod length, pod weight and total seed weight in both crosses. However, high genetic advance with high heritability was found for pod length in one cross only. Gunasekaran *et al.* (1998) studied induced polygenic mutations in cowpea and reported high heritability and high genetic advance (as percentage of mean) for days to 50 per cent flowering, plant height, clusters per plant, seeds per pod and seed yield per plant in the M_2 progeny. Vardhan and Savithramma (1998 a) reported high heritability and genetic advance for plant height, number of primary branches, number of secondary branches, seed yield per plant and green pod yield. Vardhan and Savithramma (1998 b) reported high heritability and genetic advance for green pod yield, pods per plant, plant height and number of secondary branches per plant in 29 cowpea strains.

Khan *et al.* (1999) while studying M_3 mutants in green gram observed high heritability and genetic advance for number of fertile branches, number of pods and total plant yield. Sharma (1999) observed high genetic advance coupled with high heritability for plant height among 42 diverse genotypes of cowpea. Tyagi *et al.* (2000) reported high estimates of heritability and genetic advance among 24 diverse genotypes of cowpea for days to 50 per cent flowering, plant height, seed yield per plant and days to maturity indicating additive gene action. Nehru and Manjunath (2001) while evaluating 14 genotypes of cowpea reported high genetic advance coupled with high heritability for number of pods per plant, plant height, primary branches per plant, clusters per plant, pod length, seeds per pod and 100 seed weight. However, seed yield recorded moderate genetic advance due to low PCV and moderate heritability. Singh *et al.* (2001) while studying induced variability in mungbean reported high estimates of genetic advance along with heritability (b.s.) for characters like number of pods per plant, seeds per pod and yield per plant. The high estimates of genetic advance coupled with high heritability suggest that further improvement is likely to be effective in this variety through induced mutations.

2.3 Correlation and path analysis

Estimates of correlation coefficient are the measures of association between characters and provide the basic information in identifying characters that have little or no importance in the selection programme. Robinson *et al.* (1951) observed that the correlation estimates are of potential importance, since selection is usually concerned with changing two or more traits simultaneously. Path analysis provides estimates for direct and indirect causes of yield (Wright, 1921). Dewey and Lu (1959) used correlation coefficient for the first time in plants for path analysis.

Dumbre *et al.* (1982) studied 24 cultivars of cowpea and revealed that plant height and numbers of pods per plant were significantly correlated with yield at both phenotypic and genotypic levels, while days to 50 per cent flowering and days to maturity did not show any significant association with yield. Singh *et al.* (1982) reported that plant height, number of pods per plant and number of seeds per pod were significantly and positively correlated with seed yield in cowpea. Jana *et al.* (1983) by path coefficient analysis in cowpea revealed that number of pods per plant exhibited the highest magnitude of direct effect on seed yield. Kumar *et al.* (1983) while studying correlation among seed and herbage yield per plot and other related characters in cowpea revealed that pods per peduncle, pod length, pod girth, peduncle length and days to maturity were positively and significantly correlated with seed yield and selection for these traits will be rewarding.

Chikkadyavaiah (1985) observed that seed yield was positively correlated with total number of branches per plant, fruiting branches per plant, pods per plant, number of seeds per pod and 100 seed weight in both *kharif* and summer seasons. However, path analysis revealed that plant spread, pods per plant and seeds per pod had direct effect on seed yield. Choulwar and Borikar (1985) while studying seven traits in 16 mutants along with three parental lines of cowpea showed that seed yield per plant had the greatest direct effect on harvest index. Number of seeds per pod and pod length had the greatest direct effect on seed yield and also seed yield per plant and harvest index were significantly correlated.

Natarajaratnam *et al.* (1986) while studying phenotypic correlation coefficients in cowpea for yield and other traits reported that seed yield was strongly associated with pod length and plant height. Path coefficient analysis indicated that pod weight per plant had the highest direct effect on seed yield. Patil and Bhapkar (1987 a) observed seed yield to be positively correlated with number of pods per plant and seeds per pod, which in turn were negatively correlated with each other. They suggested yield improvement by selection for pods per plant, seeds per pod and 100 seed weight.

Sharma *et al.* (1988) reported that green forage yield was positively and significantly correlated with days to first flowering, plant height, pods per plant and seeds per pod. However, seed yield was positively and significantly correlated with pods per plant, seeds per pod, days to first flowering and days to maturity. Tyagi and Koranne (1988) while studying 22 genotypes of cowpea for yield per plant and five other yield related traits observed that number of branches per plant and seeds per pod were positively and significantly correlated with yield per plant. Seed number per pod had the highest direct effect on yield per plant.

Jindal (1989) evaluated 39 lines for seven characters in *Vigna unguiculata* and by path analysis reported that branches per plant was a major component in breeding for fodder yield. Patil *et al.* (1989) reported that grain yield was highly correlated with pods per plant (0.89), 100 grain weight, cluster per plant, pod length and days to 50 per cent flowering. Path analysis indicated that pods per plant, 100 grain weight and seeds per pod had the greatest positive direct effect on yield. Tewari and Gautam (1989) observed high and positive correlation of primary branches per plant, pods per cluster, cluster per plant, 100 seed weight and seeds per pod with green pod yield in cowpea.

Patnaik and Roquib (1990) in path coefficient analysis using 25 genotypes of cowpea recommended direct selection for days to 50 per cent flowering, days to maturity and seed number per plant to improve yields. Roquib and Patnaik (1990) in phenotypic and genotypic path coefficient analysis recommended that green forage and dry matter yield may be improved by selecting for plant height, lateral and terminal leaflet area, leaf stem ratio and root nodules at 30 and 65 days after sowing. Thaware *et al.* (1991) while studying 80 genotypes of cowpea for seven components of yield observed that stem yield and forage yield were the most highly correlated components. Siddique and Gupta (1991) evaluated 50 diverse genotypes of cowpea for yield and eight other traits and found significant correlation of days to 50 per cent flowering, days to maturity, number of clusters per plant and number of pods per plant with seed yield per plant.

Sarma *et al.* (1992) association studies on 21 M_3 micromutants for seven traits reported positive association of seed yield with number of clusters per plant, number of pods per plant and number of seeds per pod. Thaware *et al.* (1992) studied path analysis in 30 genotypes of forage cowpea and indicated that stem weight had the highest positive direct effect on forage yield followed by leaf weight. Oseni *et al.* (1992) in studies on 36 diverse lines of cowpea obtained positive correlations between seed yield per plant and number of pods per plant ($r = 0.35$) and between days to flowering and seed yield ($r = 0.82$). Days to flowering had the greatest direct effect on seed yield followed by 100 seed weight. The major contributors to seed yield were days to flowering, 100 seed weight, days to pod filling and pod length.

Golasangi *et al.* (1992) while evaluating the F_2 generation in cowpea for twelve characters reported that pod yield per plant had the greatest direct effect on seed yield. Siddique and Gupta (1992) studied yield correlations in 50 genotypes of cowpea and reported that the most important yield contributing traits were pods per plant, 100 seed weight and seeds per pod. Altinbas and Sepetoglu (1993) while studying 75 accessions of cowpea observed that seed yield per plant was significantly correlated with pods per plant, seeds per pod, and branches per plant. The results of path analysis revealed that pods per plant was the most important yield component affecting seed yield per plant.

Damarany (1994) carried out association analysis in 15 genotypes for 13 characters in cowpea and observed that seed yield was positively correlated with number of pods, weight of pods, seeds per plant, plant height and number of branches per plant. Sawant (1994) while studying 10 varieties and 45 crosses of cowpea observed that seed yield per plant was significantly and positively correlated with branches per plant, flowers per plant, pods per plant, pod length, seeds per pod, 100 seed weight and harvest index. Path analysis revealed that pods per plant had the highest direct effect on seed yield followed by 100 seed weight, seeds per pod, days to 50 per cent flowering, flowers per plant, harvest index, plant height and pod length.

Mishra *et al.* (1994) observed positive correlation between leaf area, length, and diameter and pod weight with green pod yield per plant in cowpea. Path analysis revealed that pod length had the greatest direct effect on pod yield, while direct but negative effect was observed for number of leaves per plant and pod weight. Tamilselvam and Das (1994) while studying 40 hybrids (derived from 10 lines x 4 testers) observed that seed yield was positively correlated with plant height, number of branches, number of clusters, number of pods per plant, pod length, number of seeds per pod and 100 seed weight.

Murugan *et al.* (1995) while studying M_2 and M_3 mutants of cowpea reported high positive correlation of seed yield with number of clusters and number of pods. It was also observed that many non-significant correlations in M_2 were altered to significant correlations in M_3 generation. Mathur (1995) while studying genetic variability among F_2 progeny from 2 crosses reported the greatest variability for seed yield. He also observed correlation between seed yield and other yield contributing characters.

Arvindhan and Das (1995) studied nine fodder yield related traits in 14 lines, 3 testers and their 42 hybrids and observed that green fodder yield was significantly and positively associated with leaf area index, specific leaf weight, number of branches, dry matter yield, leaf stem ratio and crude protein content. Path analysis revealed that dry matter yield and leaf area index had the greatest direct effects on green fodder yield.

Naidu *et al.* (1996) while studying 73 cowpea genotypes reported that seed yield was consistently significantly and positively correlated with pods per plant, pod length and seeds per pod. Based on the association analysis, they revealed that number of pods per plant, pod length, seeds per pod and seed weight should be considered while formulating breeding programmes in cowpea. Ponmariammal and Vijendradas (1996) while studying six parents and their 30 F_1 progeny observed significant correlations of plant height, number of branches and dry matter with green fodder yield. Association analysis revealed direct effects of days to flowering, plant height, number of leaves, number of branches and leaf stem ratio on green fodder yield.

Hamid *et al.* (1996) reported significant positive correlation of seed yield with 100 grain weight and non-significant correlation with pods per plant and pod length. Path analysis revealed maximum direct effect of 100 grain weight and indirect influence via pod length on seed yield. Correlation studies by Sreekumar *et al.* (1996) in 18 cultivars of cowpea reported that yield of green pods was positively correlated with number of fruiting points per plant, pods per plant, pod length and seeds per pod. Gowda (1996) while evaluating 40 F_2 progenies of three cowpea crosses observed that yield was positively and significantly correlated with number of pods per plant, number of seeds per pod and 100 seed weight.

Kar *et al.* (1996) reported in ten *Vigna unguiculata* genotypes that pod yield was strongly associated with fibre percentage and seeds per pod.

Path analysis showed that the pod length and fibre content were the main determinants of pod yield. Golasangi *et al.* (1996) studied correlation between 12 quantitative characters of cowpea under two different spacing (45x10 cm and 45x30 cm) in F_2 generation. Seed yield showed significant positive association with number of pods per plant and pod length in normal spacing and under wider spacing seed yield was significantly and positively associated with number of pods per plant, pod yield per plant, length of pod and number of seeds per plant. Path analysis revealed direct effects of number of pods, clusters per plant and pod length on yield.

Sharma and Mishra (1997 a) while studying 42 cowpea genotypes of Indian and exotic origin reported high positive phenotypic correlation between grain yield and number of pods per peduncle (r = 0.68), seeds per pod (r = 0.50) and harvest index (r = 0.49). On the other hand, association of grain yield with days to 50 per cent flowering, days to pod formation and days to maturity was found to be negative at both genotypic and phenotypic levels. Singh and Singh (1997) observed that number of clusters per plant, number of seeds per pod and total biomass made the greatest direct contribution to seed yield. Parihar *et al.* (1997) observed significant and positive correlation of seed yield with clusters, flowers per plant, pods per plant, plant height, pod set, pod length, seeds per pod and 100 seed weight.

Rangaiah and Nehru (1998) while studying path analysis in F_2 segregating populations of two cowpea crosses reported positive correlation of seed weight with all the traits studied. The highest correlation was found for pod weight and number of pods per plant. Pod weight and number of pods per plant showed high direct effects for grain yield. Singh *et al.* (1998) by path coefficient analysis in 45 indigenous and exotic collections reported that grain yield per plant was positively and significantly associated with clusters per plant, pods per plant and total biomass per plant. Pods per plant and biomass recorded the highest direct

Table 4.1 Analysis of variance for 12 characters in M_3 mutants of cowpea

Sr.No	Character	Mean sum of squares		
		Replication (2)	Treatment (101)	Error (202)
1	Days to 50 % flowering	8.19	18.75*	6.76
2	Days to maturity	75.00	47.18	49.00
3	Plant height (cm)	1013.75*	146.43	125.16
4	Plant spread (cm)	410.36*	8.95	6.99
5	No.of branches per plant	5.93*	0.76	0.63
6	Pod length (cm)	1.72	5.73*	3.68
7	No. of pods per plant	1693.20*	63.99	53.48
8	No.of seeds per plant	119419.50*	9732.09	11370.73
9	Fresh biomass (g)	118101.00*	8603.91	7450.05
10	Dry biomass (g)	5916.97*	394.03	458.40
11	Test weight (g)	2.26	14.96*	1.29
12	Grain yield per plant (g)	1929.54*	150.82	138.18

*, ** Significant at 5 per cent and 1 per cent probability respectively.
Values in parenthesis indicate degrees of freedom

effects on grain yield. Vardhan and Savithramma (1998 a) while studying 102 accessions of cowpea reported significant positive association of green pod yield per plant with pod length, pod width, fresh pods per plant, biomass and harvest index. Vardhan and Savithramma (1998 b) reported high positive association of green pod yield with pods per plant. Green pods per plant, pod length, pod width and number of primary branches are major traits contributing to yield.

Borah and Khan (1999) reported in 60 genotypes of cowpea that green fodder yield was positively significantly correlated with number of leaves, leaflet width, days to 50 per cent flowering, dry matter yield, dry weight of leaves and dry weight of stem. Also the highest positive direct effect on fodder yield was exhibited by dry matter yield followed by leaf stem ratio and plant height.

Nagaraj and Savithramma (2000) by correlation and path coefficient analysis in F_2 generation of two crosses reported significant positive correlation of green pod yield with number of pods per plant and number of primary branches per plant. Number of pods per plant was an important yield determinant with high direct effect. Number of primary branches per plant exhibited high indirect effect via number of pods per plant in both the crosses. Tyagi *et al.* (2000) while studying genetic variability among 24 diverse genotypes of cowpea reported high significant positive correlation of seed yield per plant with days to 50 per cent flowering, plant height, pod length, number of pods per plant, seed weight per pod and 100 seed weight. High seed weight per pod (0.55), number of pods per plant (0.391), 100 seed weight (0.210) and days to maturity (0.191) had substantial direct effect on seed yield. Kalaiyarasi and Palanisamy (2000) by path analysis in F_4 population reported that protein content had high positive effect on seed yield while pod length and 100 seed weight had positive indirect effect on seed yield through number of pods per plant, number of seeds per pod and crude protein content.

2.4 Genetic diversity

The genetic differences between individuals or genetic stocks with respective individual traits or an array of traits is referred to as genetic diversity. The genetic diversity in a population is due to the inherent genetic variations present in the gene pool of the population. The knowledge of genetic divergence is best exploited in selecting parents for different hybridization programmes.

Mahalanobis (1928) described the concept of D^2 statistics as a quantitative tool for estimating genetic divergence between the populations. Mahalanobis *et al.* (1949) applied D^2 statistic in the statistical study of anthropometric data of Uttar Pradesh. Rao (1948) suggested a more flexible method, which would replace the measurement of large number of characters with relatively few measurements. Rao (1952) suggested the application of D^2 statistics to plant breeding for the assessment of genetic diversity. Moll *et al.* (1962) observed no relationship between geographical distribution and genetic diversity. Similar results were reported by Murthy and Arunachalam (1966).

Kumar *et al.* (1982) grouped 50 cowpea genotypes into seven clusters with the traits days to maturity, pod length, pod width and 100 grain weight contributing most for genetic divergence. The maximum inter cluster distance was observed between cluster III and IV indicating that crossing between genotypes of these clusters will be rewarding.

Jindal (1985) grouped 52 indigenous and exotic varieties of cowpea into eight clusters by studying genetic divergence of ten yield related traits. The clustering did not reflect the geographical origin of varieties. Chikkadyavaiah (1985) by studying genetic divergence of yield related traits grouped 207 indigenous and 117 exotic genotypes of cowpea into 23 clusters. Jindal and Gupta (1985) grouped 39 strains of cowpea into five clusters of which two clusters were monogenotypic. Of all the seven traits studied leaf number per plant and branch number per plant contributed most to the genetic divergence.

Marangappanavar (1986) by studying 46 genotypes of cowpea reported that 32 Indian genotypes were grouped into 13 clusters while 14 exotic varieties were grouped into 10 clusters. However, inter cluster patterns were not consistent with geographical distribution. Patil and Bhapkar (1987 b) grouped 28 indigenous and 21 exotic genotypes of cowpea into 16 clusters. The exotic genotypes were grouped into 6 clusters while the indigenous genotypes were distributed in 12 different clusters. Cluster IX (CO 1) and cluster XV (Russian giant) recorded the maximum genetic distance of 17.17 and were recommended as source of genetic divergence for breeding programme.

Thiyagarajan *et al.* (1988) grouped 12 hybrids of cowpea and their seven parents into seven clusters based on D^2 values, for ten characters. The characters days to 50 per cent flowering, 100 seed weight and plant height contributed most to the genetic divergence. Thiyagarajan and Natarajan (1989) used D^2 statistics and grouped 30 geographically diverse accessions of cowpea into four clusters. Number of pods per plant, number of seeds per pod and seed yield per plant made a large contribution to genetic divergence. Dharmalingam and Kadambavanasundaram (1989) grouped 40 genotypes of cowpea into 13 clusters by evaluating data on eight characters. The genotypes CO 2 and G 5 belonging to the most divergent clusters were recommended for heterosis breeding.

Sarma and Talukdar (1991) on the basis of D^2 values grouped 36 mutant lines of greengram into nine clusters. The important feature highlighted was that mutants from same parent were grouped under different clusters and likewise mutants from different parents were clustered together. The D^2 values revealed that the clusters I and IX were the most divergent. Renganayaki and Rangasamy (1991) evaluated 22 genotypes of mungbean, 20 genotypes of urdbean and 6 genotypes of cowpea. The genotypes of the three species not only resolved into distinct clusters, but also remained exclusive of other species. The characters 100 seed weight, pod length and seed yield contributed most towards genetic divergence. Sonawane and Patil (1991) by D^2 analysis grouped 47 indigenous and 17 exotic strains of cowpea into six clusters and inter cluster hybridization programme was suggested. Sarma *et al.* (1992) grouped 21 micromutants of greengram into eight distinct clusters. It was also observed that all high yielding micromutants fall in the clusters with shorter plant height.

Rewale *et al.* (1996) by D^2 statistics grouped 70 genotypes of cowpea into 19 clusters of which 11 clusters were monogenotypic. Days to flower initiation, days to 50 per cent flowering, days to maturity, number of inflorescence per plant, pods per plant, pod length, 100 seed weight, seed yield per plant and harvest index were major contributors to divergence. Genotypes from clusters XVII, XVI and III were recommended for hybridization.

Sharma and Mishra (1997 a) grouped 42 Indian and exotic genotypes of cowpea into 6 different clusters with days to 50 percent flowering, plant height, pods per peduncle and harvest index contributing maximum towards genetic divergence. The inter cluster average D^2 was maximum between strains of cluster III and VI and minimum between clusters I and II. Thaware *et al.* (1997) grouped 30 genotypes of forage cowpea into seven clusters based on D^2 analysis of seven quantitative traits. Number of branches and leaves per plant made maximum contribution towards divergence.

Vishwanathan *et al.* (1998) grouped 72 cowpea genotypes into 5 clusters with the highest inter cluster distance between clusters III and IV (2818.82). Out of the seven traits studied, 100 seed weight contributed maximum (33.5 %) to the divergence followed by days to maturity (27.25 %). Tyagi *et al.* (1999) grouped 24 early maturing cowpea genotypes into 3 clusters of which cluster I and II showed maximum inter cluster distance and recommended the genotypes in these clusters as parents in hybridization programme to develop early maturing varieties.

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MATERIAL AND METHODS

3. MATERIAL AND METHODS

The present investigation " Path analysis and genetic diversity in cowpea (*Vigna unguiculata* (L.) Walp.) was conducted during *kharif*, 2001 at Botany Farm, College of Agriculture, Pune. The details of the material used and methods followed are described in this chapter.

3.1 Material

Three varieties of Cowpea viz., (1) No. 889 (2) Sangavi local (3) GC 10 were treated with gamma radiations of 15, 25, 35 KR doses at Bhabha Atomic Research Centre, Mumbai in February, 2000. The M_1 was raised immediately during summer, 2000 and about 350 single plant selections of M_1 were evaluated in replicated trials during *kharif*, 2000 by Miss. P.S. Pillai (M.Sc. student). From the M_2 population of 7000 plants, 99 high yielding M_2 mutant plants and three parents were selected for the present investigation. The list of mutants, their original parents and dose of gamma radiation are given in Table 3.1.

3.2 Methods

3.2.1 Experimental design

In all 102 lines (99 mutants and 3 parents) were used to conduct the experiment. The experiment was conducted in randomized block design with three replications. Each entry was represented by single row of 4.5 m length with a spacing of 45 cm between rows and 15 cm between plants.

3.2.2 Sowing and cultural practices

The land was prepared by ploughing followed by two cross harrowings. The basal dose of 30 kg N, 45 kg P_2O_5 and 30 kg K_2O per

Table 3.1 List of cowpea mutants and their source

Sr.No	Variety	Dose (KR)	M_2 Plant number	M_2Yield per plant (g)
1	No. 889	10	11--1	47.00
2	No. 889	10	24--1	44.00
3	No. 889	10	8--1	43.80
4	No. 889	10	18--3	39.40
5	No. 889	10	28--7	35.80
6	No. 889	10	725--4	35.60
7	No. 889	10	13--1	35.50
8	No. 889	10	23--1	34.80
9	No. 889	10	12--7	34.40
10	No. 889	10	37--20	33.40
11	No. 889	10	25--7	33.10
12	No. 889	10	745--15	32.10
13	No. 889	10	6--7	31.80
14	No. 889	10	19--1	31.80
15	No. 889	10	6--2	31.60
16	No. 889	10	12--4	31.60
17	No. 889	10	25--10	31.20
18	No. 889	10	25--3	30.60
19	No. 889	10	22--13	30.10
20	No. 889	10	8--3	30.00
21	No. 889	10	20--6	30.00
22	No. 889	25	62--1	47.80
23	No. 889	25	776--10	40.80
24	No. 889	25	57--1	39.10
25	No. 889	25	78--1	38.20
26	No. 889	25	69--7	37.80
27	No. 889	25	40--5	37.70
28	No. 889	25	67--12	36.20
29	No. 889	25	76--2	35.50
30	No. 889	25	76--1	34.30
31	No. 889	25	43--1	33.80
32	No. 889	25	68--26	33.60
33	No. 889	25	782--1	31.50
34	No. 889	25	67--1	30.70
35	No. 889	25	58--3	30.40

Table 3.1 contd.....

Sr.No	Variety	Dose (KR)	M_2 Plant numbers	M_2Yield per plant (g)
36	No. 889	35	98--11	64.00
37	No. 889	35	101--8	61.50
38	No. 889	35	92--7	60.00
39	No. 889	35	96--9	57.00
40	No. 889	35	114--30	55.70
41	No. 889	35	673--3	54.10
42	No. 889	35	108--2	53.30
43	No. 889	35	101--28	52.00
44	No. 889	35	119--26	50.20
45	No. 889	35	18--14	50.00
46	No. 889	35	684--14	48.30
47	No. 889	35	97--5	47.80
48	No. 889	35	110--30	45.00
49	No. 889	35	96--12	44.80
50	No. 889	35	108--8	41.70
51	No. 889	35	108--5	41.10
52	No. 889	35	109--1	40.00
53	No. 889	35	108--2	39.80
54	No. 889	35	645--12	39.70
55	No. 889	35	96--7	38.40
56	No. 889	35	118--20	38.00
57	No. 889	35	683--6	37.40
58	No. 889	35	119--17	37.00
59	No. 889	35	105--22	36.30
60	No. 889	35	120--24	35.10
61	No. 889	35	121--18	35.70
62	No. 889	35	684--7	35.60
63	**No. 889**	**Parent**		**25.00**
64	No. 889	35	680--1	34.80
65	No. 889	35	98--2	34.40
66	No. 889	35	713--14	34.00
67	No. 889	35	113--18	34.00
68	No. 889	35	105--19	33.60
69	No. 889	35	691--18	33.40

Table 3.1 contd.....

Sr.No	Variety	Dose (KR)	M_2 Plant numbers	M_2Yield per plant (g)
70	No. 889	35	120--18	33.00
71	No. 889	35	116--28	32.70
72	No. 889	35	117--16	32.10
73	No. 889	35	89--1	31.50
74	No. 889	35	113--26	31.50
75	No. 889	35	121--24	31.40
76	No. 889	35	102--20	31.10
77	No. 889	35	118--4	31.00
78	No. 889	35	715--15	30.80
79	No. 889	35	121--5	30.60
80	No. 889	35	707--17	30.30
81	No. 889	35	117--18	30.10
82	No. 889	35	93--1	30.10
83	No. 889	35	107--16	30.00
84	No. 889	35	707--3	30.00
85	Sangavi local	10	161--8	38.70
86	Sangavi local	10	517--2	37.10
87	Sangavi local	25	231--25	44.00
88	Sangavi local	25	403--18	37.60
89	Sangavi local	25	199-27	34.50
90	Sangavi local	25	229--27	30.30
91	**Sangavi local**	**Parent**		**11.00**
92	Sangavi local	25	198--1	30.00
93	Sangavi local	35	282--12	42.10
94	Sangavi local	35	480--7	35.30
95	GC 10	10	308--6	42.50
96	**GC 10**	**Parent**		**12.00**
97	GC 10	10	599-1	37.20
98	GC 10	10	313--4	35.70
99	GC 10	10	320--8	32.00
100	GC 10	10	313--22	31.00
101	GC 10	25	624--1	42.40
102	GC 10	25	359--2	30.40

hectare was applied at the time of sowing in the form of Suphla (15:15:15) and SSP. The seeds were sown by dibbling on 29th June, 2001. The usual cultural practices like thinning, weeding, irrigation were suitable followed during entire period of crop growth. In order to protect the crop from Aphids two sprays of endosulphan were given at 0.2 % concentration at 30 days and 40 days after sowing. A spray of cypermethrin was undertaken to control leaf eating caterpillars and pod borers after 60 days of sowing.

3.2.3 Harvesting

The crop was harvested when majority of the pods in each of the line attained maturity.

3.2.4 Observations recorded

Following observations were recorded on five randomly selected plants from each treatment in each replication and averages were worked out.

3.2.4.1 Days to 50 per cent flowering

The number of days required from sowing to the day on which 50 per cent of the plants flowered was recorded as days to 50 per cent flowering.

3.2.4.2 Days to maturity

The number of days required from sowing to complete maturity were considered as days to maturity.

3.2.4.3 Plant height (cm)

Plant height was measured from ground level to the tip of the plant in centimeters at maturity on randomly selected plants.

3.2.4.4 Plant spread (cm)

Maximum spread of the plant was recorded at maturity on randomly selected plants.

3.2.4.5 Number of branches per plant

Total number of branches on each of the observational plants were counted and recorded at the time of harvest.

3.2.4.6 Pod length (cm)

The length of five pods on randomly selected observational plants were measured and the average pod length for each plant was worked out.

3.2.4.7 Number of pods per plant

The total number of mature pods present at harvesting were counted and recorded on randomly selected plants.

3.2.4.8 Number of seeds per plant

The harvested mature pods of each observational plant were threshed and total number of seeds were counted.

3.2.4.9 Fresh biomass (g)

The observational plants were uprooted at harvest and weighed to record the fresh biomass of the plants.

3.2.4.10 Dry biomass (g)

The observational plants after recording the fresh biomass were dried in the field for one week and the dry biomass was recorded.

3.2.4.11 Test weight (g)

Hundred seeds from each of the observational plant were counted and the average was taken as test weight of M_3 line.

3.2.4.12 Grain yield per plant (g)

The weight of seed of each of the five selected plants was recorded separately and average was worked out to give the grain yield per plant.

3.3 Statistical analysis

The mean values of five randomly selected observational plants for twelve different traits were used for statistical analysis. The following statistical measures/parameters were worked out for presentation of the data on different quantitative attributes.

3.3.1 Analysis of variance (ANOVA)

The analysis of variance was done as suggested by Panse and Sukhatme (1985) in the following form.

Source of variation	Degree of freedom	MSS	Expected mean sum of squares
Replication	r - 1	Mr	$\sigma e^2 + t\,\sigma^2 r$
Treatment	t - 1	Mt	$\sigma e^2 + r.\,\sigma^2 t$
Error	(r - 1) (t - 1)	Me	$\sigma^2 e$
Total	(rt - 1)	-	

Where,

r = number of replications

t = number of treatments

3.3.2 Genotypic coefficients of variation (GCV)

It was estimated as per the formula suggested by Burton (1952)

$$GCV = \sqrt{\sigma^2 g} \;/\; X \times 100$$

Where,

$\sigma^2 g$ = Genetic variance

X = General mean of the character

3.3.3 Phenotypic coefficient of variation (PCV)

It was estimated as per the formula suggested by Burton (1952).

$$PCV = \sqrt{\sigma^2 p} \;/\; X \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

X = General mean of the character

3.3.4 Heritability percentage

Heritability percentage in broad sense was calculated as per the formula given by Burton (1952).

$$h^2 \text{ (b.s.)} = Vg / Vp \times 100 \quad \text{or} \quad h^2 \text{ (b.s.)} = \sigma^2 g / \sigma^2 p \times 100$$

Where,

h^2 (b.s) = Heritability broad sense

$\sigma^2 g$ (Vg) = Genotypic variance

$\sigma^2 p$ (Vp) = Phenotypic variance

3.3.5 Genetic advance

Genetic advance was calculated by the formula given by Johnson *et al.* (1955).

$$G.A = K \times (\sigma^2 g / \sigma^2 p) \times \sigma p \quad \text{or} \quad G.A. = K \times h^2 \times \sigma p$$

Where,

K = Selection differential which is 2.06 at 5 per cent selection intensity

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

σp = Phenotypic standard deviation

3.3.6 Correlation

To understand the association among the characters, genotypic and phenotypic correlation coefficients were worked out by adopting method described by Singh and Chaudhary (1977).

3.3.6.1 Phenotypic correlation coefficients

$$rp = \text{Phenotypic covariance } (X . Y) \; / \sqrt{\text{Variance Xp . Variance Yp}}$$

Where,

rp = Phenotypic correlation coefficient between character X and Y

p = Phenotypic

3.3.6.2 Genotypic correlation coefficient

$$rg = \text{Genotypic covariance } (X . Y) \; / \sqrt{\text{Variance Xg. Variance Yg}}$$

Where,

rg = Genotypic correlation coefficient between character X and Y

g = Genotypic

Significance of correlation coefficients were tested by using 't' test (Panse and Sukhatme, 1985).

3.3.7 Path analysis

Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959). If y is the effect and X_1 is the cause, the path coefficient for the path from cause X_1 to the effect 'y' is $\sigma X_1/\sigma y$. Direct and indirect effects were worked out by using genotypic correlations as below

Direct effect of X_1 on $Y = PX_1 . Y$

Where,

PX_1 = Path coefficient of X_1 on Y.

Similarly, direct effects of other attributes on yield were worked out.

Indirect effect of X_1 via X_2 on Y = $PX_2Y \times r X_1X_2$

Where,

PX_2Y = Path coefficient of the component character X_2 on Y

$r X_1X_2$ = Genotypic correlation between X_1 and X_2

Similarly, indirect effects in all possible combinations were calculated for all component characters.

The residual effect (R) was calculated as below :

$$R = [1 - (PX_1Y . rX_1Y) - (PX_2Y . rX_2Y) .... (PX_nY . rX_nY)]^{1/2}$$

3.3.8 Mahalanobis generalized distance

The generalized distance between two populations is defined by Mahalanobis (1936) as :

$$D^2 = \lambda i.j.di.dj$$

Where,

$\lambda i.j$ = Reciprocal matrix to the common dispersion matrix

di = Difference between the mean values of two population for i^{th} character

dj = Difference between the mean values of two populations of j^{th} character

Estimation of D^2 values from the above formula is very complicated in the present study. Since it requires the inversion of the twelveth order determinant and then the evaluation of 12 (12+1) / 2 terms whose sum is D^2. It was found convenient to work with a set of uncorrelated characters constructed from the original measurements. D^2 with such transformed variable is reduced to the evaluation of simple sum of squares. Transformation was done by using pivotal condensation method (Singh and Choudhary, 1977). The coefficients for transformation were obtained by dividing the first row of the reduced matrix by the square root of corresponding pivotal condensation elements.

3.3.9 Determination of gene constellation

Tocher's method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for finding the cluster because a cluster is not a well defined term. The only criteria appears to be that any two groups belonging to the same cluster should at least on an average show a smaller D^2 than those belonging to the two different clusters. A simple device suggested by K.D. Tocher is to start with the two closely associated groups and find a third group which has the smallest D^2 from the two. Similarly, the fourth is chosen to have the smallest D^2 from the first three and so on. If at any stage the average D^2 of a group from those already listed appears to be high, then this group does not fit in the former groups and is therefore taken outside the former cluster. The groups of the first cluster are then omitted and the rest are treated similarly. It is also useful to calculate the change in average D^2 within a cluster due to inclusion of an additional group. If the changes are appreciable, then the newly added group has to be considered as outside the cluster.

3.3.10 Average intra and inter-cluster D^2 and D values

3.3.10.1 Average intra-cluster D^2

$$D^2 = \Sigma D_i^2/n$$

Where,

Di is the sum of distances between all possible combinations (n) of the population included in a cluster.

3.3.10.2 Average inter-cluster D^2

$$D^2 = \frac{\Sigma \text{ Distance between the population of cluster i and j}}{\text{ni. nj}}$$

Where,

ni = Number of populations in the cluster i

nj = Number of populations in cluster j

3.3.10.3 Cluster means

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included in that cluster.

3.3.11 Genetic diversity as an index for selecting desirable parents for hybridization

The possible limits to parental divergence within which there were reasonably high chances for occurrence of heterosis were calculated following Arunachalam and Bandopadhyay (1984). They advised to delineate the divergence among parents into four divergence classes. To take into account the variable magnitude of variation in parental divergence, the mean (m) and standard deviation(s) of the values of divergence were calculated. The divergence classes were defined as follows :

DC_1 = D > or = m + s

DC_2 = D < (m + s) and > or = m

DC_3 = D > or = (m - s) and < m

DC_4 = D < (m - s)

They postulated that two parents whose genetic divergence falls between (m - s) and (m + s), i.e. in the classes DC_2 and DC_3 when crossed have higher chances of producing high frequency and magnitude of heterosis when compared to a cross whose parental divergence fall outside the limits [(m - s), (m + s)].

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RESULTS

4. EXPERIMENTAL RESULTS

The experiment was undertaken to study the genetic variability, heritability, genetic advance, correlations, path analysis and genetic diversity studies in M_3 lines of cowpea during *kharif*, 2001. The observations were recorded on 12 yield and yield contributing characters at various stages of crop growth. The results obtained are described in this chapter.

4.1 Analysis of variance

The analysis of variance (Table 4.1) revealed significant treatment sum of squares for days to 50 per cent flowering, pod length and test weight indicating substantial variability for these traits.

4.2 Mean performance

The data on mean performance for 12 characters of mutant lines of cowpea are presented in Table 4.2

4.2.1 Days to 50 per cent flowering

The mutant 231-25 (50.33 days) was the earliest for days to 50 per cent flowering followed by 61-8, 24-1, 18-3 and 645-12. The mutant lines 6-7, 320-8, 6-2, 12-4 and 105-22 (all showing 62.67 days) were late for 50 per cent flowering. Out of the 24 mutants which showed earliness, seventeen (16.67 %) lines showed significantly early 50 per cent flowering over the population mean (56.85 days).

4.2.2 Days to maturity

The mutant 57-1 (93.33 days) was the earliest to mature followed by 96-9, 19-26, 118-20, 121-18, 161-8 and 231-25 (all showing 94 days). The mutants 25-7, 782-1, 110-30, 13-18 and 117-16 (all taking 99.33 days)

Table 4.1 Analysis of variance for 12 characters in M_3 mutants of cowpea

Sr.No	Character	Mean sum of squares		
		Replication (2)	Treatment (101)	Error (202)
1	Days to 50 % flowering	8.19	18.75*	6.76
2	Days to maturity	75.00	47.18	49.00
3	Plant height (cm)	1013.75*	146.43	125.16
4	Plant spread (cm)	410.36*	8.95	6.99
5	No.of branches per plant	5.93*	0.76	0.63
6	Pod length (cm)	1.72	5.73*	3.68
7	No. of pods per plant	1693.20*	63.99	53.48
8	No.of seeds per plant	119419.50*	9732.09	11370.73
9	Fresh biomass (g)	118101.00*	8603.91	7450.05
10	Dry biomass (g)	5916.97*	394.03	458.40
11	Test weight (g)	2.26	14.96*	1.29
12	Grain yield per plant (g)	1929.54*	150.82	138.18

*, ** Significant at 5 per cent and 1 per cent probability respectively.
Values in parenthesis indicate degrees of freedom

were late to mature. Among the 99 mutant lines 7 mutants showed early maturity than the population mean (94.49 days).

4.2.3 Plant height (cm)

The mutant 11-1 was the tallest having maximum height of 118 cm followed by 673-3 (112.20 cm) and 24-1 (109 cm). The mutant 161-8 was the shortest with only 79.67 cm height. From the 99 mutants studied 67 were taller than population mean (91.67cm) and 8 (7.84 %) of them were significantly taller than population mean.

4.2.4 Plant spread (cm)

The population mean for plant spread was 37.50 cm. The mutant 707-3 showed the highest plant spread of 42.42 cm followed by 69-7 (42.12 cm) and 118-20 (41.88 cm). However, the mutants 109-1 (34.1cm) and 98-2 (34.45 cm) were less spreading. Out of 99 mutants studied 75 (76 %) showed greater spread and 8 (8.08 %) of them were significantly higher than the population mean.

4.2.5 Number of branches per plant

The mutant 707-17 had maximum of 4.8 branches which is 38.5 per cent higher than the population mean. It was followed by 69-7 (4.6) and 24-1 (4.53). The mutants 624-1 (2.33), 599-1 and 320-8 (both 2.4) had minimum number of branches per plant. Forty two (42.4 %) mutants showed greater number of branches than population mean (3.39) of which 13 (13.13 %) mutants were significantly better than population mean.

4.2.6 Pod length (cm)

The population mean for this character was 16.07 cm, with a range of 11.89 (480-7) to 18.73 cm (62-1). The mutant 62-1 produced the longest pods of 18.73 cm (16.5 per cent increase in pod length) and was followed by 96-7 (18.54 cm), 8-1 (18.41 cm) and 76-2 (18.33 cm). However, the

Table 4.2 Mean performance of M_3 mutants of cowpea for different characters

Sr. No	Entry	Mutant	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No.of branches per plant	Pod length (cm)	No. of pods per plant	No.of seeds per plant	Fresh Biomass (g)	Dry Biomass (g)	Test weight (g)	Grain yield per plant (g)
1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**
1	V_1T_1	11--1	60.67	98.67	118.00	39.36	3.60	17.33	19.70	186.24	325.33	38.67	12.11	32.49
2	V_1T_1	24--1	52.33	94.67	109.00	39.65	4.53	13.15	39.70	286.98	348.00	35.33	11.24	31.50
3	V_1T_1	8--1	54.67	96.67	94.67	38.05	3.53	18.41	22.50	283.25	143.33	39.33	12.49	35.41
4	V_1T_1	18--3	52.33	94.67	95.13	36.51	4.27	16.84	21.80	255.65	220.00	36.33	13.29	33.66
5	V_1T_1	28--7	59.33	96.00	85.27	39.82	3.67	17.35	18.60	219.15	208.00	38.00	13.05	28.51
6	V_1T_1	725--4	58.00	98.67	91.40	39.84	3.00	16.54	18.70	216.01	232.00	34.00	13.56	36.01
7	V_1T_1	13--1	58.00	96.67	94.93	40.85	4.13	17.07	25.90	418.17	301.33	50.33	10.99	41.16
8	V_1T_1	23--1	56.67	96.67	93.67	36.48	3.27	15.28	22.82	303.43	165.33	57.33	13.56	41.83
9	V_1T_1	12--7	56.67	96.00	85.67	36.67	3.33	16.49	17.27	244.93	213.33	45.33	13.96	34.14
10	V_1T_1	37--20	59.33	98.00	89.20	36.12	3.67	15.65	19.63	221.32	202.67	74.00	12.85	28.70
11	V_1T_1	25--7	59.67	99.33	91.80	37.94	3.27	17.76	27.29	269.04	218.67	36.00	13.52	36.47
12	V_1T_1	745--15	58.00	96.67	93.80	40.17	3.20	16.65	26.19	164.14	232.00	36.00	13.69	22.50
13	V_1T_1	6--7	62.67	98.67	92.40	35.76	3.07	15.97	22.53	219.47	208.00	46.67	12.34	27.17
14	V_1T_1	19--1	61.33	98.67	95.87	37.61	3.27	18.17	30.06	206.44	197.33	52.00	14.43	29.89
15	V_1T_1	6--2	62.00	97.33	89.13	38.53	2.87	17.54	18.03	164.75	216.00	53.33	14.06	23.38
16	V_1T_1	12--4	62.00	97.33	85.13	35.42	3.53	15.39	19.41	177.80	281.33	51.33	13.24	23.23
17	V_1T_1	25--10	61.00	97.33	92.27	36.25	3.73	16.58	18.45	144.40	305.33	52.00	14.23	20.33
18	V_1T_1	25--3	60.67	96.67	90.73	40.67	2.87	15.38	19.83	197.63	266.67	60.67	12.87	25.53

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
19	V_1T_1	22--13	60.67	96.67	85.27	38.51	3.73	16.54	22.10	186.36	282.67	52.67	13.31	24.80
20	V_1T_1	8--3	58.67	96.67	91.87	38.91	3.33	16.37	27.13	288.14	196.00	48.00	13.31	38.36
21	V_1T_1	20--6	59.33	98.00	91.07	39.63	3.53	15.23	27.96	245.09	248.00	43.33	12.82	31.43
22	V_1T_2	62--1	59.33	95.33	94.80	38.49	3.93	18.73	16.10	216.50	156.67	54.00	12.84	28.04
23	V_1T_2	776--10	58.33	95.33	94.53	35.62	3.13	16.67	22.70	223.91	208.67	48.00	13.01	29.07
24	V_1T_2	57--1	53.00	93.33	89.20	36.17	3.40	14.14	25.90	309.44	192.00	57.33	11.49	37.19
25	V_1T_2	78--1	55.33	95.33	87.87	39.38	3.27	17.39	22.20	222.25	230.67	38.00	11.33	37.45
26	V_1T_2	69--7	59.00	96.67	95.87	42.12	4.60	16.67	21.90	251.79	328.00	64.00	12.65	31.25
27	V_1T_2	40--5	58.33	97.33	98.47	39.55	3.00	16.72	17.03	149.30	198.67	44.00	12.54	21.91
28	V_1T_2	67--12	58.67	97.33	101.80	38.42	3.00	17.54	19.73	227.17	233.33	33.33	12.79	29.23
29	V_1T_2	76--2	59.00	96.67	102.13	41.17	3.60	18.33	18.29	257.20	293.33	54.00	13.29	33.43
30	V_1T_2	76--1	58.00	97.33	92.73	36.08	3.47	15.97	19.00	260.85	225.33	42.00	13.05	34.17
31	V_1T_2	43--1	60.00	96.67	92.73	37.95	3.47	16.57	21.02	243.28	226.67	39.33	13.87	33.68
32	V_1T_2	68--26	60.00	96.00	91.93	38.33	3.60	15.71	28.11	287.97	330.67	48.00	12.45	36.47
33	V_1T_2	782--1	61.67	99.33	98.13	38.21	4.13	15.77	20.14	239.21	345.33	28.67	12.55	29.94
34	V_1T_2	67--1	61.33	96.00	96.00	37.85	3.07	16.43	26.88	268.86	180.00	39.33	13.23	35.40
35	V_1T_2	58--3	59.67	98.67	89.67	39.72	2.87	15.81	19.59	258.19	174.67	34.67	12.75	33.76
36	V_1T_3	98--11	54.33	95.33	108.73	39.39	3.53	16.95	27.40	253.09	184.00	49.33	12.46	31.35
37	V_1T_3	101--8	54.67	96.00	96.80	39.52	3.27	18.01	18.10	187.25	168.00	33.33	12.97	24.58
38	V_1T_3	92--7	56.67	98.00	101.13	38.65	3.73	16.67	17.00	226.49	176.00	64.00	13.09	29.43
39	V_1T_3	96--9	56.00	94.00	96.13	38.43	3.87	16.75	21.50	195.44	294.00	30.67	13.66	27.53
40	V_1T_3	114--30	58.33	96.00	102.87	39.37	3.27	16.53	23.63	208.85	229.33	46.00	12.96	27.82
41	V_1T_3	673--3	59.00	97.33	112.20	39.19	2.80	15.87	17.60	213.00	254.67	47.33	12.92	27.06
42	V_1T_3	108--2	55.33	94.67	99.47	38.58	3.53	15.97	24.40	174.49	213.33	38.67	13.05	22.35

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
43	V_1T_3	101--28	60.33	98.67	100.87	38.18	3.27	17.21	18.20	178.79	202.67	37.33	13.75	24.59
44	V_1T_3	119--26	54.67	94.00	102.40	40.35	3.27	16.29	20.03	200.57	224.00	50.00	13.14	26.70
45	V_1T_3	18--14	58.67	98.00	95.80	37.06	3.80	16.63	22.90	234.36	197.33	54.00	13.74	31.77
46	V_1T_3	684--14	59.33	96.67	97.60	35.57	3.80	16.55	20.20	257.94	133.33	48.67	12.70	32.54
47	V_1T_3	97--5	56.00	96.67	104.80	39.69	4.00	16.99	25.50	226.76	248.00	39.33	13.25	33.73
48	V_1T_3	110--30	59.33	99.33	99.47	37.13	3.40	16.45	16.30	178.02	191.33	47.33	13.03	23.08
49	V_1T_3	96--12	57.67	96.67	106.27	39.31	3.73	18.10	25.70	334.32	248.00	49.33	13.03	43.35
50	V_1T_3	108--8	56.33	96.00	92.47	38.67	3.67	17.31	20.20	217.22	255.33	102.67	12.83	29.96
51	V_1T_3	108--5	56.67	96.00	99.00	39.76	3.20	16.87	23.50	220.69	234.67	43.33	11.79	26.12
52	V_1T_3	109--1	56.67	95.33	90.40	34.17	3.67	16.85	20.90	255.25	220.00	32.00	12.63	32.48
53	V_1T_3	108--2	57.33	97.33	93.47	35.95	4.33	15.21	29.40	262.11	244.00	44.00	12.26	32.69
54	V_1T_3	645--12	52.33	94.67	89.20	38.54	3.27	13.05	31.10	247.97	199.33	64.67	10.85	23.89
55	V_1T_3	96--7	59.33	98.00	82.73	37.17	2.67	18.54	20.90	217.09	177.33	28.67	12.71	27.27
56	V_1T_3	118--20	57.33	94.00	98.87	41.88	3.80	16.96	18.50	183.04	273.33	39.33	13.41	28.08
57	V_1T_3	683--6	59.33	98.00	96.20	40.50	4.20	17.66	21.40	232.90	293.33	40.67	13.27	31.35
58	V_1T_3	119--17	59.67	108.00	93.70	39.31	3.47	15.65	14.80	113.53	237.33	43.33	12.63	34.53
59	V_1T_3	105--22	62.00	98.67	90.87	37.48	3.60	15.53	17.30	171.01	230.00	43.33	12.77	21.75
60	V_1T_3	120--24	58.00	98.00	91.73	38.39	2.80	17.10	17.60	196.17	224.67	32.00	13.06	25.48
61	V_1T_3	121--18	56.00	94.00	95.33	39.39	3.60	16.51	18.20	221.10	200.00	45.33	13.37	30.24
62	V_1T_3	684--7	60.67	97.33	100.07	38.28	3.47	16.41	18.60	196.38	334.67	49.33	12.19	23.63
63	**No. 889**		**59.33**	**95.33**	**102.33**	**38.50**	**4.13**	**16.20**	**14.61**	**184.95**	**261.33**	**49.33**	**13.13**	**24.15**
64	V_1T_3	680--1	57.00	97.33	83.87	37.29	3.80	16.23	24.17	285.31	216.67	68.67	13.84	39.56
65	V_1T_3	98--2	57.33	98.67	85.00	34.45	2.87	14.65	21.35	277.33	180.00	30.00	13.47	37.56
66	V_1T_3	713--14	57.33	94.67	86.53	38.98	3.73	15.47	22.39	305.99	262.00	55.33	10.54	33.28

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
67	V_1T_3	113--18	60.67	99.33	95.13	38.87	2.87	17.74	21.95	225.77	153.33	52.00	13.53	30.42
68	V_1T_3	105--19	60.00	96.00	92.33	38.31	3.27	15.93	24.71	257.88	260.00	70.00	12.43	32.06
69	V_1T_3	691--18	59.33	98.67	90.53	35.91	2.93	16.45	16.38	206.24	197.33	50.67	12.91	27.16
70	V_1T_3	120--18	57.33	96.67	89.87	38.47	4.20	18.17	28.76	502.79	248.00	52.00	13.03	63.52
71	V_1T_3	116--28	58.00	95.33	84.33	37.20	3.00	17.93	17.53	173.75	228.00	35.33	12.94	22.79
72	V_1T_3	117--16	59.67	99.33	91.20	40.45	2.93	15.10	22.58	190.99	278.00	54.00	13.07	24.84
73	V_1T_3	89--1	60.00	97.33	80.87	39.19	2.87	15.41	22.55	188.82	189.33	33.67	13.69	25.96
74	V_1T_3	113--26	59.00	97.33	94.87	36.49	2.87	16.05	20.67	154.95	196.00	38.67	13.97	21.56
75	V_1T_3	121--24	59.67	96.00	108.47	38.33	3.47	16.12	17.74	190.91	306.67	48.00	13.30	25.58
76	V_1T_3	102--20	59.33	97.33	98.67	40.18	3.20	14.87	24.97	175.63	205.33	34.67	13.30	23.10
77	V_1T_3	118--4	57.00	95.33	96.20	38.51	3.33	16.01	17.19	199.01	218.67	32.00	12.50	23.42
78	V_1T_3	715--15	56.33	94.67	94.27	37.97	4.13	17.83	19.11	184.51	230.67	53.33	13.12	24.37
79	V_1T_3	121--5	57.00	95.33	87.67	40.44	2.93	15.45	24.51	259.48	269.33	40.67	12.87	33.48
80	V_1T_3	707--17	60.67	96.67	98.93	39.85	4.80	16.84	20.25	230.21	304.00	56.00	13.80	32.09
81	V_1T_3	117--18	61.33	98.67	102.27	38.31	3.60	16.01	19.61	155.33	225.33	54.67	13.40	21.38
82	V_1T_3	93--1	61.33	97.33	95.67	41.07	3.00	14.97	23.97	246.70	144.00	24.67	12.71	31.04
83	V_1T_3	107--16	58.00	96.00	83.93	37.72	3.07	15.55	21.57	234.03	269.33	40.00	11.77	27.56
84	V_1T_3	707--3	56.00	94.67	100.47	42.42	4.27	16.08	29.42	208.96	288.00	50.67	12.51	26.08
85	V_2T_1	161--8	51.67	94.00	79.67	35.51	3.13	15.91	30.30	333.04	118.67	29.33	7.65	25.62
86	V_2T_1	517--2	58.33	95.33	87.67	39.55	2.67	14.17	16.70	286.32	180.00	28.67	6.31	23.00
87	V_2T_2	231--25	50.33	94.00	92.80	36.55	3.20	13.83	39.20	289.26	162.67	40.67	7.31	20.67
88	V_2T_2	403--18	59.00	97.33	82.33	39.57	3.20	16.24	17.70	213.65	174.00	44.67	6.69	22.61
89	V_2T_2	199-27	59.33	98.00	81.33	38.35	3.00	12.79	17.38	296.09	141.33	42.00	7.62	21.53
90	V_2T_2	229--27	59.33	97.33	89.47	38.99	3.07	14.02	19.34	161.88	112.00	38.00	6.95	11.25

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
91	**Sangavi local**		**62.00**	**98.00**	**95.67**	**40.05**	**3.87**	**14.87**	**19.44**	**262.54**	**273.33**	**58.00**	**6.75**	**17.65**
92	V_2T_2	198--1	58.67	98.00	99.33	34.91	2.93	14.01	31.73	358.02	160.00	60.00	6.68	23.48
93	V_2T_3	282--12	58.33	96.67	93.93	38.87	2.80	12.75	23.30	219.39	122.67	40.67	7.85	24.05
94	V_2T_3	480--7	61.00	98.67	88.20	41.61	2.60	11.89	23.89	257.08	165.33	42.67	6.94	17.90
95	V_3T_1	308--6	58.33	96.67	105.53	35.25	4.20	15.67	25.03	314.79	318.67	40.67	7.95	26.26
96	**GC 10**		**56.00**	**95.33**	**85.20**	**35.79**	**2.80**	**14.29**	**23.70**	**206.74**	**183.33**	**36.67**	**6.69**	**14.50**
97	V_3T_1	599-1	59.67	97.33	93.40	39.17	2.40	14.99	19.60	182.91	198.00	44.67	7.64	19.54
98	V_3T_1	313--4	61.33	97.33	98.80	39.02	2.93	14.85	14.93	174.70	185.33	53.33	7.45	15.61
99	V_3T_1	320--8	62.67	97.33	92.20	37.66	2.40	15.25	21.09	230.83	245.33	42.00	7.54	16.88
100	V_3T_1	313--22	59.67	97.33	88.87	36.71	3.53	15.17	21.06	305.69	164.00	49.33	7.11	27.42
101	V_3T_2	624--1	61.33	98.00	88.60	38.92	2.33	13.49	23.50	264.35	146.67	31.33	9.01	22.96
102	V_3T_2	359--2	60.67	98.00	94.07	39.39	3.00	13.04	24.96	221.91	242.67	45.33	9.89	21.60
Mean			58.40	97.12	94.13	38.40	3.39	16.07	22.00	232.71	224.01	45.51	11.96	28.38
S.E ±			2.12	5.72	9.13	2.16	0.65	1.57	5.97	87.07	70.47	17.48	0.92	9.59
C.D at 5 %			4.2	11.32	18.08	4.27	1.28	3.1	11.82	172.39	139.54	34.61	1.84	19
C.V (%)			4.45	7.21	11.89	6.89	23.34	11.94	33.24	45.82	38.53	47.05	9.52	41.43

mutants 480-7 (11.89 cm), 282-12 and 119-27 (both 12.79 cm) recorded pod length less than population mean. Among 99 mutants studied 38 (39 %) showed higher pod length than population mean. Out of which 7 (6.8 %) were significantly superior over the population mean.

4.2.7 Number of pods per plant

The number of pods per plant ranged between 14.61 (95-5) and 39.70 (24-1) with population mean of 22.00. The mutant 24-1 recorded the highest number of pods (i.e.39.7) which was 83.3 per cent higher than the population mean and was followed by 231-25, 198-1, 645-12, 19-1 and 161-8 which produced more than 30 pods per plant (showing an increase of 38.5 %) while 119-17 (14.8) produced the least number of pods per plant. Out of 47 (47.5 %) mutants with higher number of pods per plant than the population mean, 10 (10 %) were significantly high pod producers.

4.2.8 Number of seeds per plant

The mutant 120-18 (502.79) produced maximum number of seeds per plant showing an increase of 122 per cent over the population mean (232.71) and was followed by 13-1 which produced 418.17 seeds per plant (84.7 % increase). Three other mutants viz., 198-1, 96-12 and 161-8 produced more than 330 seeds per plant showing an increase of 45.7 per cent over the population mean. The mutant 119-17 was the least (113.53) seed producer followed by 25-10 (144.40). Among the 99 mutants studied 49 (49.5 %) produced more seeds per plant than the population mean (226.38), of which 5 (5 %) were significantly superior.

4.2.9 Fresh biomass (g)

The mutant 24-1 produced the highest (348.0 g) fresh biomass followed by 782-1, 687-7, 68-26, 69-7 and 11-1 producing more than 325.29 g of fresh biomass per plant. However, 229-27 produced the lowest (112.0 g) fresh biomass followed by 761-8 (118.67 g). Fifty four (54.5 %)

mutants recorded higher fresh biomass than the population mean (224.01 g) of which 11 (11.11 %) recorded significantly higher values than the population mean.

4.2.10 Dry biomass (g)

The mutant 108-8 recorded the highest dry biomass (102.67 g) which was 130.3 per cent higher than population mean (45.51 g). The other mutants viz., 37-20, 105-19, 680-1, 645-12, 69-7 and 92-7 recorded more than 64.08 g dry biomass per plant. However, the mutants 93-1 (24.67 g) and 782-1 (28.67 g) recorded the least dry biomass. About 52 per cent i.e. 51 mutants out of 99 showed higher dry biomass than the population mean (45.51 g). However 7 mutants (7.07 %) showed significantly higher value than the population mean.

4.2.11 Test weight (g)

The population mean for this character was 11.96 g with range of 6.31 (517-2) to 14.43 g (19-1). The mutant 517-2 produced the highest test weight of 14.43 g which was 20.5 per cent higher than the population mean of 11.96 g. The other mutants viz., 25-10, 6-2 and 12-7 exhibited test weights higher than 13.9 g. However, the mutants 198-1 (6.68 g), 403-18 (6.69 g) and 596-30 (6.69 g) recorded low test weights. Out of 76 (76.7 %) mutants recording higher values than population mean, 49 (49.5 %) showed significant increase in test weight over the population mean.

4.2.12 Grain yield per plant (g)

The mutant 120-18 recorded the highest (63.52 g) grain yield per plant which was 126.9 per cent higher than population mean. The other mutants viz., 96-12, 680-1, 98-2, 78-1 and 57-1 showed more than 37 g of yield per plant and exhibited more than 32 per cent increase over population mean (28.38 g). The mutant 229-27 (11.25 g) recorded the lowest grain yield per plant followed by 596-30 (14.50 g) and 313-4

(15.61g). Forty nine mutants produced higher grain yield than population mean of which six (6.06 %) were significantly superior.

4.3 Variety and dose wise mean performance of mutant lines

In the present investigation M_3 mutants were studied to assess variability and diversity. Apart from the variation studied among M_3 mutants, efforts were made to group the mutants based on variety [No. 889 (V_1), Sangavi local (V_2) and GC 10 (V_3).] and doses of gamma irradiation [15 (T_1), 25 (T_2) and 35 (T_3) KR]. The following are the results of the means (Table 4.3) of individual groups (variety wise and dose wise).

4.3.1 Days to 50 per cent flowering

The mutants of Variety No.889 (V_1), Sangavi local (V_2) were early for days to 50 per cent flowering (Fig. 4.1). The mutants of V_1T_3 were early (–2.18 %) than parent variety (59.33 days) followed by the mutants of V_1T_2 (-1.08 per cent) and V_1T_1 (-0.96 per cent). Among the mutant population of V_2, the mutants of V_2T_1 were earlier by –11.29 per cent than parent variety (62.00 days) followed by V_2T_2 (-6.27 per cent) and V_2T_3 (-3.76 %). However, the mutants of GC 10 (V_3) contrastingly were late for days to 50 per cent flowering. The V_3T_2 mutants were late by 8.93 per cent than parent variety (56.00 days) followed by V_3T_1 (6.45 %).

4.3.2 Days to maturity

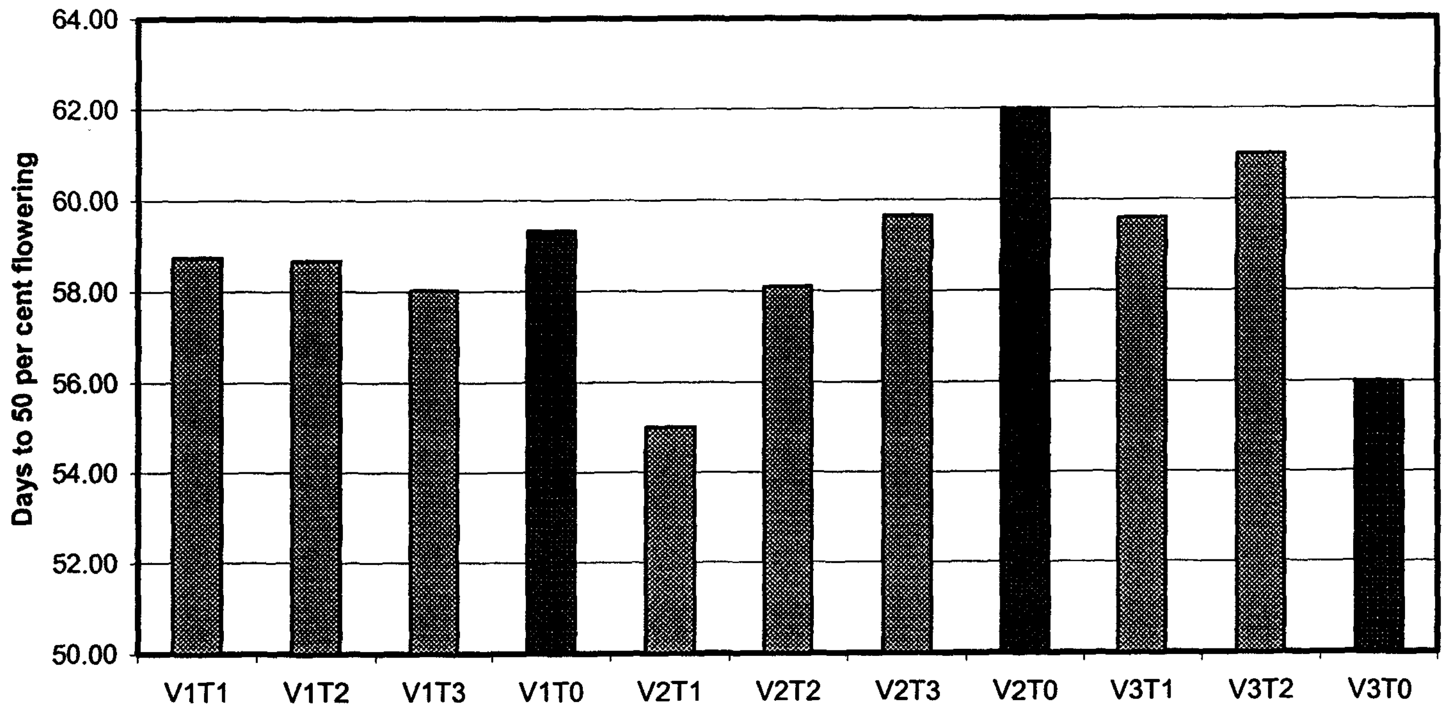
The mutants of Sangavi local (V_2) were early to mature (Fig. 4.2), with those belonging to V_2T_1 recording earliness by –3.40 per cent over the parent variety (98.00 days) followed by V_2T_2 (-0.91 %) and V_2T_3 (-0.34 %).

The mutants of No. 889 (V_1) and GC 10 (V_3) were late to mature than their respective parent varieties (both 95.33 days). The mutants of V_1T_3 took 2.13 per cent more days to mature than the parent variety

Table 4.3 Variety and dose wise mean performance of M_3 mutant lines for different characters in cowpea

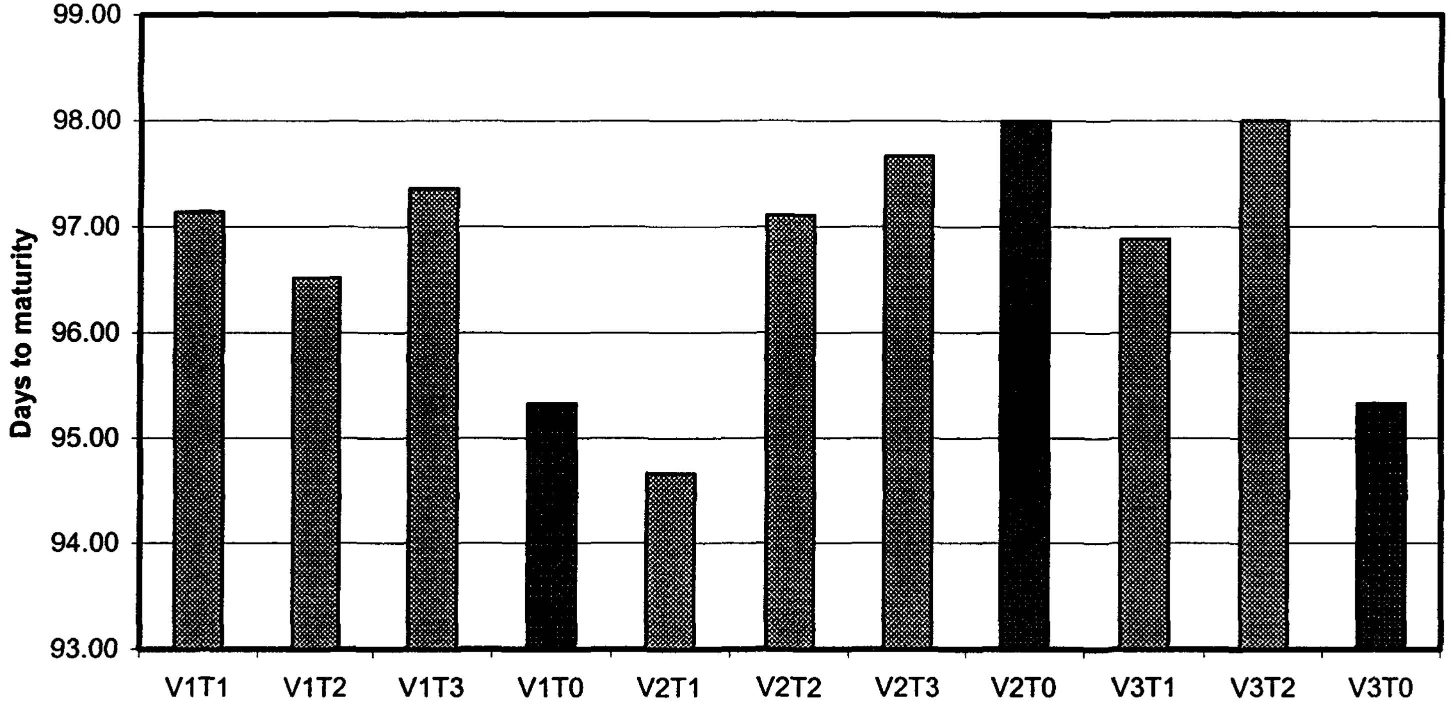
Treatment	No. of mutants	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No.of branches per plant	Pod length (cm)	No. of pods per plant	No.of seeds per plant	Fresh biomass (g)	Dry biomass (g)	Test weight (g)	Grain yield per plant (g)
V_1T_1	21	58.76 (-0.96)	97.14 (1.90)	93.16 (-8.97)	38.23 (-0.71)	3.50 (-15.44)	16.46 (1.61)	23.12 (58.24)	233.26 (26.12)	238.64 (-8.69)	46.70 (-5.34)	13.09 (-0.32)	30.79 (27.48)
V_1T_2	14	58.69 (-1.08)	96.52 (1.25)	94.71 (-7.45)	38.50 (0.01)	3.47 (-16.12)	16.60 (2.49)	21.33 (45.95)	243.99 (31.92)	237.43 (-9.15)	44.62 (-9.56)	12.70 (-3.28)	32.21 (33.39)
V_1T_3	48	58.04 (-2.18)	97.36 (2.13)	95.55 (-6.63)	38.55 (0.12)	3.48 (-15.93)	16.40 (1.25)	21.37 (46.2)	221.29 (19.65)	228.97 (-12.39)	46.29 (-6.16)	12.93 (-1.58)	29.07 (20.36)
V_1T_0	1	59.33	95.33	102.33	38.50	4.13	16.20	14.61	184.95	261.33	49.33	13.13	24.15
V_2T_1	2	55.00 (-11.29)	94.67 (-3.40)	83.67 (-12.45)	37.53 (-6.3)	2.90 (-25.00)	15.04 (1.17)	23.50 (20.88)	309.68 (17.95)	149.33 (-45.37)	29.00 (-50)	6.98 (3.46)	24.31 (37.73)
V_2T_2	5	58.11 (-6.27)	97.11 (-0.91)	90.16 (-5.76)	38.07 (-4.95)	3.21 (-16.96)	15.29 (2.86)	24.13 (24.14)	263.57 (0.39)	170.56 (-37.6)	47.22 (-18.58)	7.00 (3.74)	19.53 (10.66)
V_2T_3	2	59.67 (-3.76)	97.67 (-0.34)	91.07 (-4.81)	40.24 (0.46)	2.70 (-30.17)	12.32 (-17.13)	23.60 (21.38)	238.24 (-9.26)	144.00 (-47.32)	41.67 (-28.16)	7.39 (9.58)	20.98 (18.85)
V_2T_0	1	62.00	98.00	95.67	40.05	3.87	14.87	19.44	262.54	273.33	58.00	6.75	17.65
V_3T_1	5	59.61 (6.45)	96.89 (1.63)	94.00 (10.33)	37.27 (4.14)	3.04 (8.17)	15.04 (5.21)	20.90 (-11.81)	235.94 (14.13)	215.78 (17.7)	44.44 (21.21)	7.40 (10.54)	20.03 (38.17)
V_3T_2	2	61.00 (8.93)	98.00 (2.80)	91.33 (7.19)	39.15 (9.41)	2.67 (-4.75)	13.26 (-7.21)	24.23 (2.24)	243.13 (17.6)	194.67 (6.18)	38.33 (4.54)	9.45 (41.19)	22.28 (53.67)
V_3T_0	1	56.00	95.33	85.20	35.79	2.80	14.29	23.70	206.74	183.33	36.67	6.69	14.50

Varieties : V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
Treatments : T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR
Values in parenthesis indicate per cent deviation from parent variety.



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.1 Variety and dose wise mean performance of M_3 mutants for days to 50 per cent flowering



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.2 Variety and dose wise mean performance of M_3 mutants for days to maturity

95.33 days) followed by V_1T_1 (1.90 per cent) and V_1T_2 (1.25 per cent). The mutants of V_3 with maximum days to maturity belonged to V_3T_2 (2.80 per cent) followed by V_3T_1 (1.63 per cent).

4.3.3 Plant height (cm)

Among the mutant population of GC 10 (V_3) the mutants belonging to V_3T_1 were taller than the parent variety (85.20 cm) by 10.33 per cent followed by V_3T_2 (7.19 %).

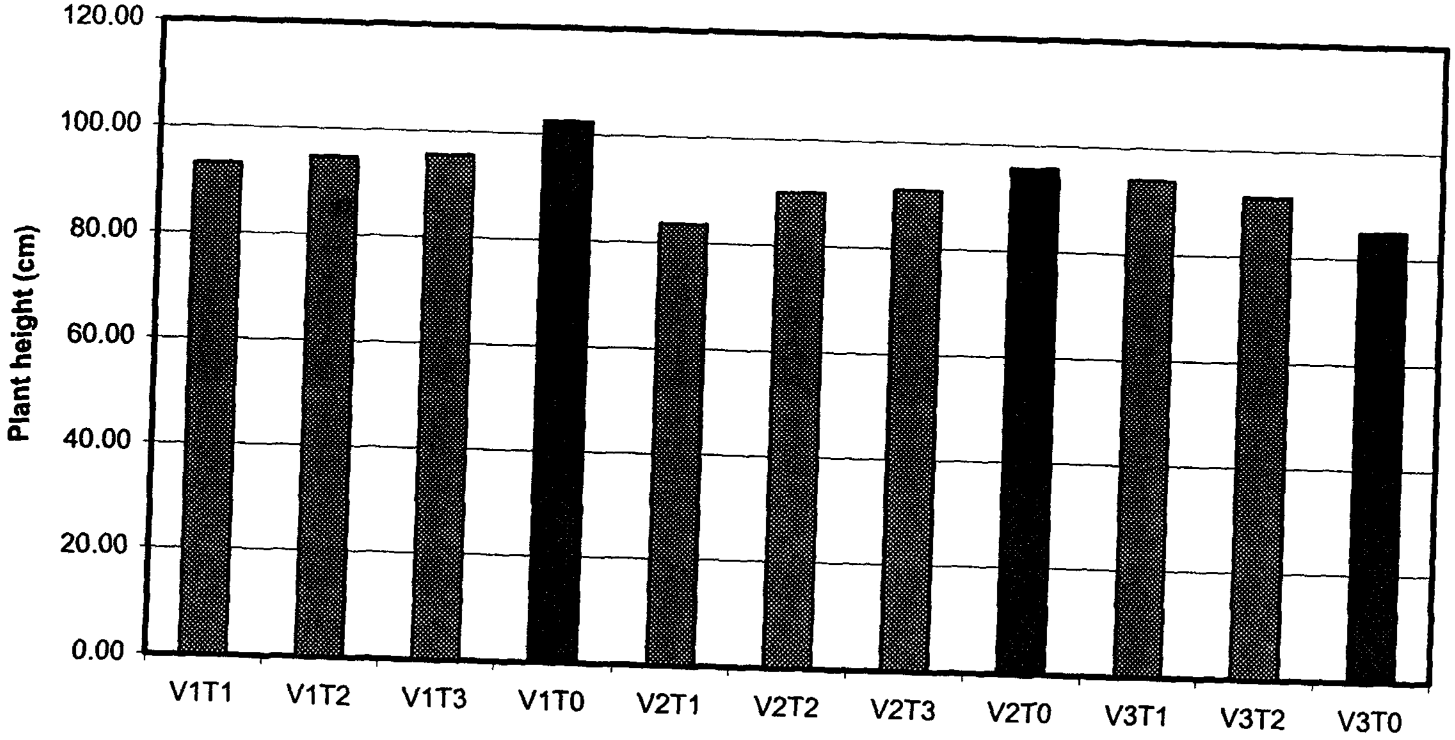
The mutant population of No. 889 (V_1) and Sangvi Local (V_2) were shorter than their parent varieties (Fig. 4.3). The mutants of V_1T_1 were shorter (–8.97 %) than parent variety (102.33 cm) followed by V_1T_2 (-7.45 %) and V_1T_3 (-6.63 %). The mutants of V_2T_1 were shorter than the parent variety (95.67 cm) by –12.45 per cent followed by V_2T_2 (-5.76 %) and V_2T_3 (-4.18 %).

4.3.4 Plant spread (cm)

In the mutant population of No. 889, the mutants of V_1T_3 recorded maximum increase of 0.12 per cent over the parent variety (102.33 cm) followed by V_1T_2 (0.01 %), while there was a decrease in plant spread by –0.17 per cent in mutants of V_1T_1 (Fig. 4.4).

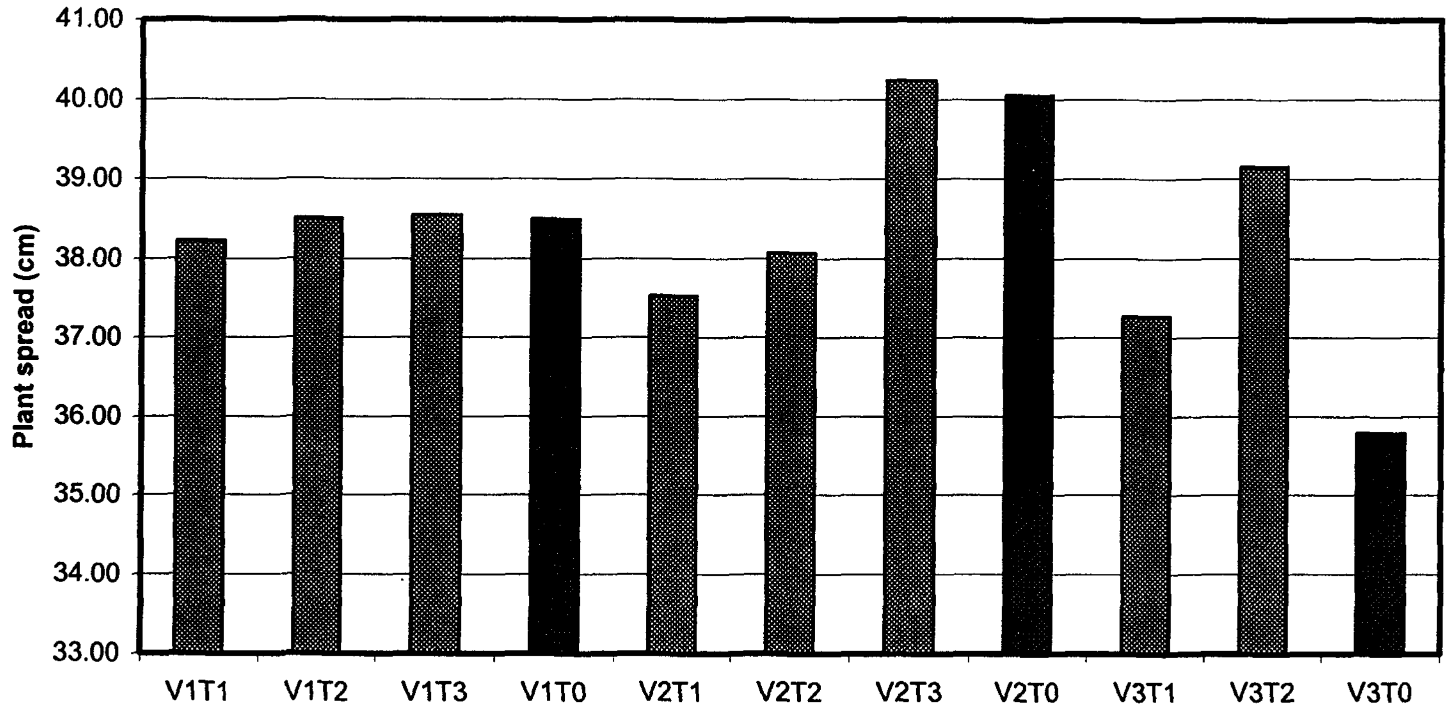
The mutant population of V_2T_3 of Sangavi local (V_2) showed an increase in plant spread by 0.46 per cent over the parent variety (40.05 cm) while there was a decrease in plant spread in V_2T_1 (-6.3 %) followed by V_2T_2 (-4.95 %).

All the mutants of GC 10 (V_3) showed an increase in plant spread. The mutants of V_3T_2 recorded maximum increase in plant spread (9.41 %) over the parent variety (35.79 cm) followed by V_3T_1 (4.14 %).



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.3 Variety and dose wise mean performance of M_3 mutants for plant height



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.4 Variety and dose wise mean performance of M_3 mutants for plant spread

4.3.5 Number of branches per plant

The mutants of No. 889 (V_1) and Sangavi local (V_2) showed a reduction in number of branches (Fig. 4.5). In the case of V_1 the mutants of V_1T_2 showed maximum reduction of –16.12 per cent over the parent variety (4.13) followed by V_1T_3 (-15.93 %) and V_1T_2 (-15.44 %). Among the mutants of V_2, those belonging to V_2T_3 showed the maximum reduction of –30.17 per cent over the parent variety (3.87) followed by mutants of V_2T_1 (-25.00 %) and V_2T_2 (-16.96 %). Among the mutants of GC 10 (V_3), those belonging to V_3T_1 showed an increase of 8.17 per cent over the parent variety (2.80) for number of branches while those belonging to V_3T_2 showed a decrease of –4.75 per cent.

4.3.6 Pod length (cm)

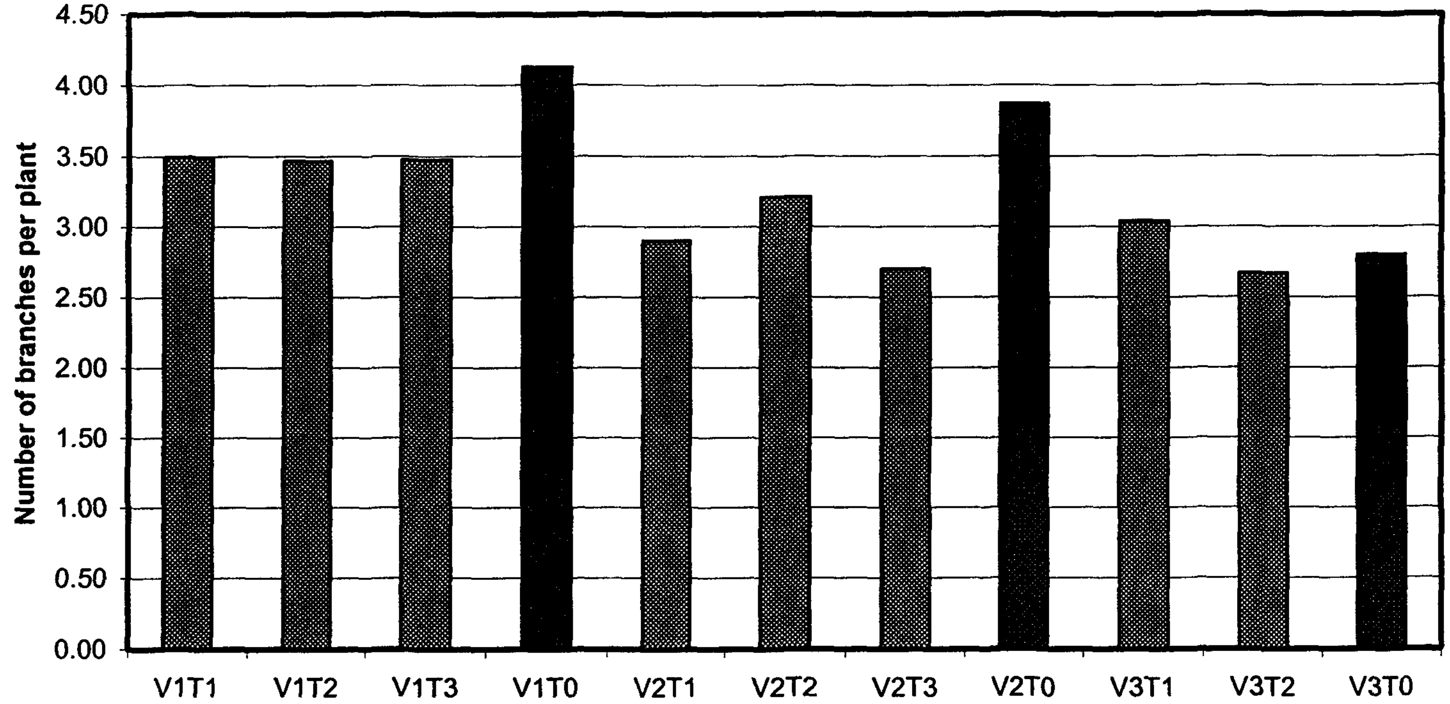
The mutant population of No. 889 (V_1) produced longer pods than the parent variety (Fig. 4.6). Increased pod length by 2.49 per cent over the parent variety (16.20 cm) was produced by mutants of V_1T_2 followed by V_1T_1 (1.61 %) and V_1T_3 (1.25 %).

Among the mutants of Sangavi local (V_2), the maximum increase of 2.86 per cent over the parent variety (14.87cm) was recorded in mutants of V_2T_1 (1.17 %). However, a drastic reduction in pod length by –17.13 per cent was observed in mutants of V_2T_3.

In the mutants of GC 10 (V_3) an increase in pod length by 5.21 per cent over the parent variety (14.29 cm) was observed in mutants of V_3T_1, while a decrease of -7.21 per cent was observed in mutants of V_3T_2.

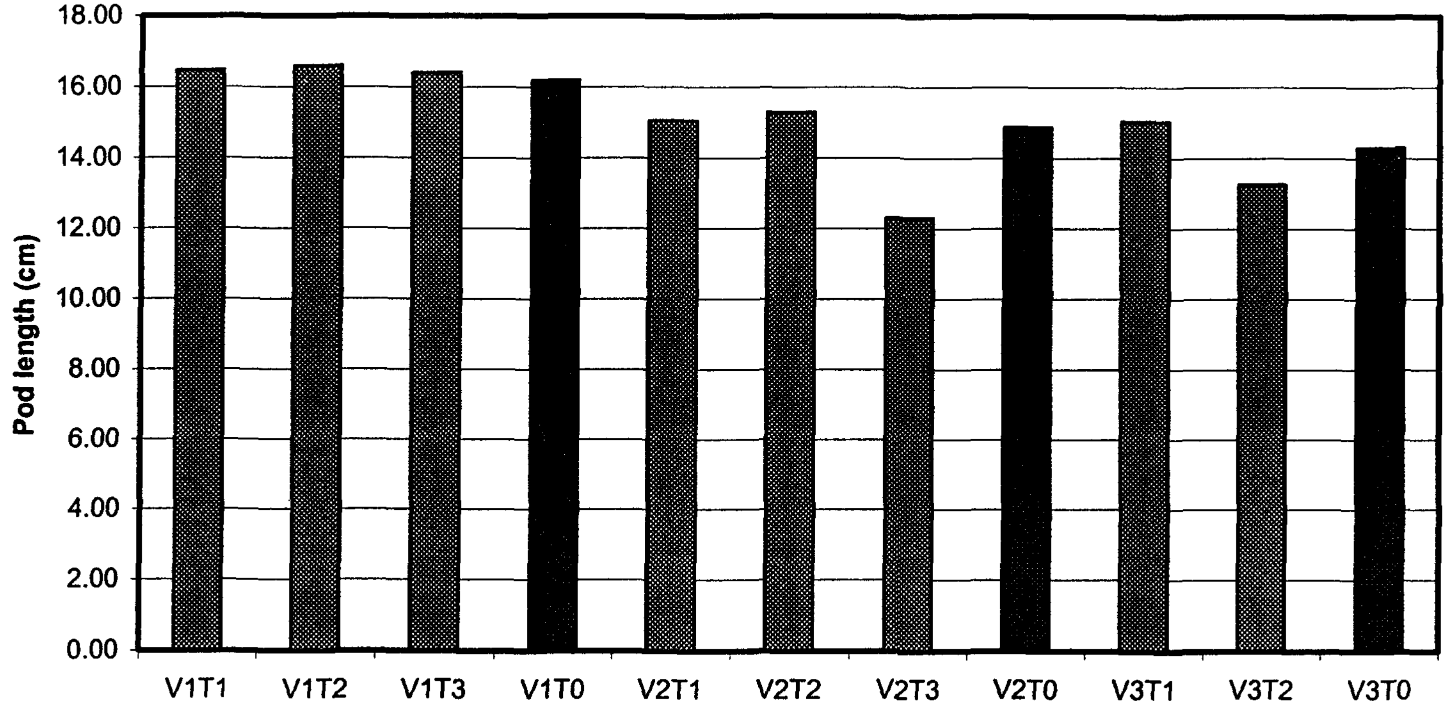
4.3.7 Number of pods per plant

The mutants of No. 889 (V_1) and Sangavi local (V_2) showed greater number of pods per plant than the parent varieties (Fig. 4.7).



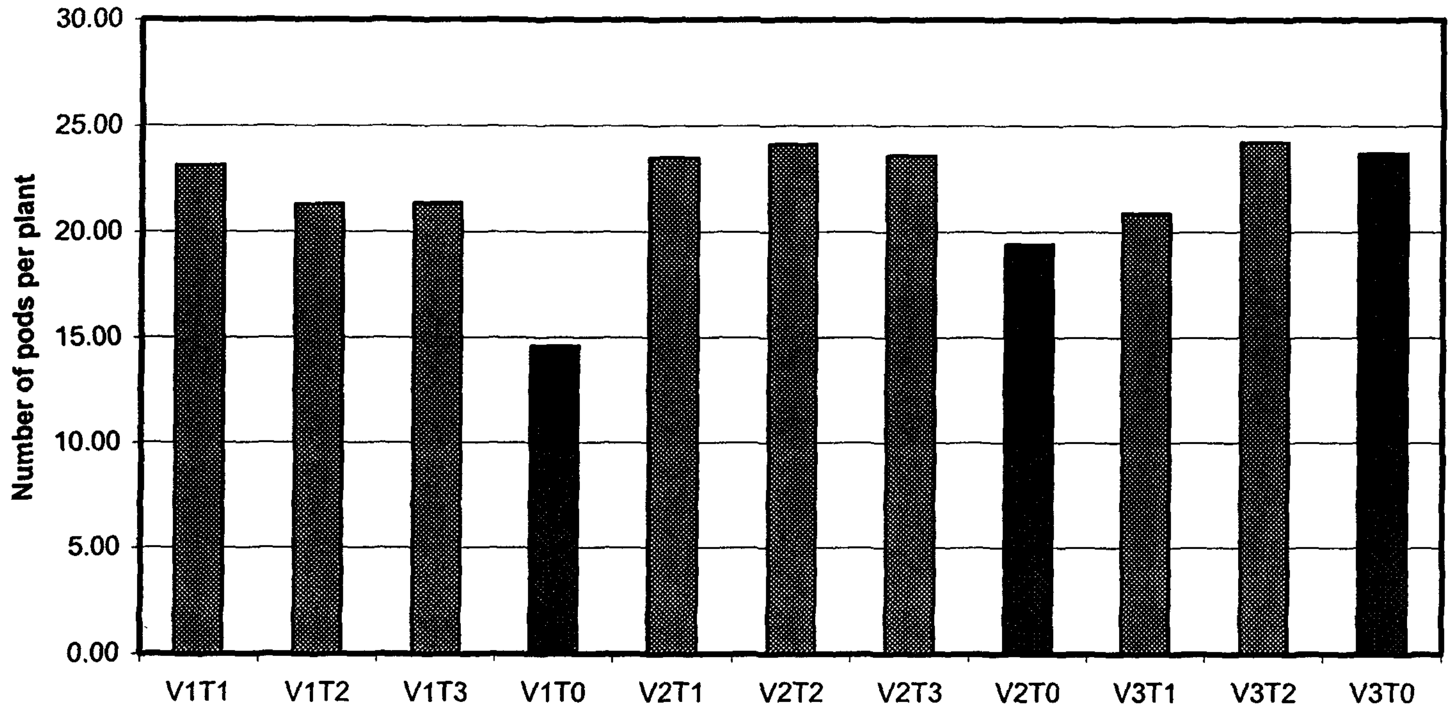
V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.5 Variety and dose wise mean performance of M_3 mutants for number of branches per plant



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.6 Variety and dose wise mean performance of M_3 mutants for pod length



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.7 Variety and dose wise mean performance of M_3 mutants for number of pods per plant

The maximum increase of 58.24 per cent over the parent variety (23.12) for number of pods per plant was observed in mutants of V_1T_1 followed by V_1T_3 (46.20 %) and V_1T_2 (45.95 %).

From the mutants of V_2, a maximum increase of 24.14 per cent from the parent variety (19.44) for number of pods per plant was recorded in mutants of V_2T_2 followed by 21.38 per cent (V_2T_3) and 20.88 per cent (V_2T_1).

In the mutants of GC 10 (V_3), an increase of 2.24 per cent from parent variety (23.70) for number of pods per plant was observed in V_3T_2 while a decrease of –11.81 per cent was observed in V_3T_1 for number of pods per plant.

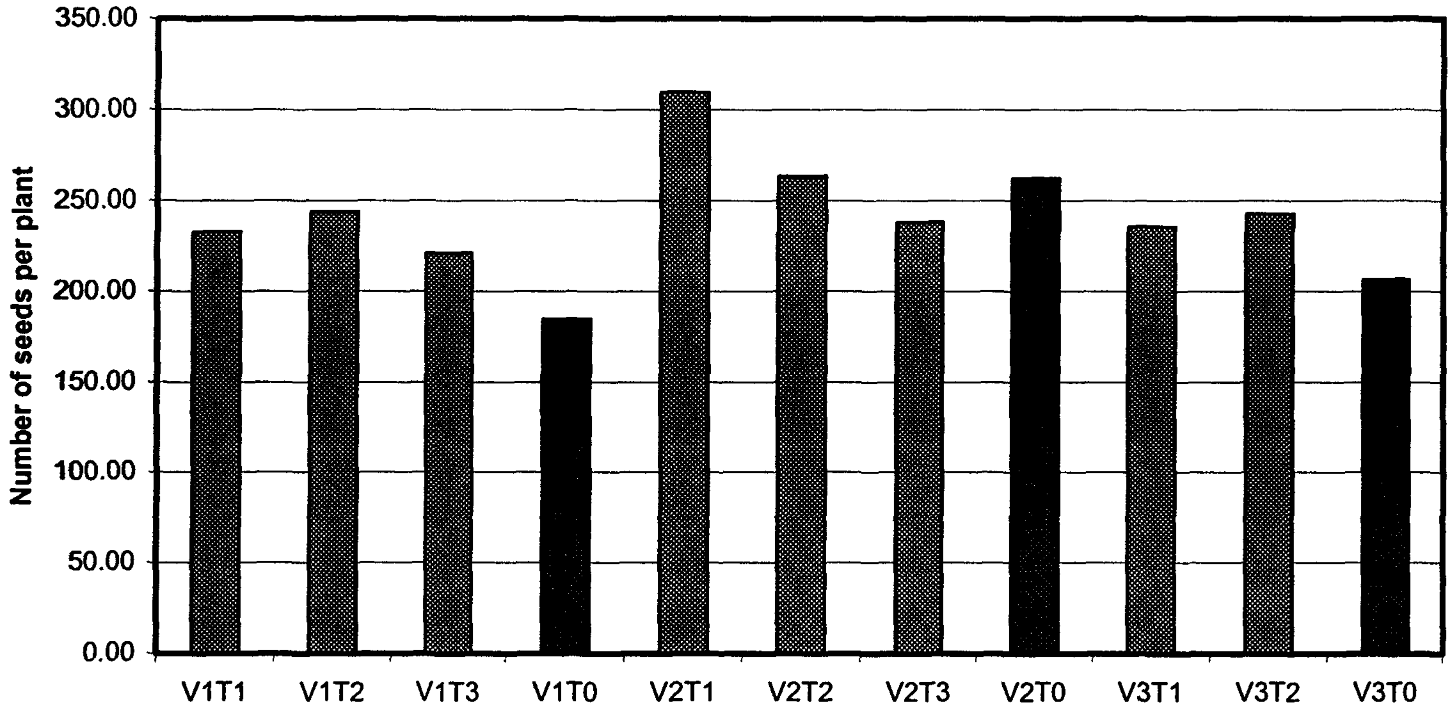
4.3.8 Number of seeds per plant

The mutant population of No. 889 (V_1) and GC 10 (V_3) showed more number of seeds per plant than parent varieties (Fig. 4.8). Among the mutants of V_1, those belonging to V_1T_2 showed maximum increase of 31.92 per cent over the parent variety (184.95) for number of seeds per plant followed by 26.12 per cent (V_1T_1) and 19.65 per cent (V_1T_3). An increase of 17.6 per cent over parent variety (206.74) was seen in mutants of V_3T_2 followed by 14.13 per cent (V_3T_1).

In Sangavi local (V_2) the mutants of V_2T_1 showed an increase of 17.95 per cent over the parent variety (262.54) followed by V_2T_2 (0.39 %). While the mutants of V_2T_3 recorded a decrease of –9.26 per cent over the parent variety.

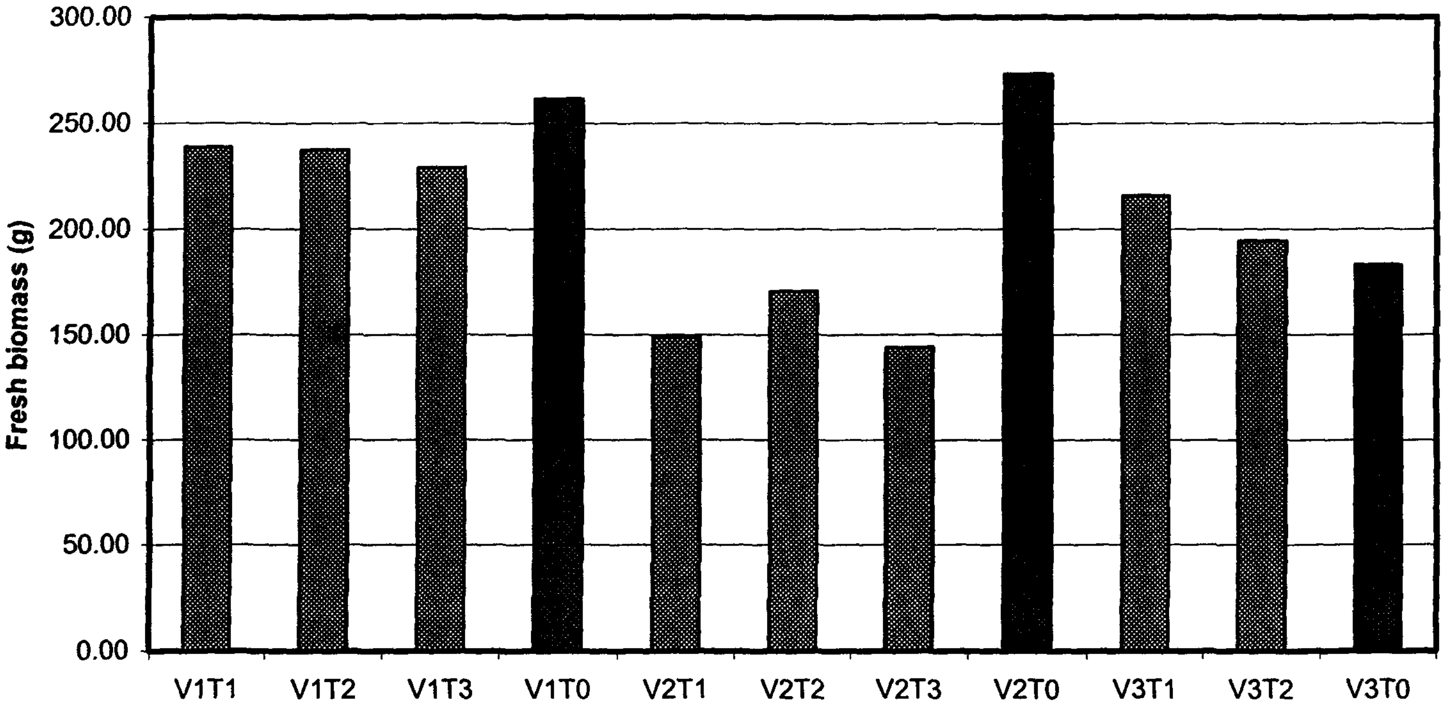
4.3.9 Fresh biomass (g)

The mutants of No. 889 (V_1) and Sangavi local (V_2) recorded a decrease in fresh biomass from parent varieties (Fig. 4.9). In V_1 the mutants of V_1T_3 recorded maximum decrease of –12.39 percent from



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.8 Variety and dose wise mean performance of M_3 mutants for number of pods per plant



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.9 Variety and dose wise mean performance of M_3 mutants for fresh biomass

parent variety (261.33 g) followed by V_1T_2 (-9.15 %) and V_1T_1 (-8.69 %). Among the mutants of V_2 (Sangavi local) maximum decrease by –47.32 per cent from parent variety (273.33 g) was recorded in mutants of V_2T_3 followed by –45.37 per cent in V_2 T_1 and –37.6 per cent in V_2T_2.

Among the mutants of V_3 (GC 10), those belonging to V_3T_1 showed a maximum increase of 17.7 per cent from parent variety (206.74 g) for fresh biomass followed by 6.18 per cent in mutants of V_3 T_2.

4.3.10 Dry biomass (g)

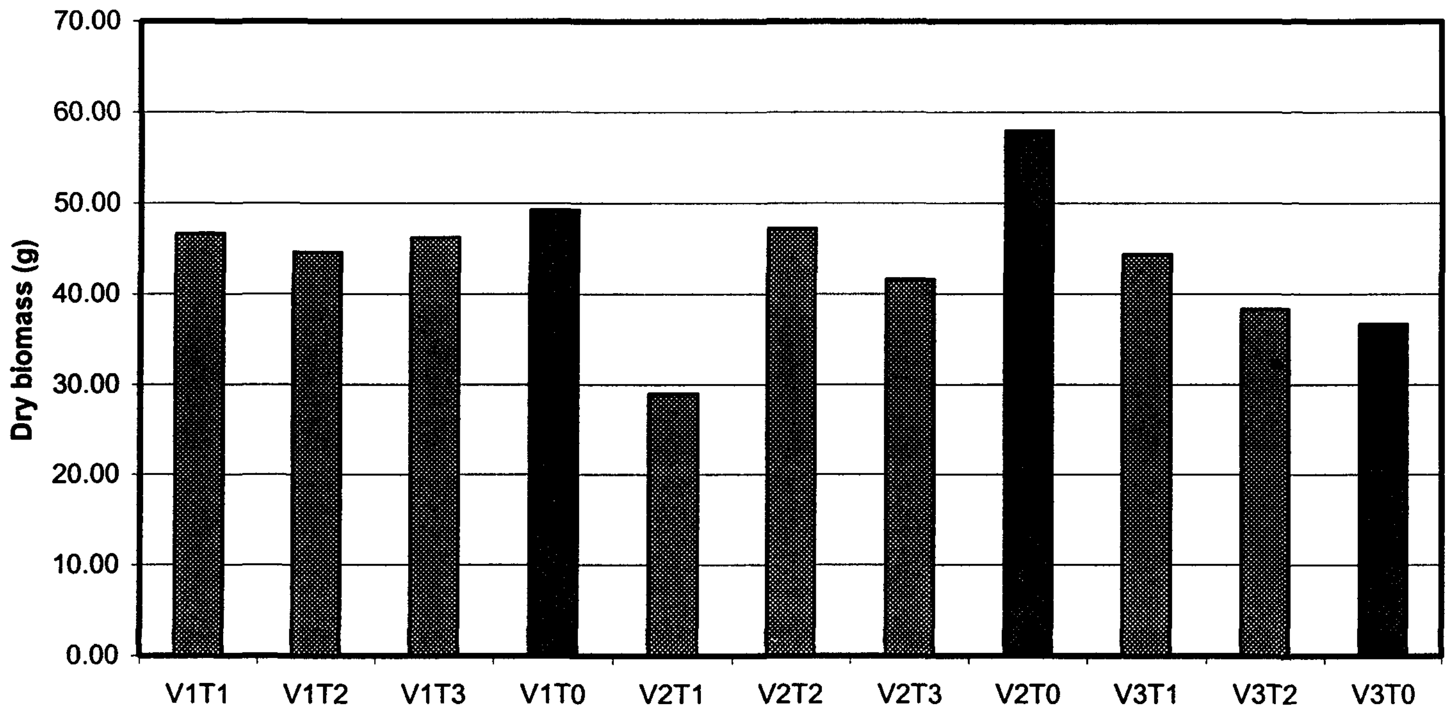
The mutants of GC 10 (V_3) showed an increase in dry biomass while those of No. 889 (V_1) and Sangavi local (V_2) recorded considerable decrease in dry biomass (Fig. 4.10). In variety V_3 the mutants of V_3T_1 recorded an increase of 21.21 per cent from parent variety (36.67 g) for dry biomass followed by 4.54 percent in mutants of V_3T_2.

Among V_1 mutants those showing a maximum decrease of –9.56 per cent for dry biomass belonged to V_1T_2 followed by V_1T_3 (-6.16 %) and V_1T_1 (-5.34 %). In V_2 the mutants of V_2T_1 showed a maximum decrease of –50.00 per cent from parent variety (58.00 g) followed by V_2T_3 (-28.16 %) and V_2T_2 (-18.58 %).

4.3.11 Test weight (g)

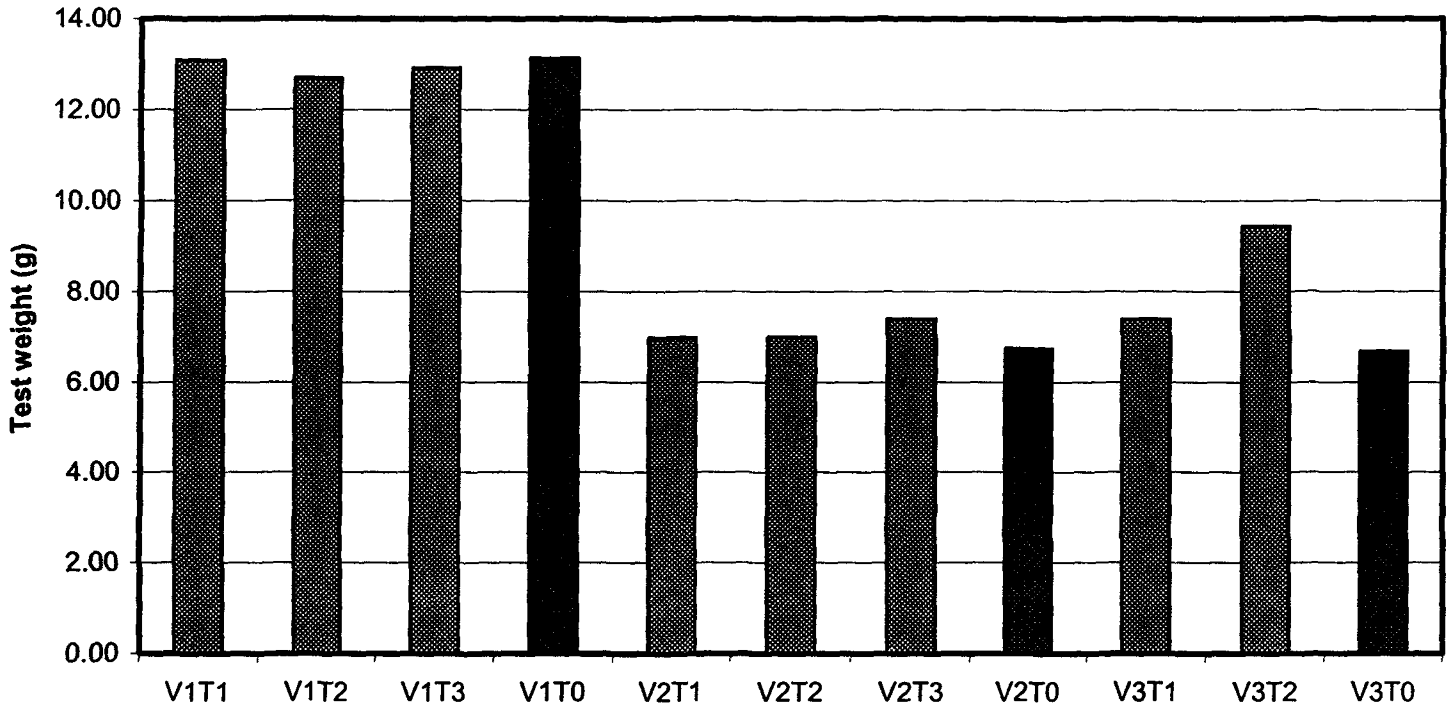
The mutants of Sangavi local (V_2) and GC 10 (V_3) showed an improvement in test weight while No. 889 (V_1) recorded a decrease in test weight (Fig. 4.11).

Among V_2 mutants those showing maximum increase of 9.58 per cent over the parent variety (6.75 g) belonged to V_2T_3 followed by V_2T_2 (3.74 %) and V_2T_1 (3.46 %). In V_3 (GC 10) the mutants of V_3T_2 recorded maximum increase of 41.19 per cent from parent variety (6.69 g) followed by V_3T_1 (10.54 %S).



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.10 Variety and dose wise mean performance of M_3 mutants for dry biomass



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.11 Variety and dose wise mean performance of M_3 mutants for test weight

A decrease in test weight by –3.28 per cent was recorded in mutants of V_1T_2 followed by V_1T_3 (-1.58 %) and V_1T_1 (-0.32 %).

4.3.12 Grain yield per plant (g)

The mutants of all the 3 varieties viz., No. 889 (V_1), Sangavi local (V_2) and GC 10 (V_3) showed improvement in yield over their parent varieties (Fig. 4.12).

In V_1 the maximum increase of 33.39 per cent over parent variety (24.15 g) for grain yield per plant was recorded in mutants of V_1T_2 followed by V_1T_1 (27.48 %) and V_1T_3 (20.36 %).

Among the mutants of V_2 those showing maximum increase by 37.73 per cent over parent variety (17.65 g) for grain yield per plant belonged to V_2T_1 followed by V_2T_3 (18.85 %) and V_2T_2 (10.66 %).

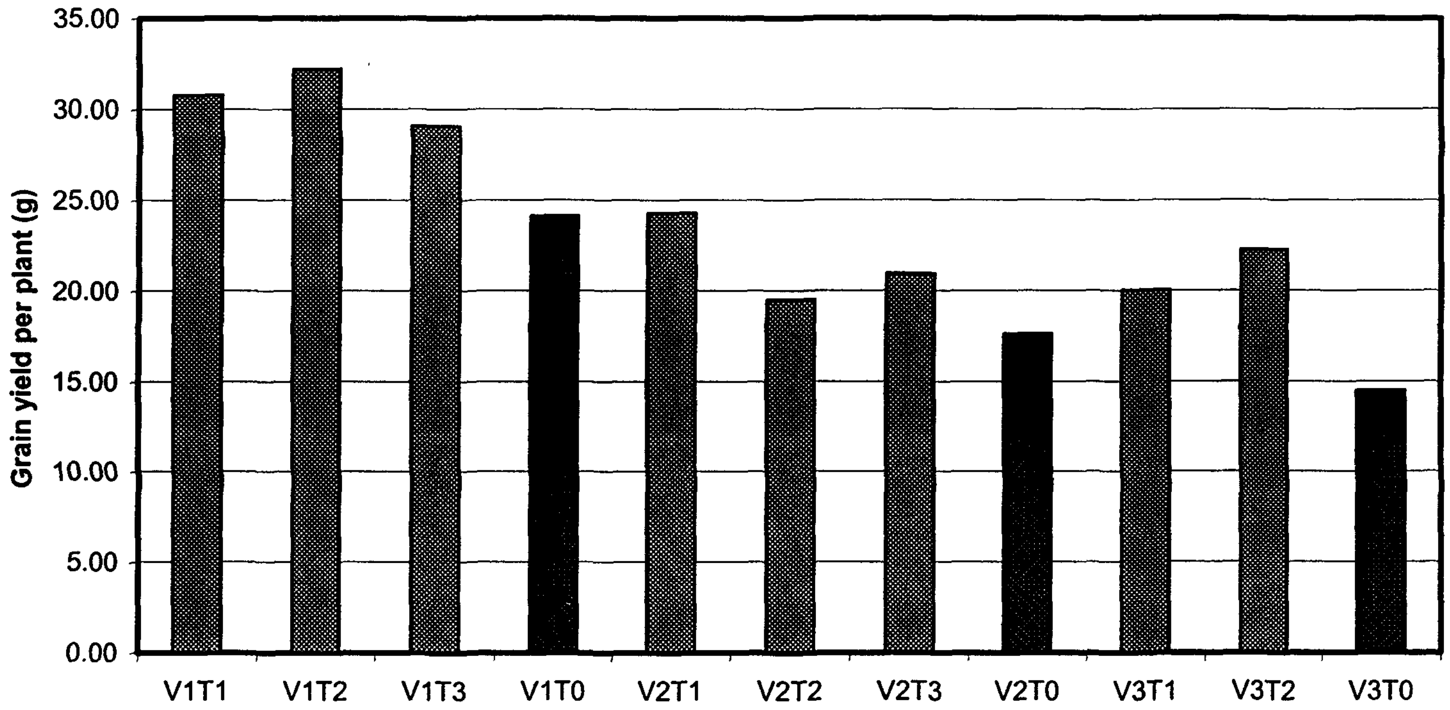
In V_3 the mutants of V_3T_2 showed the maximum improvement of 53.67 per cent over the parent variety (14.50 g) for grain yield per plant followed by mutants of V_3T_1 (38.71 %).

4.4 Components of genetic variability

The parameters of genetic variability viz., range, GCV, PCV, heritability (broad sense), genetic advance and genetic advance as per cent of mean are summarized in Table 4.4. The important findings are discussed below.

4.4.1 Coefficient of variation

The GCV values were lower than PCV values for all the twelve characters studied. The test weight recorded highest GCV estimate (17.84) followed by dry biomass (10.18), number of seeds per plant (10.04) and fresh biomass (8.76). The highest PCV value was observed for dry biomass



V_1 = No. 889; V_2 = Sangavi local; V_3 = GC 10.
T_1 = 10 KR; T_2 = 25 KR; T_3 = 35 KR.

Figure 4.12 Variety and dose wise mean performance of M_3 mutants for grain yield per plant

Table 4.4 Components of genetic variability in M_3 mutants of cowpea

Character	Components						
	Range	General mean	GCV	PCV	Heritability % (b.s)	Genetic advance	G.A as % of mean
Days to 50 % flowering	50.33 - 62.66	58.40	3.42	5.62	0.37	2.49	4.26
Days to Maturity	93.33 - 99.33	97.12	0.80	7.25	0.01	0.14	0.15
Plant height (cm)	79.66 - 118.00	94.13	2.83	12.22	0.05	1.18	1.25
Plant spread (cm)	34.17 - 42.42	38.40	2.11	7.20	0.08	0.45	1.18
No.of branches per plant	2.33 - 4.80	3.39	6.14	24.14	0.06	0.10	2.94
Pod length (cm)	11.88 - 18.72	16.07	5.15	13.00	0.15	0.64	4.00
No. of pods per plant	14.61 - 39.70	22.00	8.51	34.31	0.06	0.94	4.22
No.of seeds per plant	113.52- 502.79	232.71	10.04	46.90	0.04	8.94	3.84
Fresh biomass (g)	112.00- 348.00	224.01	8.76	39.51	0.05	9.07	4.05
Dry biomass (g)	24.66 - 102.66	45.51	10.18	48.14	0.04	1.79	3.93
Test weight (g)	6.30 - 14.43	11.96	17.84	20.22	0.77	3.81	31.86
Grain yield per plant (g)	11.25 - 63.52	28.38	7.23	42.05	0.03	0.73	2.58

(48.14) followed by number of seeds per plant (46.90), grain yield per plant (42.05) and fresh biomass (39.51).

The lowest GCV and PCV values were recorded for days to maturity (0.80) and plant spread (7.20) respectively.

The maximum difference between PCV and GCV values was observed for dry biomass followed by number of seeds per plant and grain yield per plant. The lowest difference was observed for days to 50 per cent flowering.

4.4.2 Heritability (b.s)

The heritability (b.s) estimates ranged between 1.0 and 77.0 per cent. The character test weight recorded the highest estimate (77.0 %) of heritability followed by days to 50 per cent flowering. The heritability estimate for pod length was 15 per cent and it was less than ten per cent for all other characters viz., plant spread (8 %), number of branches (6 %), number of pods per plant (6 %), plant height (5 %), fresh biomass 5 per cent, dry biomass (4 %), number of seeds per pod (4 %), grain yield (3 %) and days to maturity (1 %).

4.4.3 Genetic advance

The highest magnitude of genetic advance was observed for fresh biomass (9.07) followed by number of seeds per plant (8.94), test weight (3.81) and days to 50 per cent flowering (2.48). All the remaining characters recorded very low values for genetic advance of which number of branches (0.10) recorded the least value.

4.5 Correlation

The simple correlation coefficients among the twelve characters are presented in Table 4.5.

Table 4.5 Simple correlation coefficients of 12 characters in M_3 mutants of cowpea

Characters	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No.of branches per plant	Pod length (cm)	No. of pods per plant	No.of seeds per plant	Fresh biomass (g)	Dry biomass (g)	Test weight (g)	Grain yield per plant (g)
Days to 50 % flowering	1.0000	0.3019**	-0.0193	0.0879	-0.2115*	0.0084	-0.4221**	-0.2770**	0.1368	0.0509	0.0383	-0.2119*
Days to maturity		1.0000	-0.0069	0.0329	-0.0791	-0.0345	-0.2276	-0.2392	-0.0003	-0.0189	0.0443	0.0555
Plant height (cm)			1.0000	0.2440*	0.3255**	0.1987*	0.0357	-0.1228	0.3528**	0.0572	0.1999*	0.0400
Plant spread (cm)				1.0000	0.0712	0.0373	-0.0457	-0.1371	0.2589**	0.0046	0.0440	-0.0179
No.of branches per plant					1.0000	0.3086**	0.1398	0.2042*	0.5303**	0.2653**	0.3033**	0.3803**
Pod length (cm)						1.0000	-0.2690	-0.0898	0.1828	0.0491	0.6190**	0.3946**
No.of pods per plant							1.0000	0.5116**	0.0306	-0.0090	-0.1481	0.2462*
No.of seeds per plant								1.0000	-0.0456	0.0788	-0.2581**	0.6287**
Fresh biomass (g)									1.0000	0.1582	0.2996**	0.1673
Dry biomass (g)										1.0000	0.0857	0.1019
Test weight (g)											1.0000	0.4562**
Grain yield per plant (g)												1.0000

* ,** Significant at 5 and 1 per cent probability respectively

4.5.1 Association of grain yield with other characters

The characters number of seeds per plant (0.628), test weight (0.456), pod length (0.394), number of branches per plant (0.380) and number of pods per plant (0.246) showed significant positive association with grain yield per plant. However, days to 50 per cent flowering (-0.212) recorded significant negative correlation with grain yield.

The characters fresh biomass (0.167), dry biomass (0.102), days to maturity (0.055) and plant height (0.040) recorded nonsignificant positive correlation with grain yield, while the character plant spread (-0.017) showed nonsignificant negative correlation with grain yield per plant.

4.5.2 Association between remaining eleven characters.

The correlations between other characters at genotypic level are presented below.

Days to 50 per cent flowering recorded significant positive correlation with days to maturity (0.301). However, it was significantly and negatively correlated with number of pods per plant (0.422) number of seeds per plant (-0.277) and number of branches per plant (-0.211).

Days to maturity showed significant and negative correlation with number of seeds per plant (-0.239) and number of pods per plant (-0.227).

The characters fresh biomass (0.352), number of branches per plant (0.325), plant spread (0.244), test weight (0.199) and pod length (0.198) recorded significant positive correlation with plant height. The character plant spread showed significant positive correlation with fresh biomass (0.258).

Number of branches per plant showed significant positive correlation with fresh biomass (0.530), pod length (0.308), test weight

(0.303), dry biomass (0.265) and number of seeds per plant (0.204).

The component pod length recorded significant positive correlation with test weight (0.619) and significant negative correlation with number of pods per plant (-0.269).

Number of pods per plant recorded significant positive correlation with number of seeds per plant (0.511). The character fresh biomass was also significantly and positively correlated with test weight. All the other positive and negative associations among the characters were non-significant.

4.6 Path analysis

The direct and indirect contributions of each character as revealed by path analysis are presented in Table 4.6.

4.6.1 Direct effects

In the present study number of seeds per plant (0.872) recorded the maximum positive direct effect on grain yield per plant followed by test weight (0.606). Both these traits recorded significant positive correlation with grain yield per plant.

Among the other characters, days to maturity (0.254), pod length (0.087), plant spread (0.067) and fresh biomass (0.020) showed positive direct effects of low magnitude on grain yield per plant. However, the trait plant spread showed direct positive effect on grain yield per plant and recorded non-significant negative correlation with grain yield per plant.

The character days to 50 per cent flowering (-0.112) had maximum negative direct effect on grain yield per plant followed by number of pods per plant (-0.071), dry biomass (-0.013), number of branches per plant (-0.012) and plant height (-0.008). It is interesting to report that while

Table 4.6 Direct (diagonal) and indirect (above and below diagonal) path effects of different characters towards yield in M_3 mutants of cowpea

Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No.of branches per plant	Pod length (cm)	No. of pods per plant	No.of seeds per plant	Fresh biomass (g)	Dry biomass (g)	Test weight (g)	Corr. with grain yield per plant
Days to 50 % flowering	**-0.1122**	-0.0339	0.0022	-0.0099	0.0237	-0.0009	0.0473	0.0311	-0.0153	-0.0057	-0.0043	-0.2119*
Days to maturity	0.0768	**0.2544**	-0.0018	0.0084	-0.0201	-0.0088	-0.0579	-0.0609	-0.0001	-0.0048	0.0113	0.0555
Plant height (cm)	0.0002	0.0001	**-0.0087**	-0.0021	-0.0028	-0.0017	-0.0003	0.0011	-0.0031	-0.0005	-0.0017	0.0400
Plant spread (cm)	0.0059	0.0022	0.0165	**0.0676**	0.0048	0.0025	-0.0031	-0.0093	0.0175	0.0003	0.0030	-0.0179
No.of branches per plant	0.0025	0.0009	-0.0039	-0.0009	**-0.0120**	-0.0037	-0.0017	-0.0024	-0.0063	-0.0032	-0.0036	0.3803**
Pod length (cm)	0.0007	-0.0030	0.0174	0.0033	0.0270	**0.0874**	-0.0235	-0.0079	0.0160	0.0043	0.0541	0.3946**
No. of pods per plant	0.0303	0.0163	-0.0026	0.0033	-0.0100	0.0193	**-0.0717**	-0.0367	-0.0022	0.0006	0.0106	0.2462*
No.of seeds per plant	-0.2416	-0.2086	-0.1071	-0.1196	0.1781	-0.0784	0.4462	**0.8723**	-0.0398	0.0687	-0.2251	0.6287**
Fresh biomass (g)	0.0029	0.0000	0.0074	0.0054	0.0111	0.0038	0.0006	-0.0010	**0.0209**	0.0033	0.0063	0.1673
Dry biomass (g)	-0.0007	0.0002	-0.0008	-0.0001	-0.0035	-0.0006	0.0001	-0.0010	-0.0021	**-0.0132**	-0.0011	0.1019
Test weight (g)	0.0232	0.0269	0.1213	0.0267	0.1841	0.3757	-0.0899	-0.1566	0.1818	0.0520	**0.6069**	0.4562**

*, ** Significant at 5 and 1 per cent probability respectively

days to 50 per cent flowering recorded significant negative correlation with grain yield per plant, the characters number of pods per plant and number of branches per plant showed significant positive correlation with grain yield per plant. Two other traits (plant height and dry biomass) with negative direct effects showed non-significant positive correlation with grain yield per plant.

4.6.2 Indirect effects

Days to 50 per cent flowering had significant negative correlation with grain yield per plant, which was indirectly contributed by number of seeds per plant (-0.241) negatively, while days to maturity (0.076), number of pods per plant (0.030) and test weight (0.023) contributed positively.

The trait, number of branches per plant showed significant positive correlation with grain yield per plant, which was indirectly contributed by test weight (0.184), number of seeds per plant (0.178), pod length (0.027), days to 50 per cent flowering (0.023 and days to maturity (-0.0201).

Pod length recorded significant positive correlation with grain yield per plant which was indirectly contributed by test weight (0.375), number of pods per plant (0.019) and number of seeds per plant (-0.078). The trait, number of pods per plant showed significant positive correlation with grain yield per plant which was contributed indirectly by number of seeds per plant (0.446), days to 50 per cent flowering (0.047), test weight (-0.089), days to maturity (-0.057) and pod length (-0.023).

Number of seeds per plant recorded significant positive correlation with grain yield per plant which was contributed indirectly by days to 50 per cent flowering (0.031), test weight (-0.156), days to maturity (-0.060) and number of pods per plant (-0.036).

Test weight showed highly significant positive correlation with grain yield per plant which was indirectly contributed by pod length (0.054), days to maturity (0.011), number of pods per plant (0.010) and number of seeds per plant (-0.225).

4.7 Divergence

The genetic divergence among the 99 mutants was estimated using Mahalanobis D^2 statistics. The D^2 values ranged between 0.82 and 88.44.

4.7.1 Cluster formation

The cluster formation was done as per Tocher's method as described by Rao (1952). The 99 mutants studied with three parents were grouped into three clusters, cluster I was the largest cluster with 91 mutants followed by cluster II with 10 mutants. Cluster III was monogenotypic with a single mutant indicating wide diversity from the rest. (Table 4.7)

4.7.2 Intra and inter cluster distance

The intra and inter cluster D^2 and D values were worked out using Mahalanobis D^2 statistics. The mean D^2 values (Table 4.8) of cluster elements were used as measures of intra and inter cluster distance.

The maximum intra cluster distance was observed for cluster II (D^2= 14.98) and the lowest intra cluster distance was observed for cluster I (D^2 = 12.52). Cluster III being monogenotypic showed no intra cluster distance.

The inter cluster distance was the highest between cluster II and III (D^2 = 69.98) followed by Cluster I and III (D^2 = 45.20). The lowest inter cluster distance was observed between cluster I and II (D^2 = 38.33).

Cluster I had the largest distance from cluster III (D^2 = 45.20) followed by cluster II (38.33), while cluster II had the largest distance from cluster III (D^2 = 69.98).

Table 4.7 Distribution of 102 lines of cowpea into different clusters

Cluster number	Number of lines	Lines
I	91	11-1, 24-1, 8-1, 18-3, 28-7, 725-4, 13-1, 23-1, 12-7, 37-20, 25-7, 745-15, 6-7, 19-1, 6-2, 12-4, 25-10, 25-3, 22-13, 8-3, 20-6, 62-1, 776-10, 57-1, 78-1, 69-7, 40-5, 67-12, 76-2, 76-1, 43-1, 68-26, 782-1, 67-1, 58-3, 98-11, 101-8, 92-7, 96-9, 114-30, 673-3, 108-2, 101-28, 119-26, 18-14, 684-14, 97-5, 110-30, 96-12, 108-5, 108-8, 109-1, 108-2, 65-12, 96-7, 118-20, 683-6, 105-22, 120-24, 121-18, 684-7, 95-5, 680-1, 98-2, 713-14, 113-18, 105-19, 691-18, 120-18, 116-28, 117-16, 89-1, 113-26, 121-24, 102-20, 118-4, 715-15, 121-5, 707-17, 117-18, 93-1, 107-16, 707-3, 119-27, 282-12, 480-7, 499-1, 313-4, 320-8, 624-1, 359-2
II	10	161-8, 517-2, 231-25, 403-18, 229-27, 217-28, 198-1, 308-6, 596-30, 313-22.
III	1	119-17

Table 4.8 Average intra and inter cluster D^2 and D values in M_3 mutants in cowpea.

Clusters	I	II	III
I	12.52 (3.54)	38.33 (6.19)	45.20 (6.72)
II		14.98 (3.87)	69.98 (8.37)
III			0.00

Figure in parenthesis denotes D values.

4.8 Cluster means

The cluster means for all the 12 characters studied are presented in Table 4.9.

4.8.1 Days to 50 per cent flowering

The mutants in cluster II were early for days to 50 per cent flowering (57.33) followed closely by mutants of cluster I (58.51), while the mutants of cluster III (59.67) were late for days to 50 per cent flowering.

4.8.2 Days to maturity

Cluster means for days to maturity revealed that cluster II (96.33) was earliest to mature followed by cluster I (96.81). Cluster III (108.00) was late for days to maturity.

4.8.3 Plant height (cm)

The tallest mutants were grouped into cluster I (94.52) followed by cluster III (93.70), while the dwarf mutants were grouped into cluster II (90.65).

4.8.4 Plant spread (cm)

The mutants of cluster III (39.31 cm) had the maximum plant spread followed by cluster I (38.51 cm). Minimum plant spread was observed in cluster II (37.29 cm).

4.8.5 Number of branches per plant

The mutants with the maximum number of branches were grouped into cluster III (3.47) followed by cluster I (3.41) whereas the mutants with least number of branches were grouped into cluster II (3.26).

Table 4.9 Mean performance of clusters for 12 characters in M_3 mutants of cowpea

Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No.of branches per plant	Pod length (cm)	No. of pods per plant	No.of seeds per plant	Fresh biomass (g)	Dry biomass (g)	Test weight (g)	Grain yield per plant (g)
Clusters												
I	58.51	96.81	94.52	38.51	3.41	16.21	21.81	229.58	228.18	45.85	12.50	29.09
II	57.33	96.33	90.65	37.29	3.26	14.82	24.42	273.19	184.67	42.60	7.00	21.25
III	59.67	108.00	93.70	39.31	3.47	15.65	14.80	113.53	237.33	43.33	12.63	34.53

4.8.6 Pod length (cm)

The cluster I (16.21 cm) recorded the highest cluster mean for pod length followed by cluster III (15.65 cm). The lowest cluster mean for pod length was recorded by cluster II (14.82 cm).

4.8.7 Number of pods per plant

The mutants of cluster II (24.42) recorded maximum number of pods followed by cluster I (21.81), while the mutants of cluster III (14.80) recorded the least number of pods per plant.

4.8.8 Number of seeds per plant

Cluster II (273.19) recorded the highest mean for number of seeds per plant followed by cluster I (229.58) while the minimum number of seeds per plant was recorded by cluster III (113.53).

4.8.9 Fresh biomass (g)

The cluster mean for fresh biomass was the highest for cluster III (237.33) followed by cluster I (228.18), while cluster II (184.67) recorded the least value for fresh biomass.

4.8.10 Dry biomass (g)

The mutants with high dry biomass were grouped into cluster I (45.85) followed by cluster III (43.33) and those with low dry biomass were grouped into cluster II (42.60).

4.8.11 Test weight (g)

Cluster III (12.63) showed the highest mean for test weight followed by cluster I (12.50). The lowest mean for test weight was shown by cluster II (7.00).

4.8.12 Grain yield per plant (g)

The mutants with high grain yield per plant were grouped into cluster III (34.53 g) followed by cluster I (29.99 g), while with low grain yield per plant were grouped into cluster II (21.25 g).

4.9 Per cent contribution of various characters for divergence (%)

Among the twelve characters studied in 99 mutant lines along with three parents, test weight (35.88 %) contributed maximum for divergence followed by days to 50 per cent flowering (9.94 %), number of pods per plant (9.25 %) and pod length (7.96 %). Grain yield per plant (4.24 %) and dry weight (5.35 %) contributed the least for genetic divergence (Table 4.10).

Table 4.10 Per cent contribution of various characters to divergence

Sr.No	Characters	Per cent contribution.
1	Days to 50 % flowering	9.94
2	Days to maturity	0.95
3	Plant height (cm)	6.61
4	Plant spread (cm)	5.45
5	No.of branches per plant	5.62
6	Pod length (cm)	7.96
7	No. of pods per plant	9.25
8	No.of seeds per plant	4.71
9	Fresh biomass (g)	6.04
10	Dry biomass (g)	5.35
11	Test weight (g)	35.88
12	Grain yield per plant (g)	4.24

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DISCUSSION

5. DISCUSSION

Genetic variability and diversity are important prerequisites for success of any breeding programme and selection of elite genotypes. Genotypic and phenotypic coefficients of variation are the simple measures of variability to assess the extent of variability present in a population for a particular character. Heritability on the other hand suggests the relative role of genetic factors in expression of phenotypes (Falconer, 1989). It also acts as an index of inheritance of a particular character to its offspring. Genetic advance on the other hand measures the expected genetic gain from the selection applied in a population. Heritability along with genetic advance gives the best picture of efficiency of selection.

The study of correlations provides the interrelationships among the quantitative traits which facilitates the choice of suitable breeding method for the improvement of the crop. Where as path analysis helps to know the direct and indirect effects of characters on the yield. The D^2 statistics suggested by Mahalanobis (1936) and clustering by Rao (1952) helps to select the genetically diverse genotypes for hybridization programme.

In the present investigation, entitled "Path analysis and genetic diversity studies in M_3 lines of cowpea" attempts were made to study the variability for 12 different quantitative characters among 99 mutants lines along with three parents. The results on various aspects are discussed in this chapter under the following sub headings.

5.1 Variability

5.2 Heritability and genetic advance

5.3 Correlation

5.4 Path analysis

5.5 Genetic divergence

5.1 Variability

In the present investigation considerable amount of variability was observed for all the twelve characters studied. The variation observed for grain yield per plant ranged between 11.25 and 63.52 g with a mean of 28.38 g. The other yield related characters also showed substantial amount of variability viz., days to 50 per cent flowering (50.33 - 62.66), plant height (79.66 - 118 cm), plant spread (34.17 - 42.42 cm), number of branches per plant (2.33 - 4.8), pod length (11.88 - 18.72 cm), number of pods per plant (14.61 - 39.70), number of seeds per plant (113.52 - 502.79), fresh biomass (112 - 348 g), dry biomass (24.66 - 102.66 g) and test weight (6.30 - 14.43 g). However, the variability for days to maturity (93.33 - 99.33) was comparatively narrow.

Among the 102 genotypes (99 mutants and 3 parents) studied, mutants 231-25 (days to 50 per cent flowering), 57-1 (days to maturity), 11-1 (plant height), 707-17 (number of branches), 707-3 (plant spread), 96-7 (pod length), 24-1 (number of pods per plant and fresh biomass), 120-18 (number of seeds per plant and grain yield per plant), 108-8 (dry biomass) and 19-1 (test weight) recorded the highest *per se* performance for the respective characters.

The estimates of phenotypic coefficient of variation were higher than the estimates of genotypic coefficient of variation for all characters studied indicating the influence of environment on these traits.

The PCV estimates were high for dry biomass, number of seeds per plant, grain yield per plant, fresh biomass and number of pods per plant. These results confirmed the findings of Ramachandran *et al.* (1980), Patil and Baviskar (1987), Savant (1994), Khan *et al.* (1999) and Singh *et al.* (2001) for both grain yield per plant and number of pods per plant; Choulwar and Borikar (1986), Ariyo *et al.* (1995), Vardhan and Savithramma (1998 a), Sarma and Talukdar (1991) and Tyagi *et al.* (2000)

for grain yield per plant; Backiyarani and Nadarajan (1996), Kalaiyarasi and Palanisamy (1998) and Nehru and Manjunath (2001) for number of pods per plant and Roquib and Patnaik (1990) for fresh biomass.

Test weight recorded the highest GCV values which was in confirmation with the results of Patil and Baviskar (1987), Sawant (1994), Backiyarani and Nadarajan (1996) and Nehru and Manjunath (2001).

The characters days to maturity, plant spread, plant height and days to 50 per cent flowering had very low GCV and PCV estimates suggesting narrow range of variation for these characters. These results were in accordance with the findings of Ariyo *et al.* (1995) for days s to 50 per cent flowering. However, Thaware (1992), Sawant (1994), Vardhan and Savithramma (1998 a), Sharma (1999), Tyagi *et al.*(2000) and Nehru and Manjunath (2001) reported contrasting results for plant height.

Maximum magnitudinal difference between PCV and GCV estimates was observed for dry biomass followed by number seeds per plant and grain yield per plant suggesting considerable influence of environment on these traits. However, the differences between PCV and GCV estimates were minimum for days to 50 per cent flowering followed by test weight suggesting less influence of environment on the expression of these characters.

In the present investigation, the 99 mutants were classified into different groups based on varieties and doses of gamma radiations. The mean performance for the various characters (Table 4.3) are discussed below :

The mutants of No.889 (V_1) and Sangavi local (V_2) showed earliness for days to 50 per cent flowering for all the 3 doses of gamma radiations (T_1 = 10 KR, T_2 = 25 KR, T_3 = 35 KR) of which the mutants of V_1T_3 and V_2T_1 were the earliest for days to 50 per cent flowering suggesting that the gamma radiations of 35 KR and 10 KR dose for varieties No. 889 and Sangavi local respectively, can be employed to induce earliness. However, for the variety GC 10 the gamma radiations had a contrasting effect and resulted in delayed 50 per cent flowering.

In variability for days to maturity, the mutants of Sangavi local (V_2) were early to mature for all the three doses of gamma radiation, of which the mutants of 10 KR dose were the earliest suggesting the use of gamma radiations of 10 KR to induce earliness for days to maturity in cowpea. However, the varieties No. 889 and GC 10 had negative effect of gamma radiations and were late to mature.

Irradiation of variety GC 10 (V_3) with gamma radiation resulted in increase of plant height. Maximum increase in plant height was recorded in the mutants of V_3T_1 suggesting the use of gamma radiations of 10 KR dose to increase plant height. However, irradiation of varieties No. 889 (V_1) and Sangavi local (V_2) induced dwarfness among the mutants.

Irradiation of No. 889 (V_1), Sangavi local (V_2) and GC 10 (V_3) with 10, 25 and 35 KR of gamma radiations produced maximum increase in plant spread for V_3T_1 followed by V_3T_2 suggesting that variety GC 10 is responsive to gamma radiations for increasing plant spread. The other varieties recorded decrease in plant spread for other doses of gamma radiations.

The trait, number of branches per plant was markedly influenced by gamma irradiations. There was a substantial reduction in number of branches per plant in case of No. 889 and Sangavi local for all the doses and in GC 10 for 25 KR dose, suggesting that gamma radiations in general bring about a reduction in number of branches per plant.

There was a substantial increase in pod length for all the doses of gamma radiation in variety No. 889, 10 KR and 25 KR doses in case of

Sangavi local and 10 KR dose in case of GC 10. The results suggested that variety No. 889 is responsive for irradiations to improve pod length.

An increase in number of pods per plant was observed in all doses of gamma radiations for No. 889 and Sangavi local and a marginal increase for GC 10 for 25 KR dose suggesting that gamma radiations can be employed to induce variability and bring about an increase in number of pods per plant.

Similar to number of pods per plant, there was a substantial increase in number of seeds per plant for all doses of gamma radiations in No. 889 and GC 10 and 10 KR dose in Sangavi local. These result suggested that varieties No. 889 and GC 10 respond positively to gamma irradiations bringing about an improvement in number of seeds per plant.

The three varieties viz., No. 889, Sangavi local and GC 10 gave similar results for both fresh and dry biomass. There was a marginal reduction in fresh and dry biomass in No. 889 and Sangavi local for all the doses of gamma radiations. However, variety GC 10 responded positively to gamma radiation and produced greater fresh and dry biomass suggesting that gamma radiations can be employed to improve the biomass in the variety GC 10.

Among the 3 varieties, it was observed that gamma irradiations cause a substantial increase in test weight in varieties Sangavi local and GC 10. However, maximum increase in test weight was observed for 35 KR dose in Sangavi local and 25 KR dose in GC 10 suggesting that high doses of gamma radiations can be employed to increase the test weight in Sangavi local and GC 10. On the other hand, the radiations resulted in decrease in the test weight in No. 889.

The grain yield per plant showed an increase in all varieties and for all doses of gamma radiations. However, the maximum increase in grain yield per plant was recorded for 10 KR dose in No. 889 and Sangavi local and for 25 KR dose in GC 10. These results suggested that good variation and substantial increase in grain yield per plant can be brought about by irradiating No. 889, Sangavi local and GC 10 with gamma radiations.

5.2 Heritability and genetic advance

Heritability helps in identifying the resemblance between parents and their progeny while genetic advance provides the knowledge about expected gain for a particular character after selection (Falconer, 1989). High heritability with high genetic advance is said to be governed by additive gene action suggesting direct selection for traits. However any other results i.e. high heritability with low genetic advance or low heritability with high genetic advance are the result of non-additive gene action and selection for such traits may not be rewarding.

In the present investigation, high heritability estimates were obtained for test weight, days to 50 per cent flowering and pod length indicating least environmental influence. Similar results were obtained by Jana *et al.* (1983), Apte *et al.* (1987), Thiyagarajan (1989), Damarany (1994), Sawant (1994) and Rewale *et al.* (1995) for test weight; Dharmalingam and Kadambavanasundaram (1989) and Nehru and Manjunath (2001) for test weight and pod length and Ramachandran *et al.* (1980), Patnaik (1990), Gunasekaran *et al.* (1998) and Tyagi *et al.* (2000) for days to 50 per cent flowering.

The traits test weight (77 %) and days to 50 per cent flowering (37 %) showed high heritability estimates accompanied with good genetic advance which is due to additive gene action and direct selection for such traits is rewarding in crop improvement. These results were in accordance with Apte *et al.* (1987), Thiyagarajan and Natarajan (1989), Sawant (1994) and Rewale *et al.* (1995) for test weight and Roquib and Patnaik (1990), Gunasekaran *et al.* (1998) and Tyagi *et al.* (2000) for days to 50 per cent flowering.

Low estimates of heritability coupled with high genetic advance were observed for the characters fresh biomass and number of seeds per plant. The low heritability estimates were due to high environmental effects but high estimates of genetic advance suggest that direct selection may be rewarding.

All the other traits viz., days to maturity, plant height, plant spread, number of branches per plant, pod length, number of pods per plant, dry biomass and grain yield per plant recorded low heritability estimates coupled with low genetic advance suggesting that selection for these traits will be ineffective.

5.3 Correlation

Correlation coefficient is a statistical measure which is used to find out the degree (strength) and direction of relationship between two or more variables. The information on the interrelationship among the traits facilitates the choice of a suitable breeding method to be applied and selecting the parents for crop improvement.

In the present investigation the characters number of seeds per plant, test weight, pod length, number of branches per plant and number of pods per plant showed significant positive association with grain yield per plant indicating dependence of these characters on each other. Similar findings were reported by Sawant (1994) for test weight, pod length, number of branches per plant and number of pods per plant; by Patil *et al.* (1989), Parihar *et al.* (1997) and Tyagi *et al.* (2000) for test weight, pod length and number of pods per plant; by Damarany (1994) for number of seeds per plant, number of branches per plant and number of pods per plant; by Chikkadyavaiah (1985) for test weight and number of branches; by Gowda

(1996) for test weight and number of pods per plant; by Naidu *et al.* (1996) and Sreekumar *et al.* (1996) for pod length and number of pods per plant and by Sharma *et al.* (1988), Siddique and Gupta (1991), Sarma *et al.* (1992), Oseni *et al.* (1992) and Murugan *et al.* (1995) for number of pods per plant.

The trait days to 50 per cent flowering recorded significant negative correlation with grain yield. This result was in accordance with the findings of Sharma and Mishra (1997 a) and Tyagi *et al.* (2000). However, contrasting results were reported by Patil *et al.* (1989) and Siddique and Gupta (1999).

The other traits, viz., fresh biomass, dry biomass, days to maturity and plant height recorded non-significant positive correlation, while plant spread showed non-significant negative correlation with grain yield per plant suggesting absence of any influence of these traits on grain yield per plant. Conflicting findings were reported by Damarany (1994), Tamilselvam and Das (1994), Parihar *et al.* (1997) and Tyagi *et al.* (2000) for plant height and by Ponmariammal and Vijendradas (1996) for plant height and dry biomass.

The trait days to 50 per cent flowering recorded significant positive correlation with days to maturity. Similar results were reported by Naidu *et al.* (1996), Sharma and Mishra (1997 a) and Tyagi *et al.* (2000). However, it was significantly and negatively correlated with number of pods per plant, number of seeds per plant and number of branches per plant. These results were contradictory to the findings of Tyagi *et al.* (2000) for number of pods per plant.

The yield component pod length recorded significant positive correlation with test weight confirming the findings of Patil and Bhapkar (1987 a). However, pod length was significantly and negatively correlated with number of pods per plant, which was in accordance with the findings of Patil and Bhapkar (1987 a) and contradictory to the results of Nagaraj and Savithramma (2000).

The component days to maturity showed significant negative correlation with number of seeds per plant and number of pods per plant indicating that selection for short duration and early maturing lines may ensure more number of seeds and pods per plant.

The trait plant height showed significant positive correlation with fresh biomass, number of branches per plant, plant spread, test weight and pod length suggesting that selection for increased plant height will be rewarded with increased production of fresh biomass, number of branches per plant, plant spread, test weight and pod length.

The significant negative correlations observed for test weight with number of pods per plant may pose difficulties for improvement of these traits.

5.4 Path analysis

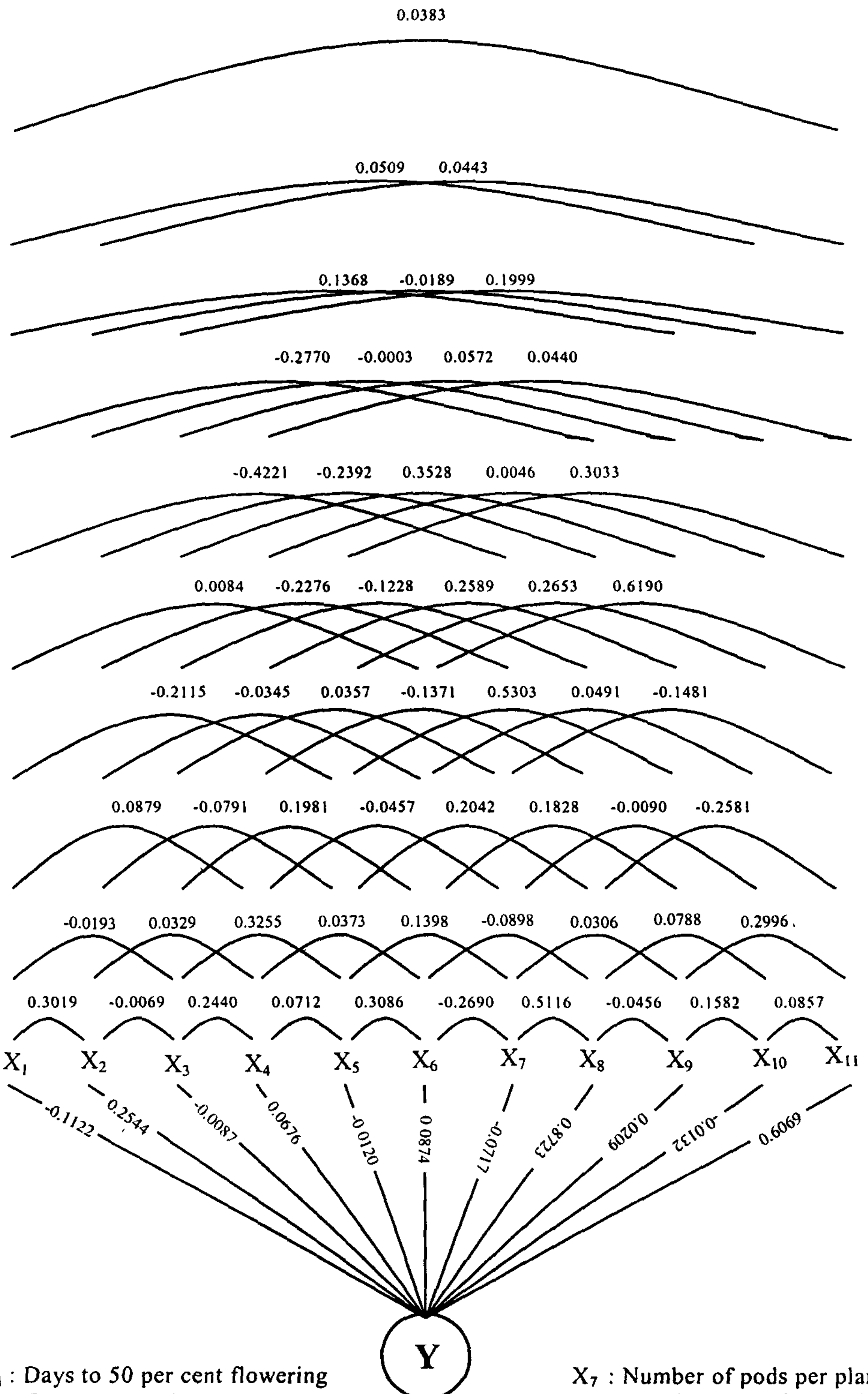
Path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation coefficient into measures of direct and indirect effects (Singh and Narayanan, 2000). In the present investigation path analysis was worked out by following Dewey and Lu (1959) to estimate the magnitude and direction of direct and indirect effects of various yield and yield contributing characters. Correlation coefficients along with path effects together provide more reliable information, which can be best used in crop improvement. If the correlation between a causal factor and direct effect is more or less of equal magnitude, it explains the true relationship between the traits and direct selection through these traits will be rewarding. However, if the correlation coefficient is positive and the direct effect is negative or negligible the indirect causal factors are to be considered in simultaneous selection (Singh and Kaker, 1977).

The direct and indirect effects of components of yield studied in 102 lines (99 mutants and 3 parents) are presented in Table 4.6 and Figure 5.1

In the present study of 12 characters, number of seeds per plant and test weight recorded high magnitudes of direct effects accompanied by highly significant correlation with grain yield per plant, indicating true and perfect relationship between them. Thus suggesting that selection for these traits viz., number of seeds per plant and test weight will be highly rewarding for improving the grain yield per plant. Earlier findings of Patil and Bhapkar (1987 a), Patil *et al.* (1989), Oseni *et al.* (1992), Gupta (1992), Sawant (1994), Hamid *et al.* (1996) and Tyagi *et al.* (2000) for test weight and Gupta (1992), Damarany (1992) and Sawant (1994) for number of seeds per plant were similar to the present results.

The trait days to maturity recorded high magnitude of direct effect towards grain yield per plant suggesting direct selections for the trait to improve grain yield. Similar results were obtained by Patnaik and Roquib (1990) and Tyagi *et al.* (2000). Days to 50 per cent flowering recorded negative direct effect of low magnitude accompanied by significant negative correlation suggesting that selection for early flowering will result in improvement of grain yield.

The yield components number of branches per plant, pod length and number of pods per plant recorded negligible direct effects to grain yield but were significantly and positively correlated with grain yield per plant indicating the indirect influence via some other traits to grain yield. This was confirmed by the high magnitude of indirect effect of test weight and number of seeds per plant through number of branches per plant. Indirect effects of test weight through pod length and indirect effect of number of



X_1 : Days to 50 per cent flowering
X_2 : Days to maturity
X_3 : Plant height
X_4 : Plant spread
X_5 : Number of branches per plant
X_6 : Pod length

X_7 : Number of pods per plant
X_8 : Number of seeds per plant
X_9 : Fresh biomass
X_{10} : Dry biomass
X_{11} : Test weight
Y : Grain yield per plant

Figure 5.1 Path diagram showing nature of causal system variables with their coefficient for path analysis in M_3 mutants of cowpea

seeds per plant through number of pods per plant. These findings suggest indirect selection of test weight and number of seeds per plant for yield improvement. Similar results were reported by Kalaiyarasi and Palanisamy (2000).

5.5 Divergence

Genetic diversity plays an important role in selection of elite and diverse genotypes as parents to obtain maximum heterosis. It would be possible to identify desirable genotypes from the genetic variability estimated, but unless a sound knowledge of divergence is available it is difficult to expect any outstanding results from the progeny.

Mahalanobis (1936) developed the concept of D^2 statistics for measuring genetic divergence. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding. This technique is extensively used in quantifying the degree of divergence between biological population at genotypic level and to assess the relative contribution of different components to total divergence at both intra and inter cluster level.

5.5.1 Clusters, intra and inter-cluster distance and mean performance

The basic concept behind formation of clusters is to obtain intra and inter cluster distances. These distances act as an index for selection of parents with diverse origin. The intra and inter cluster values are the means derived from D^2 values of cluster elements. The crossing between the genotypes in different clusters with high inter cluster D^2 values will prove to be a more correct approach to get desirable results.

In the present investigation, the 99 mutants along with 3 parents were grouped into 3 clusters as per Tochers method as described by Rao

(1952). Cluster I was the largest with 91 M_3 lines, followed by cluster II with 10 lines. The third cluster was monogenotypic. The mean D^2 values for the clusters ranged between 12.52 and 69.98 indicating the presence of good diversity in the material used for the current studies and the monogenotypic nature of the third cluster indicated maximum divergence from other groups. Wide range of diversity was also reported by earlier workers viz., Kumar *et al.* (1982) grouped 50 cowpea genotypes into seven clusters, Jindal (1985) grouped 52 indigenous and exotic varieties into eight clusters, Thiyagarajan and Natarajan (1989) grouped 30 geographically diverse accessions of cowpea into 4 clusters. Similar clustering was done by Patil and Bhapkar (1987 b), Thiyagarajan *et al.* (1988), Dharmalingam and Kadambavanasundaram (1989), Sarma and Talukdar (1991), Sarma *et al.* (1992), Rewale *et al.* (1996), Sharma and Mishra (1997 a), Viswanathan *et al.* (1998) and Tyagi *et al.* (1999).

The maximum intra cluster distance was observed for cluster II (D = 3.87) followed by cluster I (D = 3.54) indicating that the genotypes of these clusters might be differing marginally in their genetic architecture (Table 4.8 and Figure 5.2). In the case of cluster III the intra cluster distance is zero because of its monogenotypic nature.

The maximum inter cluster distance was observed between cluster II and cluster III (D = 8.37) followed by cluster I and cluster III (D = 6.72) and cluster I and cluster II (D = 6.19). These results suggest maximum divergence between genotypes of cluster II with genotypes of cluster III indicating the fact that genotypes present in one cluster differ entirely from those present in other clusters and mutation breeding through gamma rays helped to create good genetic variability.

Considering the mean performance of the three clusters for the 12 characters (Table 4.9) it was observed that cluster mean for days to 50 per cent flowering, days to maturity, plant spread, number of branches per

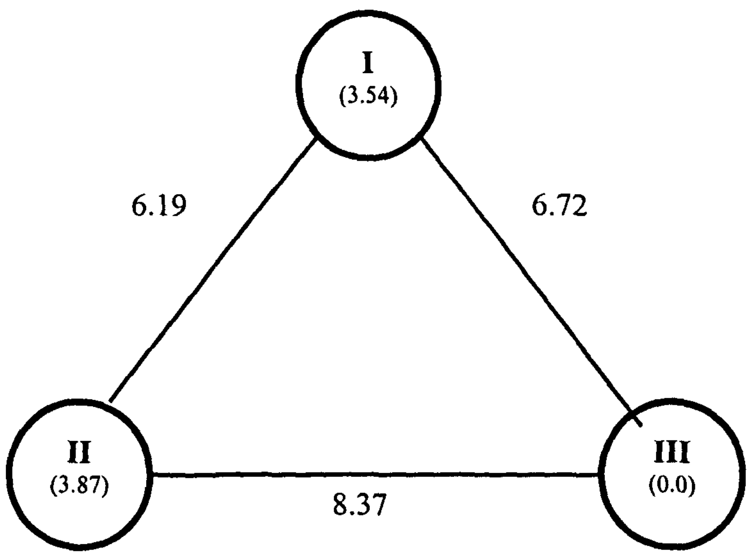


Figure 5.2 A cluster diagram showing interrelationship between three clusters

* Values in parenthesis are intra cluster values

plant, fresh biomass, test weight and grain yield per plant was maximum for cluster III. Cluster II exhibited maximum number of pods per plant and number of seeds per plant while cluster I showed maximum performance for plant height, pod length and dry biomass.

5.5.2 Relative contribution of different character towards divergence

Looking at the relative contribution of all the twelve characters towards divergence it was observed that test weight (35.88 %) contributed maximum for divergence followed by days to 50 per cent flowering (9.94 %), number of pods per plant (9.25 %) and pod length (7.96 %). These results were in agreement with the findings of Rewale *et al.* (1996), Kumar *et al.* (1982) and Renganayaki and Rangasamy (1991) for test weight and pod length; Thiyagarajan *et al.* (1988) and Rewale *et al.* (1996) for days to 50 per cent flowering and 100 seed weight; Thiyagarajan and Natrajan (1989) for pods per plant and Sharma and Mishra (1997 a) for days to 50 per cent flowering.

The traits grain yield per plant and dry biomass contributed least for genetic divergence. These findings were contradictory to the earlier results reported by Jindal and Gupta (1985), Thiyagarajan and Natarajan (1989), Renganayaki and Rangasamy (1991) and Thaware *et al.* (1997). The results obtained in the present investigation and work done by earlier workers indicate that yield indicators responsible for divergence varied substantially, which may be attributed to environment and dissimilarity of the material used for the investigation.

5.5.3 Genetic diversity as an index for selecting desirable parents for hybridization.

The present investigation on genetic diversity among the mutants of cowpea has generated valuable information which could be used in selection of elite and diverse parents to obtain maximum heterosis. Hays and Johnson (1939) and East and Hays (1942) realized that crosses between divergent parents usually produce greater heterosis than those between closely related parents. Bhatt (1970) advocated the use of multi variate analysis for selection of parents. He also stated that statistical distance of all possible cluster combination may be considered arbitrarily as a guide line and suggested crossing between individual genotypes of different clusters showing an inter cluster distance equal to statistical mean.

Arunachalam and Bandopadhyay (1984) proposed and derived a method of assorting parental diversity into 4 divergent classes (DC) viz., DC_1, DC_2, DC_3, and DC_4. To take into account the magnitude of variation in parental divergence, the mean (H) and standard deviation (S) of the intra and inter cluster divergence (D) were calculated. They showed that chances for occurrence of high frequency of heterotic crosses with high values of heterosis were more, when those parents were chosen whose divergence lies between interval M-S (DC_2) and M + S (DC_3) as compared to the crosses between parents whose divergence falls outside this interval i.e. DC_1 and DC_4.

In the present investigation attempts were made to classify the cluster combinations into 4 divergent classes as per method suggested by Arunchalam and Bandopadhyay (1984). The statistical distances (D) given in Table 4.8 represent the index of genetic diversity among clusters. The mean M calculated for 3 inter cluster and 2 intra cluster distances was 5.738 with a standard (S) deviation of 2.025. The minimum (X) and maximum (Y) values among these distances were 3.54 and 8.37, respectively. The divergent classes are presented in Table 5.1

Arunachalam and Bandopadhyay (1984) reported that crosses between divergent classes DC_2 and DC_3 will be more heterotic and promising than other combination of crosses. However, in the present

Table 5.1 Distribution of different cluster combinations into four divergent classes based on D values

	DC_4		**DC_3**		**DC_2**		**DC_1**	
X		**M-S**		**M**		**M+S**		**Y**
3.54		3.713		5.738		7.763		8.37

DC_1 : II and III

DC_2 : I and II ; I and III

DC_3 : -

DC_4 : -

investigation cluster I and II, I and III were classified under DC_2 and cluster II and III under DC_1. As no cluster combinations are classified under DC_3 it is inferred that crossing between clusters of DC_1 and DC_2 will be less heterotic and less rewarding.

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SUMMARY AND CONCLUSION

6. SUMMARY AND CONCLUSIONS

The present investigation, "Path analysis and genetic diversity in cowpea, (*Vigna unguiculata* (L.) Walp.)" was under taken with the following objectives.

1. To measure the direct and indirect contribution of various characters to yield in M_3 lines of cowpea.
2. To measure the genetic divergence between different M_3 lines.
3. To group these lines into suitable clusters and study the inter and intra cluster variations.

Three varieties of cowpea viz., (i) No. 889, (ii) Sangavi local and (iii) GC 10 were treated with gamma radiations of 15, 25 and 35 KR doses at BARC, Mumbai and the M_1 was raised during summer 2000. About 350 individual plants were evaluated in replicated trials in *kharif,* 2000 by Pillai. From the M_2 population of 7000 plants, 99 high yielding mutant lines were selected for the present investigation and evaluated in randomized block design with 3 replications during *kharif,* 2001.

The various observations recorded on yield and yield contributing traits included days to 50 per cent flowering, days to maturity, plant height, plant spread, number of branches per plant, pod length, number of pods per plant, number of seeds per plant, fresh and dry biomass, test weight and grain yield per plant.

The analysis of variance revealed significant treatment sum of squares for days to 50 per cent flowering, pod length and test weight, indicating variability for these characters in the mutants. The parameters of genetic variability revealed high GCV values for test weight, dry biomass, number of seeds per plant and fresh biomass. The highest PCV value was observed for dry biomass followed by number of seeds per plant, grain yield per plant and fresh biomass. However, the lowest PCV and GCV values were observed for days to maturity and plant spread. Days to 50 per cent flowering recorded the least difference between PCV and GCV values indicating minimal environmental influence.

Apart from the variability studies, the 99 mutants were grouped into classes depending upon the variety and doses of gamma radiation. On analysing the mean performance of these variety-treatment groups for the 12 traits, it was revealed that the gamma radiations resulted in inducing early flowering mutants and also there was increase in number of pods per plant, pod length, number of seeds per plant and grain yield per plant. However, radiations brought about reduced performance for days to maturity and biomass. Irrespective of the positive and negative effects of the radiations, the main objective of inducing variability was achieved.

The estimates of heritability (b.s.) were high for test weight, days to 50 per cent flowering and pod length. These high estimates were accompanied by substantial estimates of genetic advance indicating additive gene action.

Path analysis and correlation studies revealed that test weight and number of seeds per plant exhibited high direct effects with grain yield per plant and also recorded significant correlation with grain yield indicating true and perfect relationship between them. This also suggests that direct selection for these traits will help in improvement of yield in cowpea.

The yield component, number of branches per plant recorded negligible direct effect on grain yield but was significantly correlated with grain yield, suggesting its indirect contribution via test weight and number of seeds per plant. Similarly pod length contributed indirectly via test weight. Number of pods per plant contributed indirectly through number of seeds per plant. These findings revealed that test weight and number of seeds per plant are the most important and reliable yield indicators in mutants of cowpea.

In the present investigation the D^2 values ranged from 0.82 to 88.44 and a total of three clusters were formed with cluster I accommodating maximum 91 mutants followed by cluster II with 10 mutants. However, the cluster III was monogenotypic indicating its wide divergence from other clusters. The character test weight, was the maximum contributor towards divergence followed by days to 50 per cent flowering, number of pods per plant and pod length. The minimum contributors were days to maturity, grain yield per plant and number of seeds per plant.

Based on method suggested by Arunachalam and Bandopadhyay (1984) clusters I and II, I and III were classified under DC_2 and clusters II and III under DC_1. As no cluster combinations are classified under DC_3 it is inferred that crossing between mutants of these clusters will be less heterotic and hence less rewarding. However, the list of mutants identified (Table 6.1) as best performers for specific characters, can be carried further in the breeding programme.

Path analysis and genetic diversity studies on 99 M_3 mutants revealed 231-25, 161-8, 24-1, 120-18, 782-1 and 96-12 to be the best performers and are recommended for multi location trials to assess their adaptability.

Table 6.1 Best performing mutants for specific characters

Character	Mutant
Days to 50 per cent flowering	231-25 161-8
Days to maturity	57-1, 96-9, 119-26, 118-20, 121-18, 161-8, 231-25.
Number of branches per plant	707-17 69-7
Pod length	96-7, 8-1 76-2
Number of pods per plant	24-1 231-25
Number of seeds per plant	120-18 13-1
Fresh biomass	24-1 782-1
Test weight	19-1, 25-10 6-2
Grain yield per plant	120-18 96-12

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7. LITERATURE CITED

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* Originals not seen

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