

**ESTIMATION OF GENETIC VARIABILITY  
INDUCED THROUGH COMBINATION OF  
GAMMA RAYS AND EMS MUTAGENS IN M<sub>3</sub>  
GENERATION OF COWPEA [*Vigna unguiculata*  
(L.) Walp.]**

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COLLEGE OF AGRICULTURE  
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JUNAGADH- 362 001**

**FEB - 2021**

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OF COWPEA [*Vigna unguiculata* (L.) Walp.]**

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**IN  
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**ABSTRACT**

*Key words:* Induced mutation, M<sub>3</sub> generation, variability, heritability, genetic advance, correlation, path analysis, *Vigna unguiculata* (L.) Walp.

The present investigation was conducted to assess genetic variability, correlation and path coefficient analysis for seed yield and its attributes in cowpea treated with combination of gamma rays and EMS at Main Oilseed Research Station, Junagadh Agricultural University, Junagadh during *Kharif* 2019 in Compact Family Block Design with three replications. The observations were recorded on 10 randomly selected plants from each progeny per replication and their mean values were subjected to statistical analysis. The characters studied were days to first flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and seed yield per plant.

The analysis of variance revealed that mean sum of squares between families (mutagens) and among the progenies within the families (dose/concentration) were found highly significant for all the characters studied which indicated the presence of sufficient amount of variability between the families and among the progenies within the family. Mutagenic treatments 1, 2 and 4 expressed high genotypic and phenotypic coefficient of variation for seed yield per plant, while for number of branches per plant only phenotypic coefficient of variation was observed high in treatments 3, 4, 5, 6 and 7. High heritability coupled with high to moderate genetic advance expressed as per cent of mean were observed in treatment 4 (250Gy + 0.25% EMS) and treatment

6 (300Gy +0.25% EMS) for days to first flowering, plant height, number of clusters per plant, number of pods per plant, pod length, 100-seeds weight and seed yield per plant

In treatments 1, 5 and 7, highly significant and positive genotypic and phenotypic correlations were expressed for seed yield per plant with number of branches per plant, number of pods per plant, number of seeds per pod and 100-seeds weight. The genotypic path coefficient analysis revealed that the number of branches per plant, number of pods per plant and 100-seeds weight exhibited high and positive correlation as well as direct effects on seed yield per plant in treatments 1 and 5.

On the basis of studies, it can be concluded that additive gene action was operating for days to first flowering, plant height, number of clusters per plant, number of pods per plant, pod length and 100-seeds weight for mutagenic treatments 4 (250Gy + 0.25% EMS) and 6 (300Gy + 0.25% EMS) indicating simple selection would be rewarding for improvement of these traits. Correlation and path coefficient analysis revealed that number of branches per plant, number of pods per plant and 100-seeds weight had positive and significant association with seed yield per plant under treatments 1 and 5. Therefore, due weightage should be given to these traits for simultaneous improvement in cowpea using the mutagenic treatments 1 (100Gy + 0.25% EMS) and 5 (275Gy + 0.25% EMS).

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**CERTIFICATE-I**

This is to certify that the thesis entitled “**ESTIMATION OF GENETIC VARIABILITY INDUCED THROUGH COMBINATION OF GAMMA RAYS AND EMS MUTAGENS IN M<sub>3</sub> GENERATION OF COWPEA [*Vigna unguiculata* (L.) Walp.]**” submitted by **Mr. BURUGU CHANDRA SHEKAR GOUD** (Reg. No.- 2010118011) in partial fulfilment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **GENETICS AND PLANT BREEDING** to the Junagadh Agricultural University is a record of bonafide research work carried out by him under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma or other similar title. The candidate had fulfilled all prescribe requirements. The assistance and help received during the course of investigation have been fully acknowledged. He has successfully completed the comprehensive /preliminary examination held on **19<sup>th</sup> May, 2020** as required under the regulation for post-graduate studies. He has submitted kachha bound thesis on **30 - 12 - 2020**.

**Place:** Junagadh

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**CERTIFICATE-II**

**Date: 16-02-2021**

This is to certify that the thesis entitled “**ESTIMATION OF GENETIC VARIABILITY INDUCED THROUGH COMBINATION OF GAMMA RAYS AND EMS MUTAGENS IN M<sub>3</sub> GENERATION OF COWPEA [*Vigna unguiculata* (L.) Walp.]**” submitted by **Mr. BURUGU CHANDRA SHEKAR GOUD** to Junagadh Agricultural University, Junagadh in partial fulfillment of the requirements for award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **GENETICS AND PLANT BREEDING** after recommendation by the external examiners were defended by the candidate before the following members of the examination committee. The performance of the candidate in the oral examination was satisfactory. We, therefore, forward with recommendation.

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# CHAPTER-I

## INTRODUCTION

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Pulses form an important part of Indian dietary. They are an important source of protein and are essential adjunct to a predominantly cereal based diet and also enhance the biological value of the protein consumed. The United Nation's Food and Agriculture Organization (FAO) had recognized 11 types of pulses: dry beans, dry broad beans, dry peas, chickpeas, cowpeas, pigeonpeas, lentils, bambara beans, vetches, lupins and other pulses.

Cowpea [*Vigna unguiculata* (L.) Walp.], an annual legume, is commonly referred to as southern pea, black eye pea, crowder pea, lubia, niebe, coupe or frijole. There are various vernacular names of this crop viz., Chouli in Gujarati, Chawali in Marathi, Karamani in Tamil and Lobia in Hindi. It belongs to family *Leguminosae* and sub-family *Fabaceae*, having chromosome number  $2n = 22$ . In India, cowpea is well known since Vedic times. It is native to India (Vavilov, 1949) but tropical and central Africa is also considered as secondary centre of origin, where wild races are found even now (Ng and Marechal, 1985). According to Simmonds (1976) West Africa and India both are modern centers of diversity for this crop. However, it is generally agreed that the cowpea is an African origin as conspecific wild forms are found in Africa, but are absent in Asia. In Indian context, it is a minor pulse cultivated mainly in arid and semi-arid tracts in pockets of Punjab, Haryana, Delhi and West UP along with considerable area in Rajasthan, Meghalaya, Mizoram, Nagaland, Karnataka, Kerala, Tamilnadu, Telangana, Tripura, Maharashtra and Gujarat. The annual area and production of about 1,02,734 ha and 44,946 tonnes during 2018-19 was attained, while Karnataka state stood first in production as well as cultivated area in India (A. P. S.: District wise crop production statistics 2018-19).

Cowpea is herbaceous annual legume. Based on the growing habit, they are characterized as erect, semi-erect, prostrate (trailing) or climbing. Their growth may be indeterminate to fairly determinate, while the non-vining types tending to be more determinate. Generally, cowpea is strong tap rooted. It is a widely adapted and highly variable crop, cultivated around the world primarily for seed. Being a fast-growing

crop, it covers the ground rapidly and curbs the soil erosion. Cowpea adjusts well in a variety of cropping system and can be grown as catch crop. And also, green manure crop as it fixes atmospheric nitrogen in the soil by symbiotic bacteria to a range of 64 to 131 kg/ha (Ayanaba and Dart, 1977). Cowpea is used as a vegetable crop having nutritious component in the human diet. Cowpea is primarily grown in drier regions of the world where it is one of the most drought tolerant food legumes.

Cowpea has been referred to as “Poor man’s meat” because of its high protein content (20-25%). Its young leaves, pods and beans contain vitamins and minerals which have fueled its usage for human consumption and animal feeding (Nielsen *et al.*,1997). This crop can be grown both under irrigated and non-irrigated regimes but well-drained sandy loams or sandy soils are best suited, where soil pH is in the range of 5.5 to 6.5.

Average yield of cowpea is very low in India and year to year variation in yield is also remarkably high. There is an urgent need to make efforts for increasing the cowpea production to meet the minimum requirements as well as for ensuring the national security of fast-growing population.

Most of the crop improvement programmes attempted through conventional breeding methods have exploited only the natural variability available in the germplasm. Selection within local types exercised for a far long time, exhausted the natural genetic variability of the crop. Adequate variability is not available in the gene pool to change the plant ideotype or to correct specific deficiency of otherwise outstanding genotypes. Under such circumstances, induced mutagenesis can be efficiently employed as an alternative to induce the variability in morphological and physiological characters. Genetic improvement of a crop primarily depends upon extent of genetic variability present in the population. Experimentally induced mutations provide an important source of variability. In mutation breeding selection of appropriate mutagen and its dose is most important for obtaining wide spectrum and high frequency of desirable mutations. Hence selections of relatively better responsive genotypes to the mutagen treatment also help in achieving higher mutagenic efficiency. It is advocated that induction of viable and potential mutations in cowpea through treatment of gamma rays and ethyl methane sulphonate, because it is convenient and require lesser time than the conventional breeding particularly when intended variety is an adopted one and is deficient in few characters which are governed by major genes.

Induced mutations are highly effective in enhancing natural genetic resources and have been used in developing improved cultivars in cereals, fruits and other crops. These mutations provide beneficial variation for practical plant breeding purpose. During the past seven decades, more than 2252 mutant varieties have been officially released in the world. Hence, mutation breeding programme has proved to be a successful tool in bringing amelioration in self-pollinated crops.

Chemical mutagen generally produce induced mutations, which lead to base pair substitution especially GC to AT resulting in amino acid changes, which changes the function of proteins, but do not abolish their functions. These chemo mutagens also induce a broad variation of morphological and yield structure change in comparison to normal plants. Alkylating agents such as ethyl methane sulphonate (EMS) induce chemical modification of nucleotides, which result in mispairing and base changes. Strong biased alkylation of guanine (G) residue results, forming O<sup>6</sup>-ethyl guanine, which can pair with thymine (T) but not with cytosine (C). Through subsequent DNA repair, the original G/C pair can then be replaced with A/T. Ninety-nine per cent of mutations from alkylation of guanine induced by EMS are reported as G/C-to-A/T transitions [Greene *et al.*, 2003, Gnanamurthy and Dhanavel, 2014].

Induction of mutations with radiation has been the most frequently used method for developing mutant varieties. The prime strategy in mutation based breeding has been to upgrade the well-adapted plant varieties by altering one or two major traits, which limit their productivity or enhance their quality. In several mutation derived varieties, the changed traits have resulted in synergistic effect on increasing the yield and quality of the crop, improving agronomic inputs, crop rotation and consumer acceptance. In contrast to the currently protected plant varieties or germplasm and increasing restrictions on their use, the induced mutants have been freely available for plant breeding. Mutations are the basis for variations in characters. These variations could be of quantitative or qualitative in nature. Mutations can be induced by treatment with chemical or physical mutagens. Induced mutations have a greater advantage over the spontaneous mutations, as they occur at a higher frequency.

For any mutation breeding programme, selection of effective and efficient mutagen(s) is very essential to recover high frequency of desirable mutations (Solanki and Sharma, 1999). The increase in variance as a result of mutagenic treatments has been reported by a number of scientists in different crop plants. Future research on

induced mutations would also be important in the functional genomics of many food crops including cowpea. Despite its multifarious use, the systematic approaches to improve its yield potential are limited. The small size of flower, extremely poor seed setting on emasculated bud and narrow range of usable variation for quantitative traits impose difficulties on practicing hybridization. Hence, advocates the follow up of mutation breeding in this crop.

Exploitation of recombination variations through hybridization is less in cowpea since it is self-fertilized, due to dehiscence of anthers taking place before the opening of the flower. In addition, high rate of flower abortion nearly 70 to 75 per cent shed before anthesis and half of the remaining abort prematurely (Ojehomon, 1968). Hence, alternate methods of generating variability have gained greater importance in breeding of cowpea. In this context, artificial induction of genetic variation has been proposed as one of the quick methods of enlarging genetic variability. Gamma rays are known to influence plant growth and development by inducing cytological, genetical, biochemical, physiological and morphogenetic changes in cells and tissue (Gunckel and Sparrow, 1961).

Genetic variability is the most essential prerequisite for any successful crop improvement programme as it provides spectrum of variants for the effective selection, which can be achieved through the processes of hybridization, recombination, mutation and selection. Development of improved plant cultivar is restricted by limited genetic resources. Mutation induction could create additional genetic variability to supplement conventional crop breeding. Seven cowpea mutant varieties of radiation and chemical origin *viz.*, Amba, Shreshtha, Swarna, V-240, Co-5, Cowpea-88 and Khalleswari have been released in India. Thus, proving its role in the creation of genetic variations resulting in new varieties with better characteristics.

Correlation and path coefficient analysis are the important biometrical techniques to determine the yield components. Therefore, understanding the nature and intensity of association between seed yield and yield contributing traits. Correlation simply measures mutual relationship between both the traits, which helps for exercising selection pressure on yield attributing traits. However, in correlation studies indirect associations become more complex and confusing but path analysis helps to avoid this complication by measuring the direct influence of one trait on other and permits the

partitioning of given correlation coefficients into its components *i.e.*, direct and indirect effects.

Keeping in view of all these aspects, the present study was planned with following objectives:

1. To find out different genetic variability parameters in  $M_3$  generation
2. To estimate genotypic and phenotypic correlations among seed yield and its components in  $M_3$  generation
3. To determine the direct and indirect effects of different characters on seed yield using path coefficient analysis in  $M_3$  generation

## CHAPTER-II

### REVIEW OF LITERATURE

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A thorough understanding of the extent of variation, genetic architecture of the plant and heritability of characters among M<sub>3</sub> generation of cowpea treated with gamma rays and ethyl methyl sulphonate would help in developing sound crop improvement programmes. Genetic variability is the gift of nature and its fruitful utilization in any crop species calls for systematic collection, evaluation, description and grouping based on economic descriptors.

Genetic improvement through mutation gained attention of workers since long time and comparatively more reports are available on influence of different characters on productivity in different crops. The published literature pertaining to genetic variability, correlation and path analysis in cowpea (*Vigna unguiculata* (L.) Walp.) are reviewed here under the following sub headings:

2.1 Genetic variability parameters

2.2 Correlation coefficient

2.3 Path coefficient analysis

#### **2.1 GENETIC VARIABILITY PARAMETERS**

As the published information on mutation in cowpea [*Vigna unguiculata* (L.) Walp.] is meager, relevant literature is reviewed below. Most of the research work carried out on mutated cowpea was to create genetic variability and to find out genetic variability parameters only.

Possibility of achieving improvement in any crop plants depends on the magnitude of genetic variability present in the base population. The phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. The genotypic component being the heritable part of the total variability, its magnitude on seed yield and its component characters influences the selection strategies to be adopted by the plant breeders.

The basic requirements of plant breeding are variation and selection. Thus, analysis of variability is useful for getting information about the characters that are expected to respond the selection.

Odeigah *et al.* (1998) conducted an experiment by taking seed samples of two IITA cowpea varieties; IT84E-124 and Vita 7 treated with gamma rays, ethyl methane sulfonate (EMS) and Sodium azide ( $\text{NaN}_3$ ). The results indicated that EMS treatment and 100R gamma irradiation did not affect any improvement in the yield parameters of IT84E-124. On the other hand, for Vita 7, 100R gamma irradiation made positive changes in peduncles and pods per plant and the flowering date, while EMS affected the 100 seed weight and seeds per pod positively. Significant variation in all parameters was observed in  $M_4$  mutant lines *i.e.* seeds per pod, 100 seed weight, number of peduncles per plant and pods per plant.

Dhaka *et al.* (2013) had undertaken mutagenesis programme using ethyl methane sulphonate (EMS), methyl methane sulphonate (MMS) and sodium azide (SA) on cowpea varieties RC-19 and RC-101 and recorded observations on plant height, clusters per plant, pods per plant, seeds per pod, pod length, 100-seed weight and seed yield per plant. The estimates of various genetic parameters indicated that plant height (14.40, 13.50), cluster per plant (24.51, 14.83), pods per plant (24.81, 17.13), seed per pod (11.35, 15.48) and seed yield per plant (25.55, 17.92) exhibited relatively high genotypic as well as phenotypic coefficient of variation in both the varieties. They suggested that simple selection would be advantageous for these traits in RC-19 and RC-101 respectively. High heritability along with high genetic advance as percentage of mean were recorded for plant height, cluster per plant, pods per plant and seed yield per plant in RC-19 and for plant height, seeds per pod and seed yield per plant in RC-101.

Singh *et al.* (2013) estimated the genetic variability induced through physical and chemical mutagens in cowpea variety RC 19 in  $M_2$  generations. Observations from 10 randomly selected plants were recorded on nine quantitative traits *viz.*, plant height (cm), number of primary branches per plant, number of pods per plant, number of grains per pods, days to 50% flowering, 100 seed weight, seed yield per plant (g) and harvest index (%). The results revealed that magnitude of phenotypic coefficient of variation were distinctly high for plant height, number of pods per plant, seed yield per plant,

biological yield, harvest index and protein content at 30kR. The magnitude of phenotypic coefficient of variation were higher than genotypic coefficient of variation along with heritability and genetic advance except in protein content for family EMS 0.1%. Three progenies for biological yield per plant in family 30 kR and two progenies in EMS 0.2% for protein content, 20 progenies in each 20 kR,30 kR and EMS 0.2% families were superior than control. 11 progenies in EMS 0.1% and 3 progenies in  $\gamma$ -rays 10 kR were found superior than control and identified for high protein content which were selected for improving quality traits in cowpea.

Chattopadhyay *et al.* (2014) experimented on seventeen genotypes of vegetable cowpea (*Vigna unguiculata* cv gr. *Sesquipedalis*) collected from different places in the country to evaluate different genetic variability parameters. Observations from fifteen randomly selected plants were recorded on eight quantitative traits, viz., days to 1<sup>st</sup> flowering, days to 50% flowering, pod length (cm), pod width (cm), number of pods per plant, pod weight (g), number of seeds per pod and pod yield per plant (kg). Pod characters were taken from twelve days old immature pod from anthesis. They concluded that phenotypic coefficient of variation (PCV) agreed closely with the genotypic coefficient of variation (GCV) for all the characters except pod width and pod yield per plant but the magnitude of PCV was higher than GCV for all cases. The GCV ranged from 10.29% to 32.35%, while PCV ranged from 10.40% to 32.93%. High to moderate GCV and PCV values were found for number of pods per plant, pod yield per plant, pod weight, number of seeds per pod and pod length indicating the potential of simple selection for the improvement of these characters. Higher estimates of broad sense heritability (more than 90%) coupled with the higher genetic advance (more than 55%) were observed for number of pods per plant (99.65%, 66.53%), pod yield per plant (92.75%, 62.92%) pod weight (98.83%, 60.39%), number of seeds per pod (99.04%, 58.78%) and pod length (99.43%, 56.97%) which is indicative of additive gene action and selection based on these parameters would be more reliable.

Gnanamurthy and Dhanavel (2014) studied the effect of EMS (ethyl methane sulphonate) on induced morphological mutants and chromosomal variation in cowpea using five different doses of mutagen along with a control. They observed that the morphological and chromosomal variation was found to be mutagen sensitive in

somatic cells of cowpea and it was found to increase with increasing the concentration of EMS in cowpea plants.

Nair and Mehta (2014a) estimated genetic variability in  $M_2$  and  $M_3$  generation of cowpea var. Pusa Komal by treating with physical mutagen gamma rays (100, 200, 300, 400, 500 Gy) and chemical mutagen EMS (0.25%, 0.30%, 0.35%, 0.40% and 0.45%). High GCV and PCV was observed for number of primary branches per plant (74.27, 62.97), protein per cent (37.47, 44.14), yield per plant (37.13, 33.60) and 100 seed weight (26.11, 23.42) in  $M_2$  and  $M_3$  generations, respectively. Broad sense heritability in  $M_2$  as well as  $M_3$  generation was high for number of primary branches per plant (93.13%, 98.33%), protein per cent (89.39%, 85.86%) and 100 seed weight (77.13%, 79.58%). Genetic advance in percent of mean was estimated to be high for characters yield per plant (47.79%), protein per cent (75.06%) and number of pods per plant (72.04%), in the  $M_2$  and only protein per cent (80.23) in  $M_3$  generation of Pusa Komal, indicating the selection of these traits will be gratifying because they are governed by additive gene action.

Nair and Mehta (2014b) undertaken an experiment on cowpea [*Vigna unguiculata* (L.) Walp.] var. Arka Garima to assess the efficiency and effectiveness of physical as well as chemical mutagens and to induce viable mutation in qualitative traits. They reported that the lower and intermediate doses of gamma rays (200 and 300 Gy) and EMS (0.25% and 0.30%) can be recommended as most effective and efficient for exploring variability and isolating promising mutants. EMS induced maximum number of floral abnormalities compared to gamma ray and further stated that the induced variability generated in  $M_3$  population is more than that in  $M_2$  in Arka Garima.

Nair *et al.* (2016) studied induced chlorophyll mutations and spectrum in cowpea var. Pusa Komal and Arka Garima treated with gamma rays and EMS. They observed that broad spectrum of chlorophyll mutations (*albino*, *xantha*, *chlorina*, *viridis* and *xantha-viridis*) were obtained in treatment 500 Gy gamma rays and 0.35% (6 hrs) EMS. Chemical mutagens appeared to be more effective in inducing maximum frequencies than physical mutagen in both the varieties.

Baranda *et al.* (2018) carried out a study on genetic variability in 30 genotypes of cowpea. The results revealed that high PCV and GCV estimates were observed for plant height (37.57%, 37.14%) and number of branches per plant (24.18 %, 24.11%),

whereas low PCV and GCV was recorded for days to 75% maturity (2.66%, 1.14%). High heritability coupled with high genetic advance as per cent of mean was observed for plant height (98.00%, 75.61%), 100-grain weight (97.00%, 33.92%) and seed yield per plant (94.00%, 40.72%) indicating that these traits were mainly governed by additive gene action and were of greatly influence for direct selection for genetic improvement by pedigree selection methods of heritable traits.

### **Other Legumes**

Arulbalachandran and Mullainathan (2009) used Vamban-1 variety of black gram to induce mutation by EMS. They analysed quantitative traits in M<sub>2</sub> generation. The results showed that high and moderate PCV and GCV in M<sub>2</sub> generations was observed among the dose/concentration of mutagenic treatments for the quantitative traits such as, plant height, number of branches per plant, number of leaves per plant, number of fruit cluster per plant, number of pods per plant, number of seeds per pod and seed yield per plant. Significant variation with high PCV and GCV values were recorded almost in EMS at 0.1%. High heritability and GA as % of mean was observed for plant height, number of branches per plant, number of leaves/plants, number of days for 50% flowering, number of fruit cluster per plant, number of pods per plant, number of seeds per pod, 100 seed weight and yield per plant in gamma rays and EMS treatment at 0.1%.

Arulbalachandran *et al.* (2010) used a variety of black gram (Vamban-1) to evaluate the genetic variation on quantitative characters in M<sub>2</sub> generation derived through mutagenic treatment of gamma rays. The wider range of variation was observed for all the quantitative traits which suggested the presence of enough variation to exploit the variability. The phenotypic and genotypic coefficient of variation expressed in terms of per cent were comparatively high at 60 kR for plant height (31.69, 30.67), branches per plant (27.15, 23.36), leaves per plant (30.82, 30.12), cluster per plant (38.69, 36.71), pods per plant (39.69, 38.15), seeds per pod (24.44, 20.66), yield per plant (25.66, 24.68) and 100 seed weight (22.50, 20.42). 60 kR of gamma rays revealed highest values of heritability with genetic advance as percent of mean for plant height (89.16, 60.20), branches/plant (76.61, 74.05), leaves per plant (35.11, 37.88), cluster/plant (86.16, 37.69), pods/plant (95.31, 31.58), seeds per pod (53.76, 50.16), yield per plant (75.45, 66.82) and 100 seed weight (77.19, 84.52). They concluded wide

range of variability for different traits coupled with high heritability and high genetic advance were important yield traits Hence selection is effective for these traits.

Dhumal and Bolbhat (2012) used 675 seeds of each treatment to raise M<sub>1</sub> generation and subsequent M<sub>2</sub>, M<sub>3</sub> and M<sub>4</sub> generations in horse gram var Dapoli Kulthi-1. The M<sub>2</sub>, M<sub>3</sub>, M<sub>4</sub> and mutants were raised in next rainy season. They stated that gamma radiations and GR + EMS proved to be very effective to induce variability in quantitative traits like plant height, primary branches per plant, days required for first flowering and first pod maturity, number of pods per plant, pod length, number of seeds per pod, 1000 seed weight and yield per plant in M<sub>2</sub> and M<sub>3</sub> generations. The maximum seed yield (16.76 g) was noted in 300 Gy and minimum (11.22 g) in 200Gy as compared to control (14.54 g). The combination treatment 300Gy + 0.5% EMS had induced maximum increase in seed yield per plant (16.01 g) over control (14.54 g) while all other treatments had caused reduction in seed yield per plant.

Sridevi and Mullainathan (2012) conducted an experiment to study the effects of gamma rays and ethyl methane sulphonate (EMS) on mutagenesis of blackgram var. VBN-1. The study was carried out with various observations, such as plant height (cm), days to first flowering, number of clusters per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), seed yield/plant (g) and seed protein content (%) in M<sub>3</sub> generation. The results revealed high coefficients of phenotypic (PCV) and genotypic variation (GCV) for number of pods per plant followed by number of cluster per plant, number of seeds per pod and seed yield per plant. They advocated that high PCV and GCV observed from their high variability in turn offers good scope for selection. Heritability for number of pods per plant (87.93) and seed protein content (80.90) was very high at 15 mM EMS as compared to all other treatments and characters in M<sub>3</sub> generation. Genetic advance (GA) showed similar trends and higher values at 60 kR of gamma rays and 15 mM of EMS.

Patial *et al.* (2015) conducted an experiment to study the comparative mutagenic effectiveness and efficiency of mutagen using M<sub>2</sub> generation of two varieties of ricebean *viz.*, BRS-1 and Totru Local. Observations were recorded on days to flowering, days to maturity, pod clusters per plant, pods per cluster, seeds per pod, pod length (cm), seed yield per plant (g) and 100-seed weight (g). In both the cultivars 30kR and EMS 0.50% showed moderate to very high values of PCV, GCV,  $h^2_{bs}$  and GA for

inducing maximum variability in the characters for selection parameters *i.e.* clusters of pods per plant, pods per cluster, pod length and seeds per pod.

Usharani and Kumar (2016) estimated genetic variability in black gram (*Vigna mungo* L. Hepper) induced by gamma rays and ethyl methyl sulphonate (EMS) for different quantitative traits in M<sub>2</sub> generation. Mean performance of different quantitative traits was significantly better in 50 mM of EMS followed by 50 kR of gamma rays when compared with the control and other doses. The wide range of variation was observed in all the traits in 6 treatments and the high PCV and GCV for number of pods per plant, number of primary branches per plant and seed yield per plant. 50 kR of gamma rays revealed the highest values of heritability with genetic advance as per cent of mean for number of primary branches per plant (46.7, 38.6), number of pods per plant (93.3, 21.2), 100 seed weight (93.8, 37.5) and seed yield per plant (72.2, 26.5). Heritability coupled with genetic advance as per cent of mean were comparatively high at 50 mM of EMS for number of primary branches per plant (68.7, 38.3), pod length (78.9, 24.5) and seed yield per plant (81.7, 24.4) which indicated that these traits are under the control of additive gene action and directional selection for these traits could be effective for desired genetic improvement.

**Note:** There is no much work done and very little review are available on parameters such as correlation studies, path coefficient in mutagenic generation of cowpea as well as in other legume crops. So, taking the non-mutated legume crop review under consideration, review of literature is being collected and at the end of this research program the following parameters were studied *i.e.* correlation studies and path coefficient in M<sub>3</sub> generation of cowpea treated with gamma rays and EMS.

## **2.2 CORRELATION COEFFICIENT**

It is often observed that certain quantitative characters of economic importance are associated with each other. It is well known that different components of seed yield very often exhibit considerable degree of association among themselves and with seed yield. Therefore, to identify optimum combination of yield contributing characters in a single genotype, it is essential to know the implication of the interrelationship of various characters. In such cases, the knowledge on association between such characters is quite helpful to the plant breeders to formulate their selection strategies. The concept of correlation was given by Galton (1889) and later it was elaborated by Fisher (1918).

Correlation coefficient is useful as a basis for selecting desirable parents. The interrelationship of grain yield and its components worked out by various workers in cowpea has been reviewed here under.

Manggoel *et al.* (2012) carried out correlation analysis using 10 cowpea accessions in randomized complete block design for eight quantitative traits. Results showed positive and significant correlation between grain yield and number of peduncles plant<sup>-1</sup> ( $r = 0.716$ ), number of flowers plant<sup>-1</sup> ( $r = 0.776$ ), number of pods plant<sup>-1</sup> ( $r = 0.640$ ), pod length ( $r = 0.621$ ) and 100-seed weight ( $r = 0.690$ ). Conversely, grain yield was negatively and significantly correlated with days to 50% flowering ( $r = -0.521$ ). They implicated that pods per plant and seeds per pod as the major yield determining traits that are to be selected.

Chattopadhyay *et al.* (2014) evaluated seventeen genotypes of cowpea (*Vigna unguiculata* cv gr. Sesquipedalis) to study the correlation analysis for seven characters viz., days to 1<sup>st</sup> flowering, days to 50% flowering, pod length, pod width, number of pods per plant, pod weight and number of seeds per pod. The results stated that genotypic correlation coefficients were higher than corresponding phenotypic correlation coefficients, indicating greater contribution of genotypic factor in the growth and development. Significant and positive genotypic relationships were found for number of seeds per pod ( $r_g = 0.601$ ), number of pods per plant ( $r_g = 0.600$ ) and pod length ( $r_g = 0.487$ ) with pod yield per plant and negative phenotypic relationships were found for days to 1<sup>st</sup> flowering and days to 50% flowering. Positive and significant phenotypic correlations were observed for number of pods per plant ( $r_p = 0.577$ ) and number of seeds per pod ( $r_p = 0.575$ ) with pod yield per plant and negative correlations were exhibited for days to 1<sup>st</sup> flowering ( $r_p = -0.695$ ) and days to 50% flowering ( $r_p = -0.660$ ),

Santos *et al.* (2014) experimented 20 cowpea genotypes at two locations of Brazil to analyze correlation analysis at both genotypic and phenotypic levels for seven quantitative traits. They reported that greatest positive correlations were found between the character pairs; days to flowering (DF) x days to maturity (DM) ( $r_g = 0.8522$ ,  $r_p = 0.5276$ ); days to maturity (DM) x pod weight (PW) ( $r_g = 0.6068$ ,  $r_p = 0.3895$ ); days to maturity (DM) x number of beans per pod (NBP) ( $r_g = 0.8305$ ,  $r_p = 0.4490$ ); pod weight (PW) x number of beans per pod (NBP) ( $r_g = 0.7540$ ,  $r_p = 0.6142$ ); green pod length

(GPL) x pod weight (PW) ( $r_g = 0.5513$ ,  $r_p = 0.4726$ ); and number of pods per plant (NPP) x grain yield (YLD) ( $r_g = 0.7982$ ,  $r_p = 0.4179$ ). They concluded that grain yield may be obtained in an indirect manner with selection for increase in the number of pods per plant.

Patel *et al.* (2016) computed correlation for 11 characters using 32 cowpea genotypes. The results revealed that genotypic and phenotypic correlation coefficient for green pod yield per plant showed highly significant and positive correlation with pod length ( $r_g = 0.456$  &  $r_p = 0.312$ ) and sugar content ( $r_g = 0.269$  &  $r_p = 0.029$ ) while it was negatively correlated with days to 50 per cent flowering ( $r_g = -0.205$  &  $r_p = -0.139$ ), number of branches per plant ( $r_g = -0.159$  &  $r_p = -0.132$ ), number of clusters per plant ( $r_g = -0.153$  &  $r_p = -0.156$ ), number of pods per plant ( $r_g = -0.056$  &  $r_p = -0.091$ ), shelling % ( $r_g = -0.027$  &  $r_p = -0.015$ ) and crop duration ( $r_g = -0.069$  &  $r_p = 0.029$ ).

Sharma *et al.* (2016a) carried out correlation coefficient analysis using 60 genotypes of cowpea for 16 quantitative traits. The results revealed that seed yield per plant exhibited significant positive correlation with biological yield ( $r_g = 0.739$ ), number of pods per plant ( $r_g = 0.453$ ), number of flowers per plant ( $r_g = 0.429$ ), test weight ( $r_g = 0.421$ ), number of pods per cluster ( $r_g = 0.373$ ), pod length ( $r_g = 0.351$ ), number of seeds per pod ( $r_g = 0.343$ ), number of clusters per plant ( $r_g = 0.318$ ), harvest index ( $r_g = 0.307$ ) and plant height ( $r_g = 0.252$ ) at genotypic level. While at phenotypic level biological yield per plant ( $r_p = 0.718$ ), number of pods per plant ( $r_p = 0.419$ ), test weight ( $r_p = 0.410$ ), number of flowers per plant ( $r_p = 0.383$ ), harvest index ( $r_p = 0.340$ ), number of seeds per pod ( $r_p = 0.325$ ), pod length ( $r_p = 0.319$ ), number of clusters per plant ( $r_p = 0.272$ ), plant height ( $r_p = 0.248$ ) and number of pods per cluster ( $r_p = 0.189$ ) showed positive highly significant correlation with seed yield per plant. They concluded that main yield contributing traits are biological yield per plant, number of pods per plant, number of flowers per plant, test weight, number of pods per cluster, pod length, number of seeds per pod, number of clusters per plant, harvest index and plant height due to their direct high positive association with seed yield. They suggested possibilities of simultaneous improvement of these traits by selection to improve the seed yield.

Sharma *et al.* (2016b) conducted an experiment to evaluate 30 cowpea germplasm to analyze correlation coefficient for nine quantitative traits. The results

revealed that seed yield per plant exhibited significant positive correlation with number of pods per plant ( $r_g = 0.448$ ), number of flowers per plant ( $r_g = 0.425$ ), test weight ( $r_g = 0.464$ ), number of primary branches per plant ( $r_g = 0.340$ ), number of clusters per plant ( $r_g = 0.331$ ) and harvest index ( $r_g = 0.230$ ) at genotypic level. Number of pods per plant ( $r_p = 0.403$ ), test weight, ( $r_p = 0.451$ ), number of flowers per plant ( $r_p = 0.387$ ), number of primary branches per plant ( $r_p = 0.318$ ), harvest index ( $r_p = 0.282$ ) and number of clusters per plant ( $r_p = 0.266$ ) showed positive highly significant correlation with seed yield per plant at phenotypic level. They concluded that main yield contributing traits are number of pods per plant, number of flowers per plant, test weight, number of clusters per plant, harvest index and number of primary branches per plant. They suggested possibilities of simultaneous improvement of these traits by selection to improve the seed yield.

Lopes *et al.* (2017) conducted an experiment with 20 genotypes of cowpea to perform correlation analysis both at genotypic and phenotypic levels for nine quantitative traits. Results revealed that the highest positive correlations were observed between the pairs of traits GPM x NGP ( $r_g = 0.98$ ); NGP x HGM ( $r_g = 0.94$ ); GPL x GPM ( $r_g = 0.91$ ); GPM x YIE ( $r_g = 0.83$ ); NGP x YIE ( $r_g = 0.75$ ); DF x NBP ( $r_g = 0.72$ ), and GPL x NGP ( $r_g = 0.71$ ) at genotypic level while highest positive and significant phenotypic correlations were observed between the production components GPL x HGM ( $r_p = 0.71$ ); GPL x NGP ( $r_p = 0.66$ ); NGP x YIE ( $r_p = 0.66$ ), and GPM x NGP ( $r_p = 0.68$ ). They concluded that the traits green pod mass and number of grains per green pod are those that correlate more directly with the grain yield, allowing infer about the possibility of indirect selection for increasing the yield

Nair *et al.* (2017) evaluated 25  $F_2$  populations of inter subspecies crosses and their 14 parents to analyze correlation coefficient for 14 quantitative traits in cowpea. Results of genotypic and phenotypic correlation coefficient revealed that seed yield per plant expressed positive and significant correlation with number of pods per cluster ( $r_g = 0.3308$ ,  $r_p = 0.3004$ ), number of pods per plant ( $r_g = 0.3327$ ,  $r_p = 0.3227$ ) and dry pod yield per plant ( $r_g = 0.5378$ ,  $r_p = 0.5276$ ). They concluded that selection of these traits may be beneficial for crop improvement.

Srinivas *et al.* (2017) evaluated 30 genotypes of cowpea using randomized block design with three replications to carryout correlation coefficient analysis for 11

quantitative traits. The phenotypic correlation coefficient revealed that pod yield per plot was significantly and positively correlated with number of branches per plant (0.7659), number of nodes (0.5523), pod length (0.3960), number of seeds per pod (0.2815), number of cluster per plant (0.550), number of pods per plant (0.547), number of pods per cluster (0.524), 100 seed weight (0.2143), plant height (0.437) and protein content (0.2871) while, days for 50% flowering (-0.2081) showed significantly and negatively correlated with pod yield per plot. They concluded that pod yield per plot (Kg) had a positive and highly significant association with number of pods per plant, number of green pods per cluster, pod length (cm) average pod weight (g), number of seeds per pod and per cent of protein content having strong association which would ultimately improve the pod yield.

Al-Saady *et al.* (2018) evaluated 64 seed accessions which were collected from different governorates of Oman to study the correlation analysis for three characters *viz.*, seed length, seed width (cm) and 100 seed weight. The results showed positive and significant correlation values ( $r$ ) between three seed traits studied *viz.*, seed length vs seed width (0.620), seed length vs 100-seed weight (0.891) and seed width vs 100-seed weight (0.555).

Baranda *et al.* (2018) evaluated 30 genotypes of cowpea to study the correlation analysis for 11 characters. The results revealed that phenotypic and genotypic correlation coefficient for seed yield per plant was significantly and positively correlated with biological yield ( $r_g = 0.878$  &  $r_p = 0.817$ ), harvest index ( $r_g = 0.393$  &  $r_p = 0.319$ ), pods per plant ( $r_g = 0.372$  &  $r_p = 0.313$ ), cluster per plant ( $r_g = 0.339$  &  $r_p = 0.269$ ), plant height ( $r_g = 0.268$  &  $r_p = 0.266$ ) and 100-grain weight ( $r_g = 0.260$  &  $r_p = 0.256$ ).

Walle *et al.* (2018) evaluated 324 cowpea landraces to determine phenotypic and genotypic correlation among 18 quantitative traits at two locations. The results obtained inferred that seed yield was highly significant and positively correlated with seed length (0.26), seed thickness (0.32), seed width (0.32), hundred seed weight (0.25), number of pods per plant (0.15), number of seeds per pod (0.14), pod length (0.21), peduncle length (0.18) and number of racemes per plant (0.16) at genotypic level indicating the presence of strong inherited association between seed yield and these traits.

Kana and Kwon (2019) carried out experiment in botanical garden of Federal University Lafia with nine genotypes of cowpea which were exposed to alpha spin

nanoparticles to determine correlation among nine quantitative traits. The results revealed that significant positive correlation was found between grain yield and 100 seed weight ( $r = 0.818$ ), pod length ( $r = 0.698$ ), number of pods per plant and number of seeds per pod ( $r = 0.443$ ). They concluded that number of pods per plant, number of seeds per pod, 100 seed weight, pod length and number of branches are major component that influence yield in the cowpea varieties treated with alpha-spin nanoparticles.

Nandini and Duddukur (2019) estimated correlation coefficient using 30 cowpea genotypes with one check in randomized block design with three replications among 13 characters. The genotypic and phenotypic correlation coefficients revealed that days to 50% flowering, days to 50% pod setting, pods per plant, 100 seed weight, harvest index and biological yield showed highly significant positive association with seed yield at both phenotypic and genotypic levels. While plant height had significant negative correlation with the seed yield at both phenotypic and genotypic levels. They concluded that the selection for days to 50% flowering, days to 50% pod setting, pods per plant, 100 seed weight, biological yield may improve seed yield.

Sahu (2019) evaluated 78 germplasm lines including 3 checks of cowpea to study the association analysis for fifteen characters and reported that seed yield per plant showed positive and significant correlation with plant height (0.278), plant length (0.869), number of locules per pod (0.575) and green forage yield per day (0.259).

### **2.3 PATH COEFFICIENT ANALYSIS**

Seed yield is the ultimate result of interactions involving a number of component factors, which are interrelated. The knowledge of such interrelationship is useful in knowing the magnitude and direction of association. However, study of correlation alone for ascertaining the importance of characters may be misleading when several characters are associated with seed yield. Path analysis is simply standardized partial regression coefficient, which splits the correlation coefficients into the measures of direct and indirect effects of a set of independent variables on the dependent variable. The concept of path coefficient analysis was originally developed by Wright (1921), but the technique was first used by Dewey and Lu (1959). A brief review of work related to path analysis in cowpea is presented as under.

Path analysis was carried out by Manggoel *et al.* (2012) using 10 cowpea accessions in randomized complete block design for grain yield and its other seven component traits. The results showed that highest positive direct effect was expressed on grain yield by 100-seed weight ( $p = 1.45$ ) followed by number of flowers plant<sup>-1</sup> ( $p = 1.40$ ), number of peduncles plant<sup>-1</sup> ( $p = 0.94$ ) and number of seeds pod<sup>-1</sup> ( $p = 0.49$ ) while pod length ( $p = -1.78$ ), days to 50% flowering ( $p = -1.20$ ) and number of pods plant<sup>-1</sup> ( $p = -0.97$ ) contributed negative direct effects. They concluded that number of flowers plant<sup>-1</sup>, number of peduncles plant<sup>-1</sup> and 100-seed weight would be effective for direct selection.

Santos *et al.* (2014) carried out path analysis using 20 cowpea genotypes at two locations of Brazil. They reported that high positive direct effect on grain yield *via* days to flowering (1.3049), days to maturity (1.2962), green pod length (1.8128) and pod weight (0.6290). They concluded that selection based on these characters may be effective in yield improvement.

Patel *et al.* (2016) carried out path analysis on 32 diverse genotypes of cowpea for ten quantitative traits *viz.*, days to 50 per cent flowering, number of branches per plant, number of clusters per plant, pod length (cm), number of seeds per pod, number of pods per plant, plant height at final harvest (cm), sugar content (%) and shelling (%). The results showed that highest positive direct effect on green pod yield per plant had by pod length (0.716) followed by days to 50 per cent flowering (0.645), shelling (%) (0.398), number of pods per plant (0.289), sugar content (0.219) and plant height at final harvest (0.204). While crop duration (-0.527) showed highest negative direct effect followed by number of clusters per plant (-0.251) and number of seeds per pod (-0.180). They suggested that above traits should be considered for selection to improve green pod yield per plant.

An experiment was conducted by Sharma *et al.* (2016a) using 60 genotypes of cowpea to study path analysis for seed yield per plant and its 15 component traits. The results revealed that the highest positive direct effect at genotypic level on seed yield per plant was exhibited by biological yield (0.995) followed by harvest index (0.672), number of pods per plant (0.665) whereas number of flowers per plant (-0.129), days to maturity (-0.093), pod length (-0.028) and seed protein content (-0.018) contributed negative direct effect on seed yield. High indirect effect on seed yield per plant was

exhibited by test weight (0.381), number of seeds per pod (0.356), pod length (0.302) and number of flowers per plant (0.274) through biological yield per plant. They concluded that seed yield in cowpea can be improved by focusing on character biological yield per plant, harvest index, number of pods per plant and plant height.

Sharma *et al.* (2016b) evaluated 30 cowpea germplasm to analyze path coefficient for seed yield per plant and its component characters. The results revealed that highest positive direct effect on seed yield per plant was exhibited by pods per plant (3.927) followed by primary branches per plant (0.745) and test weight (0.133) whereas, plant height (-0.296), days to maturity (-0.835), number of flowers per plant (-1.543) and number of clusters per plant (-2.269) contributed negative direct effect on seed yield per plant. They concluded that seed yield can be improved by focusing on harvest index and number of pods per plant.

Lopes *et al.* (2017) conducted an experiment with objective to study the genetic potential of population of 20 cowpea genotypes with four replications. Path analysis showed that the highest direct and positive effect on dry grain yield was expressed by number of grains per green pod followed by main stem length, days to flowering and days to physiological maturity. While negative direct effect was expressed by number of branches per plant followed by green pod mass and green pod length.

25 F<sub>2</sub> populations of inter subspecies crosses and their 14 parents of cowpea were analyzed by Nair *et al.* (2017) to perform path analysis for seed yield per plant and 13 component traits. Results of genotypic path coefficient revealed that number of pods per cluster (0.2329), pods per plant (0.6167), dry pod yield per plant (0.3979) and harvest index (0.3683) exhibited high positive direct effect on seed yield per plant while, green pod yield per plant (-0.0309) expressed negative direct effect. They concluded that seed yield per plant could be improved through simultaneous selection of number of pods per cluster, number of pods per plant, dry pod yield per plant and harvest index for improving both seed yield and green pod yield per plant.

Srinivas *et al.* (2017) evaluated 30 genotypes of cowpea using randomized block design with three replications to carryout path analysis for seed yield and its component traits. They reported that high positive direct effect on green pod yield per plant was exhibited by number of branches per plant (0.3821), number of nodes per plant (0.0432), number of cluster per plant (0.2831), number of green pods per cluster

(0.2158), number of pods per plant (0.3888), number of seeds per pod (0.1401) and pod weight (g) (0.0476) while, negative direct effect on green pod yield per plant were contributed through plant height (-0.1763), days to 50% flowering (-0.00063), pod length(-0.0429) and pod yield per plot (-0.129).

Baranda *et al.* (2018) taken 30 genotypes of cowpea to carryout path analysis for seed yield per plant and its component trait at genotypic level. They reported that high positive direct effect on seed yield per plant was exhibited by biological yield (0.825) followed by plant height (0.366), harvest index (0.200), days to maturity (0.109), pod length (0.109),100 seed weight (0.102) and days to first flowering (0.085) while negative direct effect on seed yield per plant were contributed through number of branches per plant (-0.254) followed by number of cluster (-0.191). They summarized that biological yield, harvest index, number of pods per plant and 100-grain weight showed positive and strong correlation with seed yield per plant should be considered to be the most important yield contributing characters.

Walle *et al.* (2018) evaluated 324 cowpea landraces to determine genotypic path coefficient analysis of seed yield with other 18 traits at two locations. Genotypic path coefficient analysis revealed that days to flowering (1.852), biomass (0.588) and harvest index (0.459) at Melkassa and seed thickness (2.240), plant height (0.565), days to maturity (0.499) and biomass (0.446) at Miesso had relatively high positive direct effect on seed yield. However, seed width and 100 seed weight had exerted negative direct effect on seed yield at each location. Phenotypic path coefficient analysis showed that biomass and harvest index had exerted positive direct effect on seed yield at both locations. They concluded that seed yield can be improved by focusing on traits *viz.*, pod length, seed length, seed thickness, seed width, biomass and harvest index.

Kana and Kwon (2019) carried out path coefficient analysis using nine genotypes of cowpea which were exposed to alpha spin nanoparticles for seed yield with other 8 traits. Genotypic path coefficient analysis revealed that 100 seed weight (0.850) and number of seed per pod (0.807) showed highest direct effect on seed yield. Number of leaves showed highest indirect effect on seed yield through number of branches (0.147). They reported that 100 seed weight and mean number of seeds per pod accounted for the observed variation among the cowpea varieties used and this could suggest their

effective utilization by breeders for selecting and improving cowpea varieties using alpha spin nanoparticles.

Manohara *et al.* (2019) used 23 cowpea genotypes to study path analysis of seed yield on other 10 characters. The results indicated that straw yield (1.068) and harvest index (0.741) had highest positive direct effect on seed yield. They suggested that maximum importance should be given to these traits during the selection for achieving the higher seed yield.

Nandini and Duddukur (2019) examined 30 cowpea genotypes along with one check to study path analysis in randomized block design with three replications among 12 characters. The path analysis revealed that days to 50% flowering (0.0360,0.0043), pods per plant (0.090,0.1925), clusters per pod (0.0094,0.0072), harvest index (0.0762,0.0373) and biological yield (0.4814,0.4402) showed direct positive effect on seed yield whereas, primary branches per plant (-0.15061,-0.03448) showed direct and negative effect on seed yield at both phenotypic and genotypic levels respectively. Pod length (1.3508) and 100 seed weight (0.1762) showed direct and positive effect on seed yield at genotypic level only while it was direct and positive at phenotypic level for days to 50% maturity, days to 50% pod setting, plant height and seed yield per pod. They concluded that selection of these traits such as days to 50% flowering, days to 50% pod setting, pods per plant, 100 seed weight and biological yield may improve seed yield.

Sahu (2019) evaluated 78 germplasm lines including 3 checks of cowpea to study the path coefficient analysis for fifteen characters. She reported that maximum positive direct effect was obtained for dry matter yield per day followed by green forage yield per day, pod length and leaf width, whereas negative direct effect were obtained *via.*, dry matter yield per day followed by green forage yield, leaf length and days to maturity.

## CHAPTER-III

### MATERIALS AND METHODS

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The present investigation entitled “Estimation of genetic variability induced through combination of gamma rays and EMS mutagens in M<sub>3</sub> generation of Cowpea [*Vigna unguiculata* (L.) Walp.]” was conducted to assess the genetic variability, correlation coefficient and path coefficient analysis in cowpea treated with combination of gamma rays and EMS mutagens in M<sub>3</sub> generation of cowpea during *Kharif* 2019. Details of experimental procedure adopted, materials used and techniques followed during the course of present investigation are described as under in this chapter.

#### 3.1 LOCATION AND CLIMATIC CONDITION

Field experiment was conducted at Main Oilseed Research Station, Junagadh Agricultural University, Junagadh during the *Kharif* 2019.

Junagadh is situated in the South Saurashtra Agro-climatic Zone of Gujarat State at 21.49°N latitude and 70.43°E longitude with an elevation of 60 meters above the mean sea level on the western side at the foot hill of mountain ‘Girnar’. Climate of this region is typically subtropical characterized by moderately hot and dry summer with warm and moderately humid monsoon. The rainfall is received through the South-West monsoon between the third week of June to middle of September. July and August are the months of heavy rainfall. The decennial average rainfall of this area is 1072 mm. The soil of experimental site was medium black, alluvial with medium in organic matter. The climate of the area represented tropical condition with semi-arid in nature. The meteorological data during the experimental period is presented in Appendix-I.

#### 3.2 EXPERIMENTAL MATERIAL

##### Plant material

Two mutagens, physical mutagen *viz.*, Gamma rays at the dose of 100, 200, 225, 250, 275, 300 and 400Gy and chemical mutagen *viz.*, EMS (Ethyl Methane Sulfonate C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>S) at the dose of 0.25 per cent treated M<sub>2</sub> derived M<sub>3</sub> seeds of cowpea variety Gujarat Cowpea 5 (GC-5) were obtained from Professor and Head, Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University,

Junagadh. The basic seeds were exposed to gamma rays during 2017-18 at Bhabha Atomic Research Centre (BARC), Trombay, Mumbai.

Procedure adopted for EMS treatment of basic seed during 2017-18

1. The seeds were soaked in 0.25 per cent concentration of EMS for 6 hours and washed with normal tap water.
2. Treated seeds were tested for LD-50 value on the basis of germination test.
3. M<sub>1</sub> generation was screened in field based on LD-50 value.
4. Treatments having germination less than 50 percent and equivalent to control has been excluded.
5. From M<sub>1</sub> generation 20 superior plants of each treatment were selected on the basis of seed yield per plant. These M<sub>2</sub> progenies were grown during *kharif*-2018.
6. From M<sub>2</sub> generation, 20 superior progenies from each mutagenic treatment were selected on the basis of seed yield per plant and M<sub>3</sub> generation was sown during *kharif*-2019.

**Table 3.1 Salient features of Gujarat Cowpea -5 used in the experiment**

Characters	GC -5
<b>Pedigree</b>	GC – 2 × GC 8963
<b>Days to flowering</b>	65 – 70 days
<b>Test weight (g)</b>	8 – 9g
<b>Seed colour</b>	Brown
<b>Days to maturity</b>	65 – 70 days
<b>Yield</b>	1000 – 1100 Kg/ ha

### Mutagens

Combination of physical mutagen gamma rays and chemical mutagen Ethyl Methane Sulphonate (EMS) were used for different mutagenic treatments. The sources and mode of action of these mutagens are summarized below:

**Table 3.2 The sources and mode of action of mutagens used**

Mutagen	Source	Mode of action
Gamma Rays (Physical Mutagen)	Seeds were treated with <sup>60</sup> Co gamma cell 2.8 kR per minute at Bhabha Atomic Research Center, Trombay, Bombay.	Ionization
Ethyl Methane Sulphonate (EMS) C <sub>2</sub> H <sub>5</sub> OSO <sub>2</sub> CH <sub>3</sub> (Chemical Mutagen)	HI-Media; Bombay Chemical	Alkylation

### 3.3 EXPERIMENTAL DETAILS

The 20 superior progenies of cowpea treated with combination of gamma rays and EMS were sown on 29<sup>th</sup> July, 2019 in a Compact Family Block Design with three replications at Main Oilseed Research Station, Junagadh Agricultural University, Junagadh. Each progeny was sown in a single row plot of 2m length with a spacing of 45 cm × 10 cm. All the recommended agronomical practices along with timely plant protection measures were followed for the successful raising of the crop.

**Table 3.3: Details of treatments used in the present study along with doses**

Mutagen	Treatment	Doses
Gamma rays + EMS	T <sub>1</sub>	100Gy + 0.25% EMS
	T <sub>2</sub>	200Gy + 0.25% EMS
	T <sub>3</sub>	225Gy + 0.25% EMS
	T <sub>4</sub>	250Gy + 0.25% EMS
	T <sub>5</sub>	275Gy + 0.25% EMS
	T <sub>6</sub>	300Gy + 0.25% EMS
	T <sub>7</sub>	400Gy + 0.25% EMS
Control	T <sub>8</sub>	0Gy (Control – untreated)

### 3.4 CHARACTERS STUDIED

Ten competitive plants from each progeny were randomly selected excluding terminal ones to minimize border effects. The observations were recorded on these ten randomly selected plants from each progeny and from each replication and their mean

values were used for statistical analysis. The procedure adopted for recording the observations is described as under.

**1) Days to first flowering**

The number of days taken from sowing to the appearance of first flower.

**2) Days to maturity**

The numbers of days required from planting to maturity when more than 80 % of pods on the plant had matured.

**3) Plant height (cm)**

Plant height was measured from the base of the plant to tip of the plant at maturity in centimeters (cm).

**4) Number of branches per plant**

Effective (pod bearing) branches for each plant were counted and recorded at maturity.

**5) Number of clusters per plant**

The number of clusters per plant were counted at the time of maturity.

**6) Number of pods per plant**

Total number of pods per plant was counted for each plant.

**7) Pod length (cm)**

Five pods from each randomly selected plant were selected and the length of pod was measured from the base to the tip of the pod at the time of harvesting and average values were worked out.

**8) Number of seeds per pod**

The number of seeds in five randomly selected pods from observational plants were counted and average number of seeds per pod was computed.

**9) 100-seeds weight (g)**

100 dried seeds were counted from each selected plant and weighed on electric balance in grams.

**10) Seed yield per plant (g)**

Pods harvested from individual plant were sun-dried separately. Threshed and cleaned seeds were weighed on electric balance to obtain seed yield per plant in grams.

**3.5 STATISTICAL ANALYSIS**

The replication-wise mean values of ten randomly selected plants in each progeny were used for the statistical analysis for different character under study. The data recorded for various characters were statistically analyzed at the Computer Cell, Department of Genetics and Plant Breeding, College of Agriculture, J.A.U., Junagadh for the various parameters viz., genetic variability, genotypic and phenotypic correlations and path coefficient analysis.

**3.5.1 Analysis of variance**

The data collected on randomly selected ten plants of M<sub>3</sub> generation for individual characters were averaged and average values were subjected to statistical analysis according to Compact Family Block Design (Panse and Sukhatme, 1985). The analysis was carried out in two stages by taking mutagens as family and treatments (doses of mutagens) as progeny.

The structure of ANOVA for family (mutagens) is given in Table 3.4

**Table 3.4 Analysis of variance when families (mutagens) were raised in Compact Family Block Design**

Source	d.f.	MS	Expected mean squares
<b>Replication</b>	(r-1)	M <sub>1</sub>	$\sigma^2_{e1} + \sigma^2_r + \sigma^2_{e1}$
<b>Family</b>	(f-1) (r-1)	M <sub>2</sub>	$\sigma^2_f$
<b>Error</b>	(f-1)	M <sub>3</sub>	$\sigma^2_{e1}$

Where,

- r = number of replication
- f = number of family
- M<sub>1</sub> = Mean sum of square due to replication
- M<sub>2</sub> = Mean sum of square due to family
- M<sub>3</sub> = Mean sum of square due to error
- $\sigma^2_{e1}$  = Error variance
- $\sigma^2_f$  = Family variance
- $\sigma^2_r$  = Replication variance

The analysis for the progenies under each family was done separately for each character. The form of analysis of variance for progenies was constructed as shown in Table 3.5.

**Table 3.5 Analysis of variance of progenies (Dose/concentration of mutagen) within the family raised in Compact Family Block Design**

Source	d.f.	MS	Expected mean squares
Replication	(r-1)	M <sub>4</sub>	$\sigma^2_{e2} + p\sigma^2_r$
Progeny within family	(p-1)	M <sub>5</sub>	$\sigma^2_{e2} + r\sigma^2_p$
Error	(r-1)(p-1)	M <sub>6</sub>	$\sigma^2_{e2}$

Where,

- r = number of replication
- P = number of progeny within each family
- M<sub>4</sub> = Mean sum of square due to replication
- M<sub>5</sub> = Mean sum of square due to progeny within family
- M<sub>6</sub> = Mean sum of square due to error
- $\sigma^2_{e2}$  = Error variance
- $\sigma^2_p$  = Progeny variance
- $\sigma^2_r$  = Replication variance

Before making comparison, a test of homogeneity of error variance for progenies was carried out for each character by applying Bartlett's test of homogeneity as described by Panse and Sukhatme (1985).

### 3.5.2 Estimation of components of variance

The phenotypic, genotypic and error variances were estimated as follows:

- For progenies within family

$$\sigma^2_{e2} = M_6$$

$$\sigma^2_{g2} = (M_5 - M_6)/r$$

$$\sigma^2_{p2} = \sigma^2_{g2} + \sigma^2_{e2}$$

Where,

- r = Number of replication
- M<sub>5</sub> = Mean sum of square due to progeny within family
- M<sub>6</sub> = Mean sum of square due to error
- $\sigma^2_{e2}$  = Error variance
- $\sigma^2_{g2}$  = Genotypic variance of progeny within family
- $\sigma^2_{p2}$  = Phenotypic variance of progeny within family

The standard error of mean (S.Em.) was calculated using following formula:

- For progeny within family

$$\text{S.Em.} = \sqrt{\frac{\sigma_{e2}^2}{r}}$$

Where,

$\sigma_{e2}^2$  = Error variance of progeny within family

r = Number of replication

The critical difference (C.D.) for comparing mean of any two progeny was computed using following formula:

- For progeny within family

$$\text{C.D.} = \text{S.Em.} \times \sqrt{2} \times 't'$$

Where,

't' = Table value of 't' at 5% level of significance and error degree of freedom.

The coefficient of variation (CV) was determined as per under given formula:

- For progeny within family

$$\text{C.V. (\%)} = \frac{\sqrt{\sigma_{e2}^2}}{\bar{X}} \times 100$$

Where,

$\bar{X}$  = Mean of the character.

$\sigma_{e2}^2$  = Error variance of progeny within family

### 1) Phenotypic Range

It is the difference between maximum value and minimum value in a particular trait.

Range = Maximum value – Minimum value

While comparing the range of different traits, it is necessary to make it unit less.

Hence, coefficient of range was calculated as per the following formula:

$$\text{Coefficient of range (\%)} = \frac{\text{Range}}{\text{Maximum value} + \text{Minimum value}} \times 100$$

### 2) Phenotypic coefficient of variation (PCV %)

The phenotypic coefficient of variation, which measures the magnitude of phenotypic variation present in a particular character, was estimated as per the formula suggested by Burton (1952).

- For progeny within family

$$\text{PCV (\%)} = \frac{\sigma_{p2}^2}{\bar{X}} \times 100$$

Where,

PCV (%) = Phenotypic coefficient of variation for progeny within family

$\sigma_{p2}^2$  = Phenotypic standard deviation for progeny within family

$\bar{X}$  = Mean of the character

### 3) Genotypic coefficient of variation (GCV %)

The genotypic coefficient of variation, which measures the magnitude of genotypic variation present in a particular character, was estimated as per the formula suggested by Burton (1952).

- For progeny within family

$$\text{GCV (\%)} = \frac{\sigma_{g2}^2}{\bar{X}} \times 100$$

Where,

GCV (%) = Genotypic coefficient of variation for progeny within family

$\sigma_{g2}^2$  = Phenotypic standard deviation

$\bar{X}$  = Mean of the character

### 4) Heritability (Broad sense)

Heritability in broad sense, which is the ratio of genotypic variance ( $\sigma_g^2$ ) and phenotypic variance ( $\sigma_p^2$ ), was calculated by using the formula suggested by Allard (1960).

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

### 5) Genetic advance (GA)

The expected genetic advance at 5% selection intensity was estimated by using formula as suggested by Allard (1960).

$$\text{GA} = k \times \sigma_{p2} \times h^2$$

Where,

GA = Genetic advance under selection

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

$\sigma_{p2}$  = Phenotypic standard deviation

$h^2$  = Heritability value of the character

**6) Genetic advance as percentage of mean**

The genetic advance expressed as percentage of mean was calculated as under:

$$\text{Genetic advance as percentage of mean} = \frac{\text{Genetic advance (GA)}}{\text{Mean of character } (\bar{X})} \times 100$$

**3.5.3 Correlation coefficients**

Correlation coefficient is the measurement of relationship between two or more series of variables. The genotypic correlation coefficient provides a measure of genotypic association between different characters, while phenotypic correlation includes both genotypic as well as environmental influences. The phenotypic and genotypic correlation coefficients of all the pair of characters were worked out as per Al-Jibouri *et al.* (1958). The data were subjected to covariance analysis from which different components of mean sum of products were estimated.

The format of analysis of covariance is given as under in Table 3.6.

**Table 3.6 Analysis of covariance for experimental design**

Source of variance	d.f.	Mean sum of products	Expectation of mean sum of products
Replication	(r-1)	MP <sub>r</sub>	-
Progeny within family	(t-1)	MP <sub>t</sub>	Cov <sub>e(x,y)</sub> + r Cov <sub>g(x,y)</sub>
Error	(r-1)(t-1)	MP <sub>e</sub>	Cov <sub>e(x,y)</sub>

Where,

r = Number of replication

t = Number of progeny within family

Cov<sub>e(x,y)</sub> = Environment covariance between two characters X and Y

Cov<sub>g(x,y)</sub> = Genotypic covariance between two characters X and Y

**(i) Genotypic covariance**

$$\text{Genotypic covariance (Cov } g_{(x,y)}) = (MP_t - MP_e) / r$$

Where,

MP<sub>t</sub> = Mean sum of products due to progeny within family between two characters X and Y.

MP<sub>e</sub> = Mean sum of products due to error between two characters X and Y.

$r$  = Number of replications

**(ii) Phenotypic covariance**

$$\text{Phenotypic covariance (Cov } p_{(x,y)}) = (\text{Cov } g_{(x,y)} + \text{MP}_e)/r$$

Where,

$\text{MP}_e$  = Mean sum of products due to error between two characters X and Y.

$r$  = Number of replications

**(iii) Error covariance**

$$\text{Error covariance (Cov } e_{(x,y)}) = \text{MP}_e$$

Where,

$\text{MP}_e$  = Mean sum of products due to error between two characters X and Y.

The genotypic, phenotypic and error variances and covariances were used for calculating the genotypic and phenotypic correlation coefficients, respectively as suggested by Al-Jibouri *et al.* (1958). Now, genotypic and phenotypic correlation coefficients were worked out according to formula described below;

**(a) Genotypic correlation coefficient**

$$\text{Genotypic correlation coefficient (} r_{g_{(x,y)}} \text{)} = \frac{\text{Cov}_{g_{(x,y)}}}{\sqrt{\sigma_{g_x}^2 \sigma_{g_y}^2}}$$

Where,

$\text{Cov}_{g_{(x,y)}}$  = Genotypic covariance for two characters X and Y.

$\sigma_{g_x}^2$  = Genotypic variance for character X.

$\sigma_{g_y}^2$  = Genotypic variance for character Y.

**(b) Phenotypic correlation coefficient**

$$\text{Phenotypic correlation coefficient (} r_{p_{(x,y)}} \text{)} = \frac{\text{Cov}_{p_{(x,y)}}}{\sqrt{\sigma_{p_x}^2 \sigma_{p_y}^2}}$$

Where,

$\text{Cov}_{p_{1,2}}$  = Phenotypic covariance for two characters X and Y.

$\sigma_{p_x}^2$  = Phenotypic variance for character X.

$\sigma_{p_y}^2$  = Phenotypic variance for character Y.

**(c) Test of significance**

The test of significance for correlation coefficient was done by calculating ‘t’ value using following formula.

$$t = \frac{r_{(x,y)}}{\sqrt{(1-r_{(x,y)}^2)}} \times \sqrt{(n-2)}$$

Where,

- ‘t’ = Calculated value of ‘t’
- $r_{(x,y)}$  = Correlation coefficient of characters X and Y
- n = Number of observations

The calculated ‘t’ value was compared with table ‘t’ value at n-2 degrees of freedom to test the significance of correlation coefficient.

**3.5.4 Path Coefficient Analysis**

Path coefficient is a standardized partial regression coefficient and measures the direct and indirect influence of one variable upon another thereby permitting the separation of the correlation coefficient into the component of direct and indirect effects.

The path coefficient analysis was carried-out as per the method suggested by Dewey and Lu (1959). Genotypic correlation coefficients of 9 variables with seed yield per plant were used to estimate the path coefficient for the direct effects of various independent characters on seed yield per plant. The direct effects designated as 'P' were calculated by increasing the underlying correlation matrix as per Doolittle method described by Steel and Torrie (1960).

$$r_{1y} = P_{1y} + P_{2y}r_{1.2} + \dots, \dots, \dots + P_{9y} r_{1.9}$$

$$r_{2y} = P_{1y} r_{1.2} + P_{2y} + \dots, \dots, \dots + P_{9y} r_{2.9}$$

$$\begin{matrix} , & , & , & , & , \\ , & , & , & , & , \end{matrix}$$

$$r_{9y} = P_{1y} r_{1.9} + P_{2y} r_{2.9} + \dots, + P_{9y}$$

Where,

$r_{1y}$ ,  $r_{2y}$ ,  $r_{3y}, \dots, \dots, r_{9y}$  are the genotypic correlations of days to first flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and 100-seeds weight, respectively with seed yield per plant.

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$P_{1y}, P_{2y}, P_{3y}, \dots, \dots, P_{9y}$  are the direct effects of characters *viz.*, days to first flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and 100-seeds weight, respectively with seed yield per plant.

The coefficient of determination was calculated by using the following relationship:

$$1 = P^2_{1.y} + 2P_{1.y} r_{1.2}P_{2.y} + 2P_{1.y} r_{1.3}P_{3.y} + 2P_{1.y} r_{1.4}P_{4.y} + 2P_{1.y} r_{1.5}P_{5.y} + 2P_{1.y} r_{1.6}P_{6.y} + 2P_{1.y} r_{1.7}P_{7.y} + 2P_{1.y} r_{1.8}P_{8.y} + 2P_{1.y} r_{1.9}P_{9.y} + \dots + P^2_{8.y} + 2P_{8.y} r_{8.9}P_{9.y} + P^2_{9.y} + R^2$$

The residual variation ( $R$ ) is the variation, on dependent character *i.e.* seed yield per plant due to uncontrolled causes was estimated by subtracting this value from unity.

## **CHAPTER-IV**

### **EXPERIMENTAL RESULTS**

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The present investigation entitled “Estimation of genetic variability induced through combination of gamma rays and EMS mutagens in M<sub>3</sub> generation of cowpea [*Vigna unguiculata* (L.) Walp.]” was carried out by evaluating different M<sub>3</sub> progenies of cowpea variety GC-5 treated with different combinations of mutagens for ten quantitative characters. The experimental results obtained on different aspects are described under the following heads:

- 4.1 Analysis of variance
- 4.2 Genetic variability parameters
- 4.3 Correlation coefficients
- 4.4 Path coefficient analysis

#### **4.1 ANALYSIS OF VARIANCE**

The analysis of variance for Compact Family Block Design (CFBD) was carried out for different 10 characters and it is presented in Table 4.1. The analysis of variance between families revealed that mean sum of squares between families were highly significant for all the characters studied. The Bartlett’s test of homogeneity of error variance for all the families indicated that the error variance was homogenous for all characters except for number of clusters per plant, number of pods per plant and 100-seeds weight as showed by non-significance of chi-square values. The analysis of variance among all progenies within families indicated significant difference among 20 progenies means for all characters studied.

#### **4.2 GENETIC VARIABILITY PARAMETERS**

The magnitude of genetic variability in particular, decides the effectiveness of selection. It is an established fact that greater the variability among the genotypes, better is the chance for further improvement in the crop. Assessment of variance has been the most dependable statistical measure to find the mutagenic effect on the polygene. The results obtained on various parameters of genetic variability are presented as under:

Table 4.1 Analysis of variance (mean squares) between families and between progenies within families in M<sub>3</sub> generation for different characters in cowpea

Source of variation	df	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Seed yield per plant (g)
<b>Analysis of variance between families</b>											
Replication	2	0.26	0.81	540.48*	0.73	0.88	3.00	2.28	11.54**	0.11	28.82**
Family	7	788.32**	2.30**	5703.28**	35.89**	120.73**	229.82**	5.78**	34.36**	475.21**	141.44**
Error	14	1.21	0.42	129.21	0.30	1.04	3.57	0.68	1.51	0.07	3.98
$\chi^2$ test		NS	NS	NS	NS	S	S	NS	NS	S	NS
<b>Analysis of variance between progenies within families</b>											
<b>Treatment 1 (100Gy + 0.25% EMS)</b>											
Replication	2	1.06*	0.12	65.28	0.15	0.02	16.87**	1.89	4.83*	0.14*	0.72
Progeny	19	4.22**	4.75**	269.44**	1.17**	0.80**	6.12**	5.36**	3.21**	1.39**	57.43**
Error	38	0.27	0.54	24.85	0.14	0.05	2.04	0.68	1.19	0.03	1.18
<b>Treatment 2 (200Gy + 0.25% EMS)</b>											
Replication	2	0.60	0.12	45.88	0.07	0.13	1.47	0.73	3.66	0.05	3.99
Progeny	19	7.30**	5.13**	561.23**	0.54**	1.07**	8.45**	7.18**	3.01**	0.71**	10.10**
Error	38	0.59	0.59	54.19	0.10	0.12	1.49	0.85	1.24	0.02	1.36
<b>Treatment 3 (225Gy + 0.25% EMS)</b>											
Replication	2	1.59	0.02	118.20	0.08	5.37**	1.91	1.38	1.44	0.04	2.17
Progeny	19	5.08**	4.82**	810.33**	0.66**	3.44**	10.20**	6.59**	3.92**	0.76**	4.32**
Error	38	0.56	0.56	54.38	0.17	0.29	0.89	0.78	1.21	0.04	0.97
<b>Treatment 4 (250Gy + 0.25% EMS)</b>											
Replication	2	3.73**	0.05	618.28**	0.34	0.16	4.91	0.63	2.26*	0.08	3.46
Progeny	19	6.05**	7.20**	722.23**	0.60**	2.05**	11.65**	5.85**	1.97**	1.34**	20.85**
Error	38	0.43	0.73	53.30	0.15	0.13	1.89	0.75	0.64	0.09	1.38

Table 4.1 Conti.....

Table 4.1 Conti.....

Source of variation	df	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Seed yield per plant (g)
<b>Treatment 5 (275Gy + 0.25% EMS)</b>											
<b>Replication</b>	2	0.2	1.35	502.67**	0.23	1.38**	2.34	0.46	3.08*	0.07	7.34*
<b>Progeny</b>	19	4.70**	7.37**	551.20**	0.80**	3.07**	17.54**	4.05**	3.09**	2.71**	10.97**
<b>Error</b>	38	0.46	0.75	53.77	0.14	0.24	1.59	0.5	0.85	0.07	1.42
<b>Treatment 6 (300Gy + 0.25% EMS)</b>											
<b>Replication</b>	2	0.4	1.52	34.89	0.26	0.88*	0.21	0.79	0.67	0.01	4.96*
<b>Progeny</b>	19	6.49**	5.33**	1183.31**	0.53**	4.85**	6.98**	9.84**	1.83**	2.50**	7.82**
<b>Error</b>	38	0.51	0.48	53.6	0.11	0.22	0.8	1.01	0.65	0.11	1.18
<b>Treatment 7 (400Gy + 0.25% EMS)</b>											
<b>Replication</b>	2	0.5	0.19	23.22	1.60**	0.08	0.08	0.27	3.65*	0.15	6.65**
<b>Progeny</b>	19	2.07**	8.77**	520.92**	0.34**	2.20**	10.97**	4.32**	5.79**	2.39**	5.49**
<b>Error</b>	38	0.19	0.54	53.77	0.11	0.22	1.09	0.77	0.81	0.08	1.16
<b>Treatment 8 (control)</b>											
<b>Replication</b>	2	0.65	0.42	36.58	0.07	0.13	0.21	0.86	2.52*	0.12*	27.42**
<b>Progeny</b>	19	2.34**	8.77**	261.62**	0.41**	1.13**	4.40**	5.36**	1.08**	1.45**	15.17**
<b>Error</b>	38	0.28	0.76	53.43	0.12	0.09	0.21	0.76	0.5	0.03	1.19

\* and \*\* Significant at 5 and 1 per cent levels, respectively

Chi-square for Bartlett's test of homogeneity of error variances, S= Significant; NS = Non-significant

**4.2.1 Mean performance**

The M<sub>3</sub> progeny wise mean values of cowpea variety GC-5 treated with different combinations of gamma rays and EMS mutagens for all the 10 characters along with standard error of mean (S.Em), critical difference (C.D.) and coefficient of variation (C.V. %) is given in Appendix-II. The treatment wise summary is also presented in Table 4.2. Treatment wise mean performance is presented as under:

Perusal of Table 4.2 indicates that among the developmental traits, desirable effects of mutagens were showed on days to first flowering and days to maturity over control, while for plant height there was no gain found for short stature. The lowest days to first flowering was observed by treatment 5 (47.67 days) followed by treatment 1 (49.03 days) and treatment 4 (49.80 days). For the trait days to maturity, only two treatments *i.e.* treatment 4 (65.55 days) and treatment 2 (65.72 days) showed earliness than control treatment 8 (65.86 days). The remaining treatments were late maturing than control. Generally, cowpea is to be used for vegetable purpose, dwarf and compact plant type with determinate growth habit is desirable. But in the present study, none of the mutagen was effective in reducing plant height. The lowest plant height was recorded by control treatment 8 (85.63 cm).

Looking to the economical traits (Table 4.2), number of branches per plant was the highest in treatment 1 (4.65) followed by treatment 2 (3.84). Treatment 4 recorded the lowest number of branches (2.52) among all the mutagenic treatments. The highest (10.11) number of clusters per plant was recorded in treatment 3 followed by treatment 7 (7.77) and treatment 1 (7.26). The lowest number of clusters per plant was recorded by control treatment 8 (5.12). Maximum number of pods per plant was observed in treatment 5 (15.73) followed by treatment 4 (14.35) and treatment 2 (14.10), while minimum number of pods per plant was recorded by treatment 1 (9.69). Pod length was highest for treatment 1 (10.23) followed by treatment 2 (10.17) whereas, the lowest pod length was observed in treatment 6 (9.25). Treatment 1 (9.26) recorded the highest number of seeds per pod followed by treatment 3 (8.73) and treatment 4 (8.21). The control showed lowest number of seeds per pod (6.89). Maximum 100-seeds weight was observed in treatment 5 (14.45) followed by treatment 7 (12.47) and treatment 6 (12.04). Treatment 4 recorded the lowest (6.53) 100-seeds weight. The highest mean seed yield per plant (12.76) was observed in treatment 1 followed by treatment 4 (10.70) and treatment 5 (9.46). The lowest seed yield per plant (8.36) was recorded in treatment 6.

**Table 4.2 Treatment wise mean performance, phenotypic range and coefficient of range for different characters in M<sub>3</sub> generation of cowpea**

<b>Treatment</b>	<b>Parameter</b>	<b>Days to first flowering</b>	<b>Days to maturity</b>	<b>Plant height (cm)</b>	<b>Number of branches per plant</b>	<b>Number of clusters per plant</b>
T <sub>1</sub>	Mean	49.03	65.98	102.66	4.65	7.26
	Phenotypic range	46.6-51.7	63.3-68	81.9-123.1	3.4-5.9	6.1-8.3
	Coefficient of range	5.18	3.55	20.10	26.70	15.03
T <sub>2</sub>	Mean	53.29	65.72	97.82	3.84	6.87
	Phenotypic range	49.9-56.1	63.6-67.6	74.7-126.8	2.5-4.5	5.5-8.1
	Coefficient of range	5.81	3.04	25.83	28.87	19.03
T <sub>3</sub>	Mean	52.08	66.13	107.22	2.73	10.11
	Phenotypic range	50.3-54.2	63.3-68	67-135	1.6-3.5	8.3-11.8
	Coefficient of range	3.66	3.55	33.65	38.10	17.41
T <sub>4</sub>	Mean	49.80	65.55	103.58	2.52	7.04
	Phenotypic range	45.3-52	62-67.6	70.9-130.2	1.7-3.1	5.4-9.2
	Coefficient of range	6.91	4.37	29.48	29.16	26.12
T <sub>5</sub>	Mean	47.67	65.90	112.32	3.53	6.31
	Phenotypic range	46.2-50	62.3-67.6	81.1-142.3	2.5-4.4	4.4-8.1
	Coefficient of range	3.98	4.10	27.40	27.71	29.68
T <sub>6</sub>	Mean	53.45	65.92	114.00	2.54	7.07
	Phenotypic range	51-55.7	63.3-67.6	73.9-151.4	1.5-3.1	4.3-9.3
	Coefficient of range	4.37	3.31	34.36	33.19	36.39
T <sub>7</sub>	Mean	57.51	66.12	114.63	2.73	7.77
	Phenotypic range	55.9-58.7	62.8-68.2	88.1-138.4	2.2-3.2	6.3-9.4
	Coefficient of range	2.47	4.14	22.19	17.86	19.87
T <sub>8</sub>	Mean	57.25	65.86	85.63	2.72	5.12
	Phenotypic range	54.4-58.5	61.9-68.1	66.1-103.9	1.7-3.3	4.1-7
	Coefficient of range	3.63	4.74	22.24	31.21	25.95

**Table 4.2 Conti.....**

**Table 4.2 Conti.....**

<b>Treatment</b>	<b>Parameter</b>	<b>Number of pods per plant</b>	<b>Pod length (cm)</b>	<b>Number of seeds per pod</b>	<b>100-seeds weight (g)</b>	<b>Seed yield per plant (g)</b>
T <sub>1</sub>	Mean	9.69	10.23	9.26	8.52	12.76
	Phenotypic range	7.5-12.7	5.7-11.9	7.4-11.6	6.5-9.5	6.5-22.2
	Coefficient of range	25.99	34.99	21.78	18.55	54.70
T <sub>2</sub>	Mean	14.10	10.17	7.75	8.54	8.36
	Phenotypic range	10.7-16.7	5.5-12.2	6.2-10.2	7.3-9.4	5.6-12.2
	Coefficient of range	21.58	37.72	24.71	12.26	36.95
T <sub>3</sub>	Mean	12.92	9.99	8.73	8.80	8.50
	Phenotypic range	10.3-17.1	6.4-11.9	6.9-10.9	7.3-9.5	6.6-11.3
	Coefficient of range	24.68	29.95	22.56	13.01	26.07
T <sub>4</sub>	Mean	14.35	9.78	8.21	6.53	10.70
	Phenotypic range	9.8-17.8	6.3-11.2	7.2-10.1	5.5-8.5	7.4-16.7
	Coefficient of range	28.92	27.61	16.70	21.13	38.42
T <sub>5</sub>	Mean	15.73	9.77	7.96	14.45	9.46
	Phenotypic range	10.7-18.7	6.8-11.2	6.9-10.8	11.9-15.8	6.4-13.5
	Coefficient of range	27.38	24.53	21.54	14.09	35.60
T <sub>6</sub>	Mean	10.80	9.25	7.36	12.04	8.36
	Phenotypic range	8-13.2	5.4-11.8	6.6-9.9	10.3-13.5	6.1-11.4
	Coefficient of range	24.35	37.20	20	13.35	30.04
T <sub>7</sub>	Mean	13.69	9.93	8.40	12.47	9.07
	Phenotypic range	10.9-18.1	6.8-10.9	6.6-12.5	10.5-13.5	6.7-12.2
	Coefficient of range	24.90	23.25	30.52	12.26	29.05
T <sub>8</sub>	Mean	12.68	10.05	6.89	7.20	8.73
	Phenotypic range	9.4-14.7	5.3-11.3	6.0-8.6	5.5-7.8	5.2-12.8
	Coefficient of range	21.73	35.68	18.20	17.39	41.90

**4.2.2 Phenotypic range and coefficient of range**

Character wise phenotypic range and coefficient of range for different mutagenic treatments are presented in Table 4.2 are described as under:

**4.2.2.1 For Treatment 1 (100Gy + 0.25% EMS)**

Seed yield per plant (6.5-22.2g) recorded maximum phenotypic range of variation with coefficient of range 54.70%. The moderate phenotypic range of variation was observed for pod length (5.7-11.9 cm), number of branches per plant (3.4-5.9), number of pods per plant (7.5-12.7 pods), number of seeds per pod (7.4-11.6 seeds), plant height (81.9-123.1 cm), 100-seeds weight (6.5-9.5 g) and number of clusters per plant (6.1-8.3) with 34.99%, 26.70%, 25.99%, 21.78%, 20.10%, 18.55% and 15.03% coefficient of range, respectively. There was narrow range of variation (below 15 %) for days to first flowering (46.6-51.7 days) and days to maturity (63.3-68 days) with 5.18% and 3.55% coefficient of range, respectively.

**4.2.2.2 For Treatment 2 (200Gy + 0.25% EMS)**

The moderate phenotypic range of variation was observed for pod length (5.5-12.2 cm), seed yield per plant (5.6-12.2 g), number of branches per plant (2.5-4.5), plant height (74.7-126.8 cm), number of seeds per pod (6.2-10.2 seeds), number of pods per plant (10.7-16.7 pods), number of clusters per plant (5.5-8.1) and 100-seeds weight (7.3-9.4 g) with 37.72%, 36.95%, 28.87%, 25.83%, 24.71, 21.58%, 19.03% and 12.26% coefficient of range, respectively. There was narrow range of variation (below 15 %) for days to first flowering (49.9-56.1 days) and days to maturity (63.6-67.6 days) with 5.81% and 3.04% coefficient of range, respectively.

**4.2.2.3 For Treatment 3 (225Gy + 0.25% EMS)**

The moderate phenotypic range of variation was observed for number of branches per plant (1.6-3.5), plant height (67-135 cm), pod length (6.4-11.9 cm), seed yield per plant (6.6-11.3 g), number of pods per plant (10.3-17.1 pods), number of seeds per pod (6.9-10.9 seeds) and number of clusters per pod (8.3-11.8) with 38.10%, 33.65%, 29.95%, 26.07%, 24.68%, 22.56% and 17.41% coefficient of range, respectively. Narrow range of variation (below 15 %) was observed for 100-seeds weight (7.3-9.5 g), days to first flowering (50.3-54.2 days) and days to maturity (63.3-68 days) with 13.01%, 3.66% and 3.55% coefficient of range, respectively.

**4.2.2.4 For Treatment 4 (250Gy + 0.25% EMS)**

The moderate phenotypic range of variation was observed for seed yield per plant (7.4-16.7 g), plant height (70.9-130.2 cm), number of branches per plant (1.7-

3.1), number of pods per plant (9.8-17.8 pods), pod length (6.3-11.2 cm), number of clusters per plant (5.4-9.2), 100-seeds weight (5.5-8.5 g) and number of seeds per pod (7.2-10.1 seeds) with 38.42%, 29.48%, 29.16%, 28.92%, 27.61%, 26.12%, 21.13% and 16.70% coefficient of range, respectively. There was narrow range of variation for days to first flowering (45.3-52 days) and days to maturity (62-67.6 days) with 6.91% and 4.37% coefficient of range, respectively.

#### **4.2.2.5 For Treatment 5 (275Gy + 0.25% EMS)**

The moderate phenotypic range of variation was observed for seed yield per plant (6.4-13.5 g), number of clusters per plant (4.4-8.1), number of branches per plant (2.5-4.4), plant height (81.1-142.3 cm), number of pods per plant (10.7-18.7 pods), pod length (6.8-11.2 cm) and number of seeds per pod (6.9-10.8 seeds) with 35.60%, 29.68%, 27.71%, 27.40%, 27.38%, 24.53% and 21.54% coefficient of range, respectively. There was narrow coefficient of range for 100-seeds weight (14.09 %), days to maturity (4.10 %) and days to first flowering (3.98 %).

#### **4.2.2.6 For Treatment 6 (300Gy + 0.25% EMS)**

The moderate phenotypic range of variation was observed for pod length (5.4-11.8 cm), number of clusters per plant (4.3-9.3), plant height (73.9-151.4 cm), number of branches per plant (1.5-3.1), seed yield per plant (6.1-11.4 g), number of pods per plant (8-13.2 pods) and number of seeds per pod (6.6-9.9 seeds) with 37.20%, 36.39%, 34.36%, 33.19%, 30.04%, 24.35% and 20% coefficient of range, respectively. There was narrow coefficient of range for 100-seeds weight (13.35 %), days to first flowering (4.37 %) and days to maturity (3.31%).

#### **4.2.2.7 For Treatment 7 (400Gy + 0.25% EMS)**

Number of seeds per pod (6.6-12.5 seeds), seed yield per plant (6.7-12.2 g), number of pods per plant (10.9-18.1 pods), pod length (6.8-10.9 cm), plant height (88.1-138.4 cm), number of clusters per plant (6.3-9.4) and number of branches per plant (2.2-3.2) recorded moderate phenotypic range of variation with coefficient of range 30.52%, 29.05%, 24.90%, 23.25%, 22.19%, 19.87% and 17.86% respectively. There was narrow coefficient of range for 100-seeds weight (12.26 %), days to maturity (4.14 %) and days to first flowering (2.47 %).

#### **4.2.2.8 For Treatment 8 (control)**

The moderate phenotypic range of variation was observed for seed yield per plant (5.2-12.8 g), pod length (5.3-11.3 cm), number of branches per plant (1.7-3.3), number of clusters per plant (4.1-7), plant height (66.1-103.9 cm), number of pods per

plant (9.4-14.7 pods), number of seeds per pod (6-8.6 seeds) and 100-seeds weight (5.5-7.8 g) with coefficient of range 41.90%, 35.68%, 31.21%, 25.95%, 22.24%, 21.73%, 18.20% and 17.39% respectively. Narrow coefficient of range was expressed by days to maturity (4.74 %) and days to first flowering (3.63 %).

### **4.2.3 Phenotypic coefficient of variation (PCV)**

Phenotypic coefficients of variation (PCV) for different mutagenic treatments in M<sub>3</sub> generation of cowpea are presented in Table 4.3.

#### **4.2.3.1 For Treatment 1 (100Gy + 0.25% EMS)**

The high phenotypic coefficient of variation was observed for seed yield per plant (35.09%). Moderate PCV was recorded for number of pods per plant (19.02%), number of branches per plant (15.72%), number of seeds per pod (14.75%), pod length (14.65%) and plant height (10.05%) while, low PCV was recorded for 100-seeds weight (8.16%), number of clusters per plant (7.58%), days to first flowering (2.57%) and days to maturity (2.14%).

#### **4.2.3.2 For Treatment 2 (200Gy + 0.25% EMS)**

Phenotypic coefficient of variation for treatment 2 was high for seed yield per plant (24.84%) while, it was moderate for number of seeds per pod (17.46%), pod length (16.92%), number of branches per plant (15.90%), plant height (15.27%) and number of pods per plant (13.84%). Low PCV was recorded for number of clusters per plant (9.64%), 100-seeds weight (5.84%), days to first flowering (3.17%) and days to maturity (2.24%).

#### **4.2.3.3 For Treatment 3 (225Gy + 0.25% EMS)**

The high phenotypic coefficient of variation was observed for number of branches per plant (33.70%) while, moderate PCV was recorded for seed yield per plant (16.78%). number of seeds per pod (16.65%), pod length (16.49%), plant height (16.33%), number of pods per plant (15.46%) and number of clusters per plant (11.40%). Low PCV was recorded for 100-seeds weight (6.04%), days to first flowering (2.88%) and days to maturity (2.10%).

#### **4.2.3.4 For Treatment 4 (250Gy + 0.25% EMS)**

The high phenotypic coefficient of variation was observed for number of branches per plant (29.66%) and seed yield per plant (25.73%). Moderate PCV was recorded for plant height (16.05%), pod length (16.01%), number of pods per plant (15.80%), number of seeds per pod (12.66%), number of clusters per plant (12.55%)

while, low PCV was recorded for days to first flowering (3.05%) and days to maturity (2.61%).

#### **4.2.3.5 For Treatment 5 (275Gy + 0.25% EMS)**

Phenotypic coefficient of variation for this treatment was high for number of branches per plant (23.67%) and seed yield per plant (22.70%). Moderate PCV was recorded for number of clusters per plant (17.22%), number of pods per plant (16.71%), number of seeds per pod (15.87%), pod length (13.29%) and plant height (13.19%) while, low PCV was recorded for 100-seeds weight (6.75%), days to first flowering (2.88%) and days to maturity (2.54%).

#### **4.2.3.6 For Treatment 6 (300Gy + 0.25% EMS)**

The high phenotypic coefficient of variation was observed for number of branches per plant (30.33%), seed yield per plant (21.53%) and pod length (21.52%) while, moderate PCV was recorded for number of clusters per plant (19.26%), plant height (18.19%), number of pods per plant (15.66%) and number of seeds per pod (13.88%). Low PCV was recorded for 100-seeds weight (7.91%), days to first flowering (2.97%) and days to maturity (2.24%).

#### **4.2.3.7 For Treatment 7 (400Gy + 0.25% EMS)**

The high phenotypic coefficient of variation for treatment 7 was observed for number of branches per plant (32.12%). Moderate PCV was recorded for number of seeds per pod (18.72%), seed yield per plant (17.82%), number of pods per plant (15.31%), pod length (14.08%) plant height (12.63%) and number of clusters per plant (12.14%) while, low PCV was recorded in 100-seeds weight (7.41%), days to maturity (2.66%) and days to first flowering (1.58%).

#### **4.2.3.8 For Treatment 8 (control)**

The high phenotypic coefficient of variation for control was observed for seed yield per plant (27.76%) while, moderate PCV was recorded for number of branches per plant (17.53%), pod length (15.07%), number of clusters per plant (12.96%), plant height (12.94%), number of seeds per pod (12.11%) and number of pods per plant (10.01%). Low PCV was recorded in 100-seeds weight (9.85%), days to maturity (2.95%) and days to first flowering (1.71%).

### **4.2.4 Genotypic coefficient of variation (GCV)**

Genotypic coefficients of variation (GCV) for different mutagenic treatments in M<sub>3</sub> generation of cowpea are presented in Table 4.3.

**Table 4.3 Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for different characters in M<sub>3</sub> generation of cowpea**

<b>Treatment</b>	<b>Parameter</b>	<b>Days to first flowering</b>	<b>Days to maturity</b>	<b>Plant height (cm)</b>	<b>Number of branches per plant</b>	<b>Number of clusters per plant</b>	<b>Number of pods per plant</b>	<b>Pod length (cm)</b>	<b>Number of seeds per pod</b>	<b>100-seeds weight (g)</b>	<b>Seed yield per plant (g)</b>
T <sub>1</sub>	<b>PCV</b>	2.57	2.14	10.05	15.72	7.58	19.02	14.65	14.75	8.16	35.09
	<b>GCV</b>	2.33	1.80	8.80	12.90	6.88	12.04	12.22	8.87	7.92	33.99
T <sub>2</sub>	<b>PCV</b>	3.17	2.24	15.27	15.90	9.64	13.84	16.92	17.46	5.84	24.84
	<b>GCV</b>	2.80	1.82	13.29	10.29	7.88	10.80	14.28	9.92	5.63	20.33
T <sub>3</sub>	<b>PCV</b>	2.88	2.10	16.33	33.70	11.40	15.46	16.49	16.65	6.04	16.78
	<b>GCV</b>	2.48	1.76	14.81	11.38	10.04	13.64	13.92	10.89	5.58	11.99
T <sub>4</sub>	<b>PCV</b>	3.05	2.61	16.05	29.66	12.55	15.80	16.01	12.66	10.92	25.73
	<b>GCV</b>	2.75	2.15	14.42	16.55	11.27	12.57	13.34	8.13	9.86	23.04
T <sub>5</sub>	<b>PCV</b>	2.88	2.54	13.19	23.67	17.22	16.71	13.29	15.87	6.75	22.70
	<b>GCV</b>	2.51	2.19	11.47	3.78	15.44	14.66	11.12	10.88	6.50	18.94
T <sub>6</sub>	<b>PCV</b>	2.97	2.24	18.19	30.33	19.26	15.66	21.52	13.88	7.91	21.53
	<b>GCV</b>	2.66	1.88	17.02	16.74	17.97	13.29	18.56	8.53	7.43	17.45
T <sub>7</sub>	<b>PCV</b>	1.58	2.66	12.63	32.12	12.14	15.31	14.08	18.72	7.41	17.82
	<b>GCV</b>	1.40	2.41	10.89	7.78	10.50	13.26	10.95	15.33	7.04	13.24
T <sub>8</sub>	<b>PCV</b>	1.71	2.95	12.94	17.53	12.96	10.01	15.07	12.11	9.85	27.76
	<b>GCV</b>	1.45	2.36	9.73	11.49	11.61	9.32	12.33	6.36	9.58	24.82

**4.2.4.1 For Treatment 1 (100Gy + 0.25% EMS)**

The high genotypic coefficient of variation was observed for seed yield per plant (33.99%). Moderate GCV was recorded for number of branches per plant (12.90%), pod length (12.22%) and number of pods per plant (12.04%) while, low GCV was recorded for number of seeds per pod (8.87%), plant height (8.80%), 100-seeds weight (7.92%), number of clusters per plant (6.88%), days to first flowering (2.33%) and days to maturity (1.80%).

**4.2.4.2 For Treatment 2 (200Gy + 0.25% EMS)**

Genotypic coefficient of variation was high for seed yield per plant (20.33%) while, moderate GCV was recorded for pod length (14.28%), plant height (13.29%), number of pods per plant (10.80%) and number of branches per plant (10.29%). Low GCV was recorded for number of seeds per pod (9.92%), number of clusters per plant (7.88%), 100-seeds weight (5.63%), days to first flowering (2.80%) and days to maturity (1.82%).

**4.2.4.3 For Treatment 3 (225Gy + 0.25% EMS)**

None of the treatment expressed high GCV whereas, moderate genotypic coefficient of variation was observed for plant height (14.81%), pod length (13.92%), number of pods per plant (13.64%), seed yield per plant (11.99%), number of branches per plant (11.38%), number of seeds per pod (10.89%) and number of clusters per plant (10.04%). Low GCV was recorded for 100-seeds weight (5.58%), days to first flowering (2.48%) and days to maturity (1.76%).

**4.2.4.4 For Treatment 4 (250Gy + 0.25% EMS)**

Only the character seed yield per plant (23.04%) had the high genotypic coefficient of variation for this treatment while, moderate GCV was recorded for number of branches per plant (16.55%), plant height (14.42%), pod length (13.34%), number of pods per plant (12.57%), number of clusters per plant (11.27%). Low GCV was recorded for 100-seeds weight (9.86%), number of seeds per pod (8.13%), days to first flowering (2.75%) and days to maturity (2.15%).

**4.2.4.5 For Treatment 5 (275Gy + 0.25% EMS)**

The moderate GCV was observed for seed yield per plant (18.94%), number of clusters per plant (15.44%), number of pods per plant (14.66%), plant height (11.47%), pod length (11.12%) and number of seeds per pod (10.88%) while low GCV was recorded for 100-seeds weight (6.50%), number of branches per plant (3.78%), days to first flowering (2.51%) and days to maturity (2.19%).

**2.4.6 For Treatment 6 (300Gy + 0.25% EMS)**

None of the trait recorded high GCV for treatment 6, while moderate genotypic coefficient of variation was observed for pod length (18.56%), number of clusters per plant (17.97%), seed yield per plant (17.45%), plant height (17.02%), number of branches per plant (16.74%) and number of pods per plant (13.29%). Low GCV was recorded for number of seeds per pod (8.53%), 100-seeds weight (7.43%), days to first flowering (2.66%) and days to maturity (1.88%).

**4.2.4.7 For Treatment 7 (400Gy + 0.25% EMS)**

Moderate genotypic coefficient of variation was observed for number of seeds per pod (15.33%), seed yield per plant (13.24%), number of pods per plant (13.26%), pod length (10.95%), plant height (10.89%) and number of clusters per plant (10.50%) while, low GCV was recorded for number of branches per plant (7.78%), 100-seeds weight (7.04%), days to maturity (2.41%) and days to first flowering (1.40%).

**4.2.4.8 For Treatment 8 (control)**

The high genotypic coefficient of variation was observed only for seed yield per plant (24.82%) while moderate GCV was recorded for pod length (12.33%), number of clusters per plant (11.61%) and number of branches per plant (11.49%). Low GCV was recorded for plant height (9.73%), 100-seeds weight (9.58%), number of pods per plant (9.32%), number of seeds per pod (6.36%), days to maturity (2.36%) and days to first flowering (1.45%).

**4.2.5 Heritability**

With the help of genotypic coefficient of variation alone, it is not possible to determine the extent of variation which is heritable. Thus, the knowledge of heritability of a character helps the plant breeders for predicting the genetic advance for any quantitative characters and aids in exercising necessary selection procedure. Broad sense heritability for different mutagenic treatments are presented in Table 4.4.

**4.2.5.1 For Treatment 1 (100Gy + 0.25% EMS)**

Very high heritability estimates were observed for 100-seeds weight (94.22%) and seed yield per plant (93.86%). High heritability estimates were observed for days to first flowering (82.37%), number of clusters per plant (82.30%), plant height (76.64%), days to maturity (70.83%), pod length (69.57%) and number of branches per plant (67.36%) while, number of pods per plant (40.06%) and number of seeds per pod (36.18%) exhibited moderate heritability values

**4.2.5.2 For Treatment 2 (200Gy + 0.25% EMS)**

Very high heritability estimates were recorded for 100-seeds weight (93.23%). High heritability estimates were observed for days to first flowering (78.26%), plant height (75.72%), pod length (71.24%), number of clusters per plant (66.77%), days to maturity (65.88%), seed yield per plant (66.98%) and number of pods per plant (60.88%) while, medium heritability was observed for number of branches per plant (41.89%) and number of seeds per pod (32.26%).

**4.2.5.3 For Treatment 3 (225Gy + 0.25% EMS)**

High heritability estimates were observed for 100-seeds weight (85.22%), plant height (82.25%), number of pods per plant (77.80%), number of clusters per plant (77.58%), days to first flowering (74.00%), pod length (71.24%) and days to maturity (70.86%) while, seed yield per plant (51.02%) and number of seeds per pod (42.78%) exhibited moderate heritability values. Low heritability estimates were observed for number of branches per plant (11.41%).

**4.2.5.4 For Treatment 4 (250Gy + 0.25% EMS)**

The trait 100-seeds weight (81.58%) expressed high heritability estimates followed by days to first flowering (81.43%), plant height (80.70%), number of clusters per plant (80.65%), seed yield per plant (80.20%), pod length (69.47%), days to maturity (67.97%) and number of pods per plant (63.30%). Whereas, number of seeds per pod (41.21%) and number of branches per plant (31.13%) exhibited moderate heritability values.

**4.2.5.5 For Treatment 5 (275Gy + 0.25% EMS)**

Very high heritability estimates were observed for 100-seeds weight (92.69%). High heritability was observed for number of clusters per plant (80.39%) followed by number of pods per plant (76.98%), days to first flowering (75.92%), plant height (75.51%), days to maturity (73.89%), pod length (70.04%) and seed yield per plant (69.62%). The trait number of seeds per pod (46.96%) exhibited moderate heritability values while, number of branches per plant (2.55%) expressed low heritability estimates.

**4.2.5.6 For Treatment 6 (300Gy + 0.25% EMS)**

High heritability estimates were observed for 100-seeds weight (88.21%) followed by plant height (87.54%), number of clusters per plant (86.98%), days to first flowering (79.69%), pod length (74.42%), number of pods per plant (72.01%), days to maturity (70.24%) and seed yield per plant (65.71%) while, number of seeds per pod

(37.80%) and number of branches per plant (30.47%) exhibited moderate heritability values.

#### **4.2.5.7 For Treatment 7 (400Gy + 0.25% EMS)**

Very high heritability estimates were observed for 100-seeds weight (90.29%). High heritability estimates were observed for days to maturity (82.13%), days to first flowering (78.41%), number of pods per plant (75.05%), number of clusters per plant (74.77%), plant height (74.33%), number of seeds per pod (67.08%) and pod length (60.51%). The trait seed yield per plant (55.21%) and number of branches per plant (5.87%) exhibited moderate and very low heritability values, respectively.

#### **4.2.5.8 For Treatment 8 (control)**

Very high heritability estimate was observed for 100-seeds weight (94.71%). High heritability estimates were observed for number of pods per plant (86.79%), number of clusters per plant (80.22%), seed yield per plant (79.95%), days to first flowering (71.10%), pod length (66.99%) and days to maturity (63.71%) while, plant height (56.50%) and number of branches per plant (42.95%) exhibited moderate heritability values. Number of seeds per pod (27.57%) exhibited low heritability values.

### **4.2.6 Genetic advance**

Genetic advance at five per cent selection intensity ( $k=2.06$ ) was estimated for different characters (Table 4.4). Treatment wise results of genetic advance are described as under:

#### **4.2.6.1 For Treatment 1 (100Gy + 0.25% EMS)**

The highest genetic advance was observed for plant height (16.29). Moderate value of genetic advance was recorded for seed yield per plant (8.65) while, low values were observed for pod length (2.15), days to first flowering (2.14), days to maturity (2.06), number of pods per plant (1.52), 100-seeds weight (1.35), number of branches per plant (1.03) and number of seeds per pod (1.02). Very low value of genetic advance was recorded for number of clusters per plant (0.93).

#### **4.2.6.2 For Treatment 2 (200Gy + 0.25% EMS)**

The highest genetic advance was observed for plant height (23.30). Low values of genetic advance were observed for seed yield per plant (2.88), days to first flowering (2.72), pod length (2.53), number of pods per plant (2.45) and days to maturity (1.99) while, it was very low for 100-seeds weight (0.96), number of clusters per plant (0.91), number of seeds per pod (0.90) and number of branches per plant (0.53).

**Table 4.4 Heritability (broad sense), genetic advance and genetic advance as percentage of mean for different characters in M<sub>3</sub> generation of cowpea**

Treatment	Parameter	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Seed yield per plant (g)
T <sub>1</sub>	h <sup>2</sup>	82.37	70.83	76.64	67.36	82.30	40.06	69.57	36.18	94.22	93.86
	GA	2.14	2.06	16.29	1.03	0.93	1.52	2.15	1.02	1.35	8.65
	GA%	4.36	3.12	15.86	21.81	12.86	15.70	20.99	10.99	15.83	67.85
T <sub>2</sub>	h <sup>2</sup>	78.26	65.88	75.72	41.89	66.77	60.88	71.24	32.26	93.23	66.98
	GA	2.72	1.99	23.30	0.53	0.91	2.45	2.53	0.90	0.96	2.88
	GA%	5.11	3.04	23.82	13.73	13.26	17.36	24.83	11.60	11.21	34.27
T <sub>3</sub>	h <sup>2</sup>	74.00	70.86	82.25	11.41	77.58	77.80	71.24	42.78	85.22	51.02
	GA	2.29	2.02	29.66	0.22	1.84	3.20	2.42	1.28	0.93	1.49
	GA%	4.39	3.06	27.66	7.92	18.21	24.78	24.20	14.67	10.61	17.64
T <sub>4</sub>	h <sup>2</sup>	81.43	67.97	80.71	31.13	80.65	63.30	69.47	41.21	81.58	80.20
	GA	2.55	2.39	27.64	0.49	1.47	2.96	2.24	0.88	1.20	4.57
	GA%	5.12	3.65	26.68	19.02	20.84	20.61	22.91	10.75	18.35	42.50
T <sub>5</sub>	h <sup>2</sup>	75.92	73.89	75.51	2.55	80.39	76.98	70.04	46.96	92.69	69.62
	GA	2.15	2.55	23.05	0.05	1.80	4.17	1.87	1.22	1.86	3.08
	GA%	4.51	3.87	20.52	1.24	28.51	26.50	19.17	15.36	12.89	32.55
T <sub>6</sub>	h <sup>2</sup>	79.69	70.24	87.54	30.47	86.98	72.01	74.42	37.80	88.21	65.71
	GA	2.61	2.14	37.40	0.50	2.45	2.51	3.05	0.80	1.73	2.45
	GA%	4.88	3.24	32.81	19.04	34.52	23.23	32.98	10.81	14.37	29.15
T <sub>7</sub>	h <sup>2</sup>	78.41	82.13	74.33	5.87	74.77	75.05	60.51	67.08	90.29	55.21
	GA	1.47	2.98	22.16	0.11	1.45	3.24	1.74	2.17	1.72	1.84
	GA%	2.55	4.50	19.33	3.89	18.69	23.66	17.54	25.86	13.78	20.26
T <sub>8</sub>	h <sup>2</sup>	71.10	63.71	56.50	42.95	80.22	86.79	66.99	27.57	94.71	79.95
	GA	1.44	2.55	12.90	0.42	1.10	2.27	2.09	0.47	1.38	3.99
	GA%	2.51	3.88	15.06	15.51	21.42	17.89	20.79	6.87	19.21	45.71

h<sup>2</sup> = Heritability, GA = Genetic advance, GA%=Genetic advance as percentage of mean.

**4.2.6.3 For Treatment 3 (225Gy + 0.25% EMS)**

The highest genetic advance was observed for plant height (29.66). Low values of genetic advance were observed for number of pods per plant (3.20), pod length (2.42), days to first flowering (2.29), days to maturity (2.02), number of clusters per plant (1.84), seed yield per plant (1.49) and number of seeds per pod (1.28) while, 100-seeds weight (0.93) and number of branches per plant (0.22) exhibited very low values of genetic advance.

**4.2.6.4 For Treatment 4 (250Gy + 0.25% EMS)**

The highest genetic advance was observed only for plant height (27.64) whereas, it was low for seed yield per plant (4.57), number of pods per plant (2.96), days to first flowering (2.55), days to maturity (2.39), pod length (2.24), number of clusters per plant (1.47) and 100-seeds weight (1.20). The character number of seeds per pod (0.88) and number of branches per plant (0.49) exhibited very low values of genetic advance for treatment 4.

**4.2.6.5 For Treatment 5 (275Gy + 0.25% EMS)**

Genetic advance estimate for treatment 5 was the highest (23.05) for plant height. Estimates were low for number of pods per plant (4.17), seed yield per plant (3.08), days to maturity (2.55), days to first flowering (2.15), pod length (1.87), 100-seeds weight (1.86), number of clusters per plant (1.80) and number of seeds per pod (1.22) while, number of branches per plant (0.05) exhibited very low value of genetic advance.

**4.2.6.6 For Treatment 6 (300Gy + 0.25% EMS)**

The highest estimate of genetic advance for treatment 6 was observed for plant height (37.40). Low values of genetic advance was observed for pod length (3.05) followed by days to first flowering (2.61), number of pods per plant (2.51), number of clusters per plant (2.45), seed yield per plant (2.45), days to maturity (2.14) and 100-seeds weight (1.73). Number of seeds per pod and number of branches per plant exhibited very low values (0.80 and 0.50, respectively).

**4.2.6.7 For Treatment 7 (400Gy + 0.25% EMS)**

The highest genetic advance was observed for plant height (22.16). Low values of genetic advance were observed for number of pods per plant (3.24), days to maturity (2.98), number of seeds per pod (2.17), seed yield per plant (1.84), pod length (1.74), 100-seeds weight (1.72), number of clusters per plant (1.45) and days to first flowering (1.47). Number of branches per plant (0.11) exhibited very low value of GA.

**4.2.6.8 For Treatment 8 (control)**

Genetic advance estimate was moderate for plant height (12.90). Low values of genetic advance were observed for seed yield per plant (3.99), days to maturity (2.55), number of pods per plant (2.27), pod length (2.09), days to first flowering (1.44), 100-seeds weight (1.38) and number of clusters per plant (1.10). Number of seeds per pod (0.47) and number of branches per plant (0.42) exhibited very low values of genetic advance.

**4.2.7 Genetic advance expressed as percentage of mean**

The estimates of genetic advance expressed as percentage of mean are presented in Table 4.4. Mutagenic treatment wise results obtained on genetic advance expressed as percentage of mean are described as under:

**4.2.7.1 For Treatment 1 (100Gy + 0.25% EMS)**

The highest genetic advance as percentage of mean was observed for seed yield per plant (67.85%) followed by number of branches per plant (21.81%) and pod length (20.99%). Moderate values of genetic advance as percentage of mean was observed for plant height (15.86%), 100-seeds weight (15.83%), number of pods per plant (15.70%), number of clusters per plant (12.86%) and number of seeds per pod (10.99%). The low values of genetic advance as percentage of mean were recorded for days to first flowering (4.36%) and days to maturity (3.12%) for treatment 1.

**4.2.7.2 For Treatment 2 (200Gy + 0.25% EMS)**

Genetic advance as percentage of mean for treatment 2 was high for seed yield per plant (34.27%) followed by pod length (24.83%) and plant height (23.82%). Moderate values of GA % was observed for number of pods per plant (17.36%), number of branches per plant (13.73%), number of clusters per plant (13.26%), number of seeds per pod (11.60%) and 100-seeds weight (11.21%) while, it was low in case of days to first flowering (5.11%) and days to maturity (3.04%).

**4.2.7.3 For Treatment 3 (225Gy + 0.25% EMS)**

The highest GA % was observed for plant height (27.66%) followed by number of pods per plant (24.78%) and pod length (24.20%). Moderate values of genetic advance as percentage of mean was observed for number of clusters per plant (18.21%), seed yield per plant (17.64%), number of seeds per pod (14.67%) and 100-seeds weight (10.61%). For number of branches per plant (7.92%), days to first flowering (4.39%) and days to maturity (3.06%) were low values of genetic advance as percentage of mean for this treatment were observed.

**4.2.7.4 For Treatment 4 (250Gy + 0.25% EMS)**

For treatment 4, the highest genetic advance as percentage of mean was observed for seed yield per plant (42.50%) followed by plant height (26.68%), pod length (22.91%), number of clusters per plant (20.84%) and number of pods per plant (20.61%) whereas, it was moderate for number of branches per plant (19.02%), 100-seeds weight (18.35%) and number of seeds per pod (10.75%) and low for days to first flowering (5.12%) and days to maturity (3.65%).

**4.2.7.5 For Treatment 5 (275Gy + 0.25% EMS)**

High genetic advance as percentage of mean was recorded for seed yield per plant (32.55%), number of clusters per plant (28.51%), number of pods per plant (26.50%) and plant height (20.52%). Moderate values of this parameter was observed for pod length (19.17%), number of seeds per pod (15.36%) and 100-seeds weight (12.89%) while, it was low for days to first flowering (4.51%), days to maturity (3.87%) and number of branches per plant (1.24%).

**4.2.7.6 For Treatment 6 (300Gy + 0.25% EMS)**

Treatment 6 showed high genetic advance as percentage of mean for number of clusters per plant (34.52%), pod length (32.98%), plant height (32.81%), seed yield per plant (29.15%) and number of pods per plant (23.23%). Moderate values were observed for number of branches per plant (19.04%), 100-seeds weight (14.37%) and number of seeds per pod (10.81%) and low values for days to first flowering (4.88%) and days to maturity (3.24%).

**4.2.7.7 For Treatment 7 (400Gy + 0.25% EMS)**

The highest genetic advance as percentage of mean for treatment 7 was observed for number of seeds per pod (25.86%) followed by number of pods per plant (23.66%) and seed yield per plant (20.26%). Moderate genetic advance as percentage of mean was recorded by plant height (19.33%), number of clusters per plant (18.69%), pod length (17.54%) and 100-seeds weight (13.78%) while, it was low for number of branches per plant (3.89%), days to maturity (4.50%) and days to first flowering (2.55%).

**4.2.7.8 For Treatment 8 (control)**

For treatment 8 (control), there was high genetic advance as percentage of mean for seed yield per plant (45.71%), number of clusters per plant (21.42%) and pod length (20.79%). Moderate values of GA% was observed for 100-seeds weight (19.21%),

number of pod plant (17.89%), number of branches per plant (15.51%) and plant height (15.06%). It was low for number of seeds per pod (6.87%), days to maturity (3.88%) and days to first flowering (2.51%) for this treatment.

### **4.3 CORRELATION COEFFICIENTS**

The correlation coefficients for each mutagenic treatment were estimated for all the combinations of 10 characters under study at phenotypic ( $r_p$ ) as well as genotypic ( $r_g$ ) levels. The genotypic correlation was higher than that of phenotypic one (except few cases) which indicates presence of influence of environment. The mutagenic treatment wise results of correlations in  $M_3$  generation of cowpea given in Table 4.5 to 4.12 between different pairs of characters are presented below:

#### **4.3.1 Correlation coefficient for treatment 1 (100Gy + 0.25% EMS)**

Correlation coefficient among different characters for treatment 1 is presented in Table 4.5. The negative relationship between seed yield per plant and other developmental character like days to first flowering, days to maturity and plant height is desirable, while positive association is desirable for yield attributing traits in cowpea. Among the developmental traits, genotypic as well as phenotypic correlation coefficient was highly significant and negative only for days to maturity with seed yield per plant ( $r_g=-0.406$ ,  $r_p=-0.325$ ). Traits like days to first flowering and plant height showed non-significant correlation with seed yield per plant. For other traits, only plant height had negative and significant correlation ( $r_g=-0.538$ ,  $r_p=-0.466$ ) with number of clusters per plant at both the levels whereas, it showed non-significant results with all other traits. Days to first flowering showed significant and positive correlation both at genotypic and phenotypic levels with 100-seeds weight ( $r_g=0.306$ ,  $r_p=0.258$ ) while, this trait had significant correlation only at genotypic level with days to first flowering ( $r_g=0.316$ ) and number of clusters per plant ( $r_g=0.356$ ). The days to maturity showed positive and significant correlation at both the levels with number of clusters per plant ( $r_g=0.434$ ,  $r_p=0.335$ ) and 100-seeds weight ( $r_g=0.622$ ,  $r_p=0.501$ ). This trait also showed positive and significant genotypic correlation with number of pods per plant ( $r_g=0.432$ ).

Looking to the yield and yield attributing traits, the genotypic as well as phenotypic correlations were significant and positive between seed yield per plant and number of branches per plant ( $r_g=0.414$ ,  $r_p=0.303$ ), number of pods per plant ( $r_g=0.389$ ,  $r_p=0.302$ ) and number of seeds per pod ( $r_g=0.429$ ,  $r_p=0.317$ ). Number of clusters per

plant showed significant and positive correlation at both the levels with number of seeds per pod ( $r_g=0.490$ ,  $r_p=0.265$ ) and 100-seeds weight ( $r_g=0.277$ ,  $r_p=0.257$ ) whereas, number of pods per plant also had significant and positive correlation with number of seeds per pod ( $r_g=0.771$ ,  $r_p=0.614$ ).

Negative and significant genotypic correlation among number of branches per plant and number of seeds per pod ( $r_g=-0.314$ ), number of pods per plant and pod length ( $r_g=-0.294$ ), pod length and number of seeds per pod ( $r_g=-0.319$ ) while, positive and significant correlation was recorded among pod length and 100-seeds weight ( $r_g=0.300$ ). Treatment 1 expressed negative and non-significant correlation between 100-seeds weight and seed yield per plant.

Considering mutagenic effect of treatment 1, seed yield per plant showed association in desirable direction with days to maturity, number of branches per plant, number of pods per plant and number of seeds per pod at genotypic and phenotypic levels.

#### **4.3.2 Correlation coefficient for treatment 2 (200Gy + 0.25% EMS)**

For treatment 2, correlation coefficient among different character is presented in Table 4.6. None of the developmental traits showed significant correlation with seed yield per plant for treatment 2. Genotypic as well as phenotypic correlation coefficient was highly significant and negative for days to first flowering with plant height ( $r_g=-0.443$ ,  $r_p=-0.302$ ) whereas, only at genotypic level with number of branches per plant ( $r_g=-0.308$ ). Days to maturity had highly significant and positive correlation only at genotypic level with number of clusters per plant ( $r_g=0.343$ ) and 100-seeds weight ( $r_g=0.334$ ) while significant and positive association was found with number of seeds per pod ( $r_g=0.315$ ). The plant height showed positive and highly significant correlation at genotypic and phenotypic levels respectively, with pod length ( $r_g=0.359$ ,  $r_p=0.282$ ) while, this trait expressed non-significant correlation with other traits.

Referring to the yield and yield attributing traits, the genotypic as well as phenotypic level showed significant positive correlation only between seed yield per plant and number of pods per plant ( $r_g=0.401$ ,  $r_p=0.326$ ). Seed yield per plant had significant and positive correlation with number of branches per plant ( $r_g=0.322$ ) while it was negative with number of seeds per pod ( $r_g=-0.276$ ) at genotypic level. Number of branches per plant showed significant and positive correlation at both levels with 100-seeds weight ( $r_g=0.459$ ,  $r_p=0.349$ ) while significant only at genotypic level with number of pods per plant ( $r_g=0.266$ ). Number of clusters per plant exhibited highly

Table 4.5 Genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients among 10 characters in  $M_3$  generation of cowpea for treatment 1 (100Gy + 0.25% EMS)

Character		Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)
Days to maturity	$r_g$	0.316*								
	$r_p$	0.235								
Plant height (cm)	$r_g$	-0.224	-0.233							
	$r_p$	-0.169	-0.097							
Number of branches per plant	$r_g$	0.005	-0.202	-0.057						
	$r_p$	-0.014	-0.205	-0.060						
Number of clusters per plant	$r_g$	0.356**	0.434**	-0.538**	-0.190					
	$r_p$	0.250	0.335**	-0.466**	-0.213					
Number of pods per plant	$r_g$	-0.020	0.432**	-0.091	-0.028	0.735**				
	$r_p$	0.043	0.194	-0.216	0.001	0.406**				
Pod length (cm)	$r_g$	0.124	0.168	-0.086	0.083	-0.101	-0.294*			
	$r_p$	0.043	0.191	-0.112	0.103	-0.02	-0.127			
Number of seeds per pod	$r_g$	0.053	0.248	-0.051	-0.314*	0.490**	0.771**	-0.319*		
	$r_p$	0.046	0.042	-0.084	-0.101	0.265*	0.614**	-0.159		
100-seeds weight (g)	$r_g$	0.306*	0.622**	-0.249	-0.071	0.277*	0.062	0.300*	-0.156	
	$r_p$	0.258*	0.501**	-0.203	-0.086	0.257*	0.088	0.229	-0.076	
Seed yield per plant (g)	$r_g$	0.200	-0.406**	0.177	0.414**	0.055	0.389**	-0.263*	0.429**	-0.233
	$r_p$	0.196	-0.325*	0.151	0.303*	0.040	0.302*	-0.222	0.317*	-0.204

\*, \*\* Significant at 5% and 1% levels, respectively.

Table 4.6 Estimates of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients among 10 characters in  $M_3$  generation of cowpea for treatment 2 (200Gy + 0.25% EMS)

Character		Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)
Days to maturity	$r_g$	-0.159								
	$r_p$	-0.142								
Plant height (cm)	$r_g$	-0.443**	0.151							
	$r_p$	-0.302*	0.175							
Number of branches per plant	$r_g$	-0.308*	0.157	-0.100						
	$r_p$	-0.066	-0.070	-0.136						
Number of clusters per plant	$r_g$	-0.203	0.343**	-0.070	0.085					
	$r_p$	-0.226	0.199	-0.043	0.051					
Number of pods per plant	$r_g$	-0.240	-0.003	-0.112	0.266*	0.345**				
	$r_p$	-0.143	-0.007	0.043	0.096	0.191				
Pod length (cm)	$r_g$	-0.083	0.190	0.359**	-0.406**	-0.003	0.106			
	$r_p$	-0.085	0.055	0.282*	-0.146	0.011	0.088			
Number of seeds per pod	$r_g$	-0.083	0.315*	-0.025	-0.325*	0.130	-0.572**	-0.024		
	$r_p$	-0.105	0.180	-0.187	-0.205	-0.010	-0.229	0.076		
100-seeds weight (g)	$r_g$	-0.062	0.334**	-0.022	0.459**	0.176	0.323*	0.001	0.194	
	$r_p$	-0.033	0.239	-0.067	0.349**	0.145	0.200	0.011	0.131	
Seed yield per plant (g)	$r_g$	-0.182	0.026	-0.107	0.322*	-0.073	0.401**	0.190	-0.276*	0.240
	$r_p$	-0.077	0.043	-0.045	0.143	-0.066	0.326*	0.057	-0.206	0.197

\*, \*\* Significant at 5% and 1% levels, respectively.

significant and positive correlation only at genotypic level with number of pods per plant ( $r_g=0.345$ ) while number of pods per plant had positive significant correlation at genotypic level with 100-seeds weight ( $r_g=0.323$ ).

Negative and significant genotypic correlation was also observed among number of branches per plant with pod length ( $r_g=-0.406$ ) and number of seeds per plant ( $r_g=-0.325$ ), number of pods per plant and number of seeds per pod ( $r_g= -0.572$ ).

Considering mutagenic effect of treatment 2, seed yield per plant showed association in desirable direction only with number of pods per plant at genotypic and phenotypic levels.

#### **4.3.3 Correlation coefficient for treatment 3 (225Gy + 0.25% EMS)**

The results presented in Table 4.7 regarding effects of treatment 3 on various characters showed that seed yield per plant had significant relationship in desirable direction only with days to maturity ( $r_g= -0.466$ ,  $r_p=-0.320$ ) at both the levels, while there was strong association between seed yield per plant and days to first flowering ( $r_g= -0.353$ ) at genotypic level only. Days to first flowering had negative and significant correlation with plant height ( $r_g=-0.394$ ,  $r_p= -0.318$ ) at both the levels, while it showed positive and significant correlation with pod length ( $r_g= 0.348$ ) and 100-seeds weight ( $r_g= 0.267$ ) at genotypic level only. Days to maturity showed negative genotypic correlation with number of branches per plant ( $r_g =-0.620$ ) and pod length ( $r_g =-0.300$ ) at genotypic level while it showed positive and significant correlation with number of seeds per pod ( $r_g= 0.683$ ,  $r_p=0.365$ ) at both the levels. Plant height showed significant negative correlation with 100-seeds weight ( $r_g=-0.399$ ,  $r_p= -0.331$ ).

Looking to the yield and yield attributing traits, none of the traits showed desirable significant correlation with seed yield per plant. Significant and positive genotypic correlation was expressed between number of branches per plant with number of seeds per pod ( $r_g=0.464$ ) and 100-seeds weight ( $r_g=0.281$ ). Negative and significant correlation was expressed at both levels among number of clusters per plant and number of seeds per pod ( $r_g= -0.634$ ,  $r_p=-0.318$ ) and only at genotypic level with number of seeds per pod ( $r_g= -0.353$ ). There were non-significant genotypic as well as phenotypic correlations among all other yield attributing traits.

Considering mutagenic effect of treatment 3, seed yield per plant showed association in desirable direction with days to maturity at both the levels and days to first flowering at only genotypic level.

**4.3.4 Correlation coefficient for treatment 4 (250Gy + 0.25% EMS)**

With reference to correlation coefficient for treatment 4 from Table 4.8, the significant and desirable association was observed between seed yield per plant and number of branches per plant ( $r_g = 0.257$ ) and number of seeds per pod ( $r_g = 0.362$ ) at genotypic level only. Whereas, it was in negative direction for number of pods per plant ( $r_g = -0.297$ ). Among the developmental traits, genotypic correlation was negatively and significantly correlated between days to first flowering and number of branches per plant ( $r_g = -0.461$ ) while it showed positive and significant correlation with days to maturity ( $r_g = 0.494$ ,  $r_p = 0.374$ ) and pod length ( $r_g = 0.559$ ,  $r_p = 0.426$ ) at both the levels. Days to maturity showed negative genotypic and phenotypic correlation with plant height ( $r_g = -0.410$ ,  $r_p = -0.304$ ), whereas it expressed negative significant correlation with number of branches per plant only at genotypic level ( $r_g = -0.396$ ). The days to maturity also showed positive and significant correlation at both the levels with pod length ( $r_g = 0.631$ ,  $r_p = 0.452$ ). Plant height showed positive and significant correlation only at genotypic level with number of seeds per pod ( $r_g = 0.331$ ) and 100-seeds weight ( $r_g = 0.355$ ). As far as the yield attributing traits are concerned the genotypic correlations were significant and positive between number of branches per plant and number of seeds per pod ( $r_g = 0.773$ ).

Mutagenic effect of Treatment 4 (250Gy + 0.25% EMS) on seed yield per plant showed association in desirable direction with number of branches per plant and number of seeds per pod at genotypic level only.

Table 4.7 Estimates of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients among 10 characters in  $M_3$  generation of cowpea for treatment 3 (225Gy + 0.25% EMS)

Character		Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)
Days to maturity	$r_g$ $r_p$	0.040 0.037								
Plant height (cm)	$r_g$ $r_p$	-0.394** -0.318*	-0.089 -0.076							
Number of branches per plant	$r_g$ $r_p$	-0.046 -0.053	-0.620** -0.244	0.286* -0.018						
Number of clusters per plant	$r_g$ $r_p$	0.041 0.032	-0.097 -0.111	-0.361** -0.293*	-0.247 -0.080					
Number of pods per plant	$r_g$ $r_p$	-0.048 -0.115	-0.070 -0.071	0.033 0.042	-0.313* -0.026	0.163 0.127				
Pod length (cm)	$r_g$ $r_p$	0.348** 0.214	-0.300* -0.187	0.235 0.155	0.078 0.008	0.054 -0.007	-0.227 -0.218			
Number of seeds per pod	$r_g$ $r_p$	0.130 0.070	0.683** 0.365**	0.216 0.086	0.464** -0.007	-0.634** -0.318*	-0.353** -0.226	0.060 0.052		
100-seeds weight (g)	$r_g$ $r_p$	0.267* 0.221	-0.052 -0.043	-0.399** -0.331**	0.281* 0.014	-0.056 -0.053	0.181 0.160	-0.045 -0.065	-0.176 -0.059	
Seed yield per plant (g)	$r_g$ $r_p$	-0.353** -0.190	-0.466** -0.320*	0.106 0.036	0.126 0.059	0.132 0.112	0.102 0.068	-0.002 -0.148	-0.091 -0.044	-0.199 -0.120

\*, \*\* Significant at 5% and 1% levels, respectively.

**Table 4.8 Estimates of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients among 10 characters in  $M_3$  generation of cowpea for treatment 4 (250Gy + 0.25% EMS)**

Character		Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)
Days to maturity	$r_g$	0.494**								
	$r_p$	0.374**								
Plant height (cm)	$r_g$	-0.027	-0.410**							
	$r_p$	0.035	-0.304*							
Number of branches per plant	$r_g$	-0.461**	-0.396**	0.237						
	$r_p$	-0.252	-0.076	0.115						
Number of clusters per plant	$r_g$	0.002	-0.202	0.046	-0.089					
	$r_p$	0.066	-0.180	0.083	-0.018					
Number of pods per plant	$r_g$	-0.079	-0.021	0.075	0.013	-0.053				
	$r_p$	-0.042	-0.031	0.043	-0.002	-0.054				
Pod length (cm)	$r_g$	0.559**	0.631**	0.102	-0.128	-0.302*	0.115			
	$r_p$	0.426**	0.452**	0.042	-0.026	-0.144	0.091			
Number of seeds per pod	$r_g$	0.184	-0.131	0.331**	0.773**	-0.035	0.067	0.115		
	$r_p$	0.160	-0.054	0.187	0.203	-0.034	0.008	0.047		
100-seeds weight (g)	$r_g$	0.059	-0.144	0.355**	-0.152	0.116	0.152	0.103	0.165	
	$r_p$	0.037	-0.147	0.254	0.057	0.032	0.106	-0.009	0.117	
Seed yield per plant (g)	$r_g$	0.013	-0.242	-0.006	0.257*	-0.031	-0.297*	-0.211	0.362**	-0.216
	$r_p$	-0.016	-0.174	0.004	0.175	-0.031	-0.173	-0.180	0.075	-0.190

\*, \*\* Significant at 5% and 1% levels, respectively.

**4.3.5 Correlation coefficient for treatment 5 (275Gy + 0.25% EMS)**

As per correlation coefficient data for treatment 5 presented in Table 4.9, trait seed yield per plant had significant and negative genotypic correlation with plant height ( $r_g=-0.268$ ) whereas, number of branches per plant also showed ( $r_g =-0.741$ ) negative genotypic correlation with seed yield per plant. The seed yield per plant had positive and significant correlation with days to maturity ( $r_g= 0.433$ ,  $r_p=0.354$ ) and 100-seeds weight plant ( $r_g=0.623$ ,  $r_p=0.473$ ) at both the levels. Number of clusters per plant showed significant and positive correlation only at genotypic level with seed yield per plant ( $r_g=0.350$ ).

Days to first flowering had significant and positive genotypic correlation with days to maturity ( $r_g=0.287$ ) and number of branches per plant ( $r_g=0.943$ ). Plant height showed positive and significant correlation with number of pods per plant ( $r_g= 0.426$ ,  $r_p=0.277$ ) and 100-seeds weight ( $r_g= 0.367$ ,  $r_p=0.289$ ) at both the levels. Attributing trait number of pods per plant expressed significant and positive correlation at both levels with 100-seeds weight ( $r_g=0.405$ ,  $r_p=0.329$ ) whereas, number of branches per plant had significant and positive genotypic correlation with number of clusters per plant ( $r_g=0.820$ ), pod length ( $r_g=0.724$ ) and number of seeds per pod ( $r_g=0.693$ ).

Considering mutagenic effect of treatment 5, seed yield per plant showed association in desirable direction with plant height, number of clusters per plant and 100-seeds weight.

**4.3.6 Correlation coefficient for treatment 6 (300Gy + 0.25% EMS)**

The correlation coefficient among different characters for treatment 6 is presented in Table 4.10. None of the trait showed desirable and significant association with seed yield per plant except days to first flowering ( $r_g= -0.306$ ) at genotypic level. There was significant and negative correlation among seed yield per plant and pod length ( $r_g= -0.459$ ,  $r_p= -0.271$ ) at both the levels while, number of clusters per plant ( $r_g= -0.363$ ) had at genotypic level only.

Among the developmental traits, days to first flowering showed significant and negative correlation with number of branches per plant ( $r_g=-0.317$ ), pod length ( $r_g=-0.317$ ) and 100-seeds weight ( $r_g=-0.281$ ) at genotypic level whereas, days to maturity and plant height showed positive correlation with other traits.

In the yield and yield attributing traits, number of branches per plant showed significant and positive correlation with number of clusters per plant ( $r_g=0.280$ ), number of pods per plant ( $r_g=0.428$ ), pod length ( $r_g=0.412$ ) and number of seeds per

Table 4.9 Estimates of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients among 10 characters in  $M_3$  generation of cowpea for treatment 5 (275Gy + 0.25% EMS)

Character		Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)
Days to maturity	$r_g$ $r_p$	0.287* 0.211								
Plant height (cm)	$r_g$ $r_p$	0.128 0.089	-0.211 -0.164							
Number of branches per plant	$r_g$ $r_p$	0.943** 0.176	0.009 0.003	-0.216 -0.124						
Number of clusters per plant	$r_g$ $r_p$	0.109 0.034	-0.137 -0.095	-0.196 -0.230	0.820** 0.118					
Number of pods per plant	$r_g$ $r_p$	0.134 0.122	-0.124 -0.065	0.426** 0.277*	-0.478** -0.106	-0.199 -0.182				
Pod length (cm)	$r_g$ $r_p$	-0.405** -0.223	0.114 0.033	0.012 0.016	0.724** 0.196	-0.087 -0.031	0.184 0.150			
Number of seeds per pod	$r_g$ $r_p$	0.044 -0.038	-0.140 -0.049	-0.081 -0.048	0.693** -0.024	-0.048 -0.022	-0.238 -0.249	0.141 0.073		
100-seeds weight (g)	$r_g$ $r_p$	0.162 0.142	0.145 0.098	0.367** 0.289*	-0.418** -0.195	-0.068 -0.038	0.405** 0.329*	0.074 0.060	-0.123 -0.050	
Seed yield per plant (g)	$r_g$ $r_p$	0.051 0.095	0.433** 0.354**	-0.268* -0.206	-0.741** -0.077	0.350** 0.241	-0.040 -0.050	-0.004 0.012	-0.127 -0.045	0.623** 0.473**

\*, \*\* Significant at 5% and 1% levels, respectively.

Table 4.10 Estimates of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients among 10 characters in  $M_3$  generation of cowpea for treatment 6 (300Gy + 0.25% EMS)

Character		Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)
Days to maturity	$r_g$	-0.248								
	$r_p$	-0.243								
Plant height (cm)	$r_g$	-0.209	0.126							
	$r_p$	-0.169	0.129							
Number of branches per plant	$r_g$	-0.317*	0.074	-0.086						
	$r_p$	-0.108	-0.064	0.012						
Number of clusters per plant	$r_g$	0.136	-0.100	-0.250	0.280*					
	$r_p$	0.141	-0.092	-0.168	0.197					
Number of pods per plant	$r_g$	0.002	0.263*	0.422**	0.428**	0.372**				
	$r_p$	-0.013	0.201	0.335**	0.173	0.289*				
Pod length (cm)	$r_g$	-0.307*	0.084	-0.169	0.412**	0.404**	0.530**			
	$r_p$	-0.216	0.023	0.383**	0.198	0.319*	0.312*			
Number of seeds per pod	$r_g$	0.058	0.580**	-0.133	0.429**	0.419**	0.779**	0.191		
	$r_p$	-0.017	0.323*	-0.056	0.076	0.23	0.356**	0.104		
100-seeds weight (g)	$r_g$	-0.281*	0.207	0.045	-0.211	-0.143	-0.235	-0.076	-0.264*	
	$r_p$	-0.253	0.172	0.031	-0.197	-0.154	-0.234	-0.028	-0.080	
Seed yield per plant (g)	$r_g$	-0.306*	0.196	-0.043	0.142	-0.363**	-0.201	-0.459**	-0.002	-0.222
	$r_p$	-0.215	-0.007	-0.089	0.079	-0.244	-0.205	-0.271*	0.066	-0.177

\*, \*\* Significant at 5% and 1% levels, respectively.

pod ( $r_g=0.429$ ), at genotypic levels. Number of clusters per plant exhibited positive and significant correlation with number of pods per plant ( $r_g= 0.372$ ,  $r_p= 0.289$ ) and pod length ( $r_g= 0.404$ ,  $r_p= 0.319$ ) both at genotypic and phenotypic levels, respectively. Whereas, it showed positive significant correlation with number of seeds per pod ( $r_g=0.419$ ) only at genotypic level. Number of pods per plant showed significant and positive correlation at both the phenotypic and genotypic levels with pod length ( $r_g=0.530$ ,  $r_p=0.312$ ) and number of seeds per pod ( $r_g=0.779$ ,  $r_p=0.356$ ). Treatment 6 expressed negative and non-significant correlation among seed yield per plant and plant height, number of pods per plant and 100-seeds weight at both the levels.

Considering mutagenic effect of treatment 6, seed yield per plant showed association in desirable direction only with days to first flowering at genotypic level.

#### **4.3.7 Correlation coefficient for treatment 7 (400Gy + 0.25% EMS)**

Perusal of data presented in Table 4.11 indicates that none of the developmental trait showed significant and desirable association with seed yield per plant. Among the yield attributing traits, 100-seeds weight showed positive and significant association with seed yield per plant ( $r_g=0.455$ ,  $r_p=0.290$ ) at both the levels, while it was significant and positive direction with number of branches per plant ( $r_g= 0.334$ ) and number of pods per plant ( $r_g= 0.327$ ) at genotypic level only. Genotypic as well as phenotypic correlation coefficient was highly significant and negative for days to first flowering with number of clusters per plant ( $r_g=-0.380$ ,  $r_p= -0.321$ ) and days to maturity with number of seeds per pod ( $r_g=-0.331$ ,  $r_p= -0.285$ ). The plant height showed negative and significant correlation at genotypic levels with number of branches per plant ( $r_g= -0.557$ ), number of clusters per plant ( $r_g= -0.277$ ) and pod length ( $r_g= -0.272$ ). Days to first flowering showed positive and significant correlation at both genotypic and phenotypic levels with number of pods per plant ( $r_g= 0.583$ ,  $r_p= 0.476$ ) and only at genotypic level with 100-seeds weight ( $r_g= 0.328$ ). Days to maturity showed positive and significant correlation at both genotypic and phenotypic levels with number of pods per plant ( $r_g= 0.382$ ,  $r_p= 0.295$ ).

Looking to the yield and yield attributing traits, the genotypic as well as phenotypic correlations were significant and positive between number of branches per plant and 100-seeds weight ( $r_g= 0.434$ ,  $r_p=0.285$ ) and only at genotypic level with number of clusters per plant ( $r_g=0.290$ ) and pod length ( $r_g=0.917$ ). Number of clusters per plant showed non-significant correlation with all other traits. Number of pods per plant showed significant and positive correlation at both the levels with 100-seeds

weight ( $r_g=0.447$ ,  $r_p=0.366$ ). Pod length also had significant and positive correlation with 100-seeds weight at both genotypic and phenotypic levels ( $r_g=0.488$ ,  $r_p=0.393$ ).

Negative and significant genotypic correlations were expressed among number of branches per plant and number of seeds per pod ( $r_g= -0.898$ ), number of pods per plant and pod length ( $r_g= -0.375$ ), number of seeds per pod and 100-seeds weight ( $r_g= -0.300$ ). Treatment 7 expressed negative and non-significant correlation between days to first flowering, plant height and number of seeds per pod traits with seed yield per plant.

Considering mutagenic effect of treatment 7, seed yield per plant showed association in desirable direction with number of branches per plant, number of pods per plant and 100-seeds weight at genotypic and/or phenotypic levels.

### 4.3.8 Correlation coefficient for treatment 8 (control)

In respect to Table 4.12 which represents the correlation coefficient among different characters for treatment 8 (control). It is known that the developmental traits are days to first flowering, days to maturity and plant height. Genotypic correlation coefficient was significant and negative for days to first flowering ( $r_g= -0.280$ ) and days to maturity ( $r_g= -0.286$ ) with seed yield per plant. However, yield attributing traits *viz.*, number of clusters per plant ( $r_g=0.494$ ,  $r_p=0.414$ ) and number of pods per plant ( $r_g=0.334$ ,  $r_p=0.291$ ) had significant and positive correlation with seed yield per plant at both the levels. The association was significant and in negative direction for pod length ( $r_g= -0.333$ ) and number of seeds per pod ( $r_g= -0.395$ ) with seed yield per plant at genotypic level only.

Days to first flowering showed negative association at both the levels with number of clusters per plant ( $r_g=-0.763$ ,  $r_p= -0.581$ ) while it had significant and positive correlation at genotypic levels with days to maturity ( $r_g= 0.284$ ) and number of clusters per plant ( $r_g=0.318$ ). Days to maturity showed non-significant correlation with all other traits. The plant height showed positive and significant correlation at genotypic levels with number of pods per plant ( $r_g= 0.268$ ) and negative phenotypic correlation with number of seeds per pod ( $r_g= -0.256$ ). Looking to the yield and yield attributing traits, the genotypic as well as phenotypic correlations were significant and positive between number of branches per plant and 100-seeds weight ( $r_g=0.543$ ,  $r_p=0.291$ ) and pod length with 100-seeds weight ( $r_g= 0.351$ ,  $r_p=0.282$ ) however, it was in negative direction between number of clusters per plant and pod length ( $r_g= -0.543$ ,  $r_p= -0.375$ ), number of pods per plant with pod length ( $r_g=-0.478$ ,  $r_p=-0.357$ ) and 100-seeds weight

Table 4.11 Estimates of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients among 10 characters in  $M_3$  generation of cowpea for treatment 7 (400Gy + 0.25% EMS)

Character		Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)
Days to maturity	$r_g$	0.028								
	$r_p$	0.017								
Plant height (cm)	$r_g$	0.001	0.072							
	$r_p$	0.017	0.089							
Number of branches per plant	$r_g$	-0.025	0.065	-0.557**						
	$r_p$	0.012	-0.070	-0.223						
Number of clusters per plant	$r_g$	-0.380**	0.026	-0.277*	0.290*					
	$r_p$	-0.321*	0.025	-0.252	0.173					
Number of pods per plant	$r_g$	0.583**	0.382**	0.028	0.093	0.133				
	$r_p$	0.476**	0.295*	0.036	-0.119	0.041				
Pod length (cm)	$r_g$	-0.102	0.043	-0.272*	0.917**	0.222	-0.375**			
	$r_p$	-0.140	0.020	-0.169	0.157	0.129	-0.179			
Number of seeds per pod	$r_g$	-0.072	-0.331**	-0.184	-0.898**	-0.234	-0.000	-0.220		
	$r_p$	-0.059	-0.285*	-0.200	-0.132	-0.206	0.082	-0.129		
100-seeds weight (g)	$r_g$	0.328*	0.105	-0.155	0.434**	0.057	0.447**	0.488**	-0.300*	
	$r_p$	0.245	0.077	-0.105	0.285*	0.042	0.366**	0.393**	-0.214	
Seed yield per plant (g)	$r_g$	-0.043	0.024	0.445**	0.334**	0.048	0.327*	-0.209	-0.225	0.455**
	$r_p$	-0.083	-0.028	0.169	0.086	-0.018	0.217	-0.079	-0.014	0.290*

\*, \*\* Significant at 5% and 1% levels, respectively.

Table 4.12 Estimates of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients among 10 characters in  $M_3$  generation of cowpea for treatment 8 (control)

Character		Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)
Days to maturity	$r_g$	0.284*								
	$r_p$	0.229								
Plant height (cm)	$r_g$	0.076	0.228							
	$r_p$	0.095	0.102							
Number of branches per plant	$r_g$	-0.017	-0.184	0.190						
	$r_p$	-0.030	-0.244	0.125						
Number of clusters per plant	$r_g$	-0.763**	0.089	-0.208	-0.039					
	$r_p$	-0.581**	-0.070	-0.168	0.049					
Number of pods per plant	$r_g$	0.318*	0.200	0.268*	0.050	0.068				
	$r_p$	0.227	0.190	0.232	-0.013	0.067				
Pod length (cm)	$r_g$	0.076	-0.138	0.015	0.413**	-0.543**	-0.478**			
	$r_p$	-0.082	-0.102	0.034	0.218	-0.375**	-0.357**			
Number of seeds per pod	$r_g$	-0.071	0.096	-0.151	-0.059	-0.137	-0.101	0.212		
	$r_p$	-0.093	0.076	-0.256*	0.036	-0.031	-0.043	0.098		
100-seeds weight (g)	$r_g$	-0.041	-0.197	0.200	0.543**	-0.178	-0.396**	0.351**	-0.152	
	$r_p$	-0.019	-0.147	0.118	0.291*	-0.128	-0.334**	0.282*	-0.095	
Seed yield per plant (g)	$r_g$	-0.280*	-0.286*	-0.206	0.335**	0.494**	0.334**	-0.333**	-0.395**	-0.252
	$r_p$	-0.233	-0.252	-0.128	0.093	0.414**	0.291*	-0.229	-0.191	-0.216

\*, \*\* Significant at 5% and 1% levels, respectively.

( $r_g=-0.396$ ,  $r_p=-0.334$ ). There was negative and non-significant correlation between seed yield per plant with plant height and 100-seeds weight for the treatment 8 (control).

Considering correlation coefficient under treatment 8 (control), seed yield per plant showed association in desirable direction with days to first flowering, days to maturity and number of branches per plant at genotypic level as well as number of clusters per plant and number of pods per plant at genotypic and phenotypic levels.

#### **4.4 PATH COEFFICIENT ANALYSIS**

The genotypic correlation coefficients calculated for different pairs of characters were subjected to genotypic path coefficient analysis for partitioning these values into the direct and indirect effects. The characters which had shown significant genotypic correlation with seed yield per plant were considered for results and discussion. The results obtained for direct and indirect effects of different characters on seed yield per plant are presented in tables.

##### **4.4.1 Path coefficient analysis for treatment 1 (100Gy + 0.25% EMS)**

Direct and indirect attribution of component character towards the yield was analyzed using only the genotypic correlation in present study. For the treatment 1 (Table 4.13), seed yield per plant showed highly significant and positive genotypic correlation with number of seeds per pod ( $r_g=0.429$ ) followed by number of branches per plant ( $r_g= 0.414$ ) and number of pods per plant ( $r_g= 0.389$ ) while, days to maturity ( $r_g=-0.406$ ) and pod length ( $r_g=-0.263$ ) was negatively and significantly correlated with seed yield per plant. The highest positive direct effect on seed yield per plant was exhibited by number of seeds per pod (0.489) followed by days to first flowering (0.444), number of branches per plant (0.409), number of pods per plant (0.357), 100-seed weight (0.330) and plant height (0.138), however, negative direct effect on seed yield per plant were contributed through days to maturity (-0.817) followed by number of clusters per plant (-0.196) and pod length (-0.060).

The highest positive indirect effect of days to maturity on seed yield per plant was exhibited *via* 100-seeds weight (0.205) followed by number of pods per plant (0.154) and days to first flowering (0.140). Number of branches per plant exhibited indirect effect on seed yield per plant *via* days to maturity (0.164) and number of pods per plant *via* number of seeds per pod (0.524) while it was negatively effected *via* days to maturity (-0.353). Number of seeds per pod exhibited maximum positive indirect effect (0.382) on seed yield per plant *via* number of pods per plant while it was

negatively effected *via* days to maturity (-0.202).

Residual effect (0.10800) was low and positive for treatment 1 in path analysis.

#### **4.4.2 Path coefficient analysis for treatment 2 (200Gy + 0.25% EMS)**

Perusal of the Table 4.14 revealed that seed yield per plant showed highly significant and positive correlation with number of pods per plant ( $r_g=0.401$ ) and number of branches per plant ( $r_g=0.322$ ). It was negatively and significantly correlated with number of seeds per plant ( $r_g=-0.276$ ).

The highest positive direct effect on seed yield per plant was exhibited by number of branches per plant (0.933) followed by number of pods per plant (0.917), number of seeds per pod (0.777), pod length (0.523) and days to first flowering (0.328). However, negative direct effect on seed yield per plant were contributed through 100-seeds weight (-0.508) followed by number of clusters per plant (-0.366) and days to maturity (-0.121).

Number of branches per plant exhibited highest positive indirect effect *via* number of pods per plant (0.243) whereas negative indirect effect was exhibited *via* number of seeds per pod (-0.253) followed by 100-seeds weight (-0.233) and pod length (-0.212). Maximum positive and indirect effect was exhibited by number of pods per plant on seed yield per plant *via* number of branches per plant (0.248) while negative indirect effect was exhibited through trait number of seeds per pod (-0.445). Similarly, number of seeds per pod exhibited maximum positive indirect effect *via* 100-seeds weight (0.098) and negative indirect effect *via* number of pods per plant (-0.525) followed by number of branches per plant (-0.303).

Residual effect for treatment 2 was low (0.61000) and positive in path analysis.

Table 4.13 Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in M<sub>3</sub> generation of cowpea for treatment 1 (100Gy + 0.25% EMS)

Characters	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Genetic correlation with seed yield per plant
Days to first flowering	<b>0.444</b>	-0.258	-0.031	0.002	-0.069	-0.007	-0.007	0.026	0.101	0.200
Days to maturity	0.140	<b>-0.817</b>	-0.032	-0.082	-0.085	0.154	-0.010	0.121	0.205	-0.406**
Plant height (cm)	-0.099	0.190	<b>0.138</b>	-0.023	0.105	-0.032	0.005	-0.025	-0.082	0.177
Number of branches per plant	0.002	0.164	-0.008	<b>0.409</b>	0.037	-0.010	-0.005	-0.153	-0.023	0.414**
Number of clusters per plant	0.157	-0.354	-0.074	-0.077	<b>-0.196</b>	0.262	0.006	0.240	0.091	0.055
Number of pods per plant	-0.008	-0.353	-0.012	-0.011	-0.144	<b>0.357</b>	0.017	0.524	0.020	0.389**
Pod length (cm)	0.054	-0.137	-0.011	0.033	0.019	-0.105	<b>-0.060</b>	-0.156	0.099	-0.263*
Number of seeds per pod	0.023	-0.202	-0.007	-0.128	-0.096	0.382	0.019	<b>0.489</b>	-0.051	0.429**
100-seeds weight (g)	0.136	-0.508	-0.034	-0.029	-0.054	0.022	-0.018	-0.076	<b>0.330</b>	-0.233

\*, \*\* Significant at 5% and 1% levels, respectively. (Residual effect = 0.10800).

Table 4.14 Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in M<sub>3</sub> generation of cowpea for treatment 2 (200Gy + 0.25% EMS)

Characters	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Genetic correlation with seed yield per plant
Days to first flowering	<b>0.328</b>	0.019	-0.021	-0.287	0.074	-0.220	-0.043	-0.064	0.031	-0.182
Days to maturity	-0.052	<b>-0.121</b>	0.007	0.146	-0.126	-0.003	0.099	0.245	-0.169	0.026
Plant height (cm)	-0.145	-0.018	<b>0.047</b>	-0.092	0.025	-0.102	0.187	-0.019	0.011	-0.107
Number of branches per plant	-0.101	-0.019	-0.004	<b>0.933</b>	-0.031	0.243	-0.212	-0.253	-0.233	0.322*
Number of clusters per plant	-0.066	-0.041	-0.003	0.079	<b>-0.366</b>	0.315	-0.001	0.100	-0.089	-0.073
Number of pods per plant	-0.078	0.004	-0.005	0.248	-0.126	<b>0.917</b>	0.055	-0.445	-0.164	0.401**
Pod length (cm)	-0.027	-0.023	0.016	-0.378	0.009	0.096	<b>0.523</b>	-0.018	-0.007	0.190
Number of seeds per pod	-0.027	-0.038	-0.001	-0.303	-0.047	-0.525	-0.012	<b>0.777</b>	-0.098	-0.276*
100-seeds weight (g)	-0.020	-0.040	-0.001	0.428	-0.064	0.295	0.007	0.150	<b>-0.508</b>	0.240

\*, \*\* Significant at 5% and 1% levels, respectively. (Residual effect = 0.61000).

**4.4.3 Path coefficient analysis for treatment 3 (225Gy + 0.25% EMS)**

The results presented in Table 4.15 revealed that seed yield per plant showed highly significant and negative correlation with days to maturity ( $r_g = -0.466$ ) and days to first flowering ( $r_g = -0.353$ ). The association between all other traits was non-significant. The highest positive direct effect on seed yield per plant was exhibited by number of branches per plant (0.425) followed by number of pods per plant (0.348) and pod length (0.277), however, negative direct effect on seed yield per plant were contributed through plant height (-0.473) followed by 100-seeds weight (-0.460), days to first flowering (-0.458), number of seeds per pod (-0.091), days to maturity (-0.087) and number of clusters per plants (-0.079).

Considerable positive indirect effect on seed yield per plant only through days to first flowering was exhibited *via* plant height (0.186) whereas it showed negative indirect effect *via* 100-seeds weight (-0.122). Days to maturity exhibited highest positive indirect effect *via* plant height (0.042) and its negative effect *via* number of branches per plant (-0.263). Remaining traits exhibited moderate to low positive or negative indirect effects.

Positive and low (0.66960) residual effect was observed in treatment 3.

**4.4.4 Path coefficient analysis for treatment 4 (250Gy + 0.25% EMS)**

With reference to Table 4.16 revealed that seed yield per plant showed highly significant and positive correlation with number of seeds per pod ( $r_g = 0.362$ ) followed by number of branches per plant ( $r_g = 0.257$ ).

The highest positive direct effect on seed yield per plant was exhibited by number of branches per plant (1.295) followed by days to first flowering (1.068), 100-seeds weight (0.148), days to maturity (0.013) and plant height (0.008). Whereas, negative direct effect on seed yield per plant were contributed through number of seeds per pod (-0.789), followed by pod length (-0.606) followed by number of clusters of plant (-0.151) followed by number of pods per plant (-0.138).

Maximum positive indirect effect was exhibited on seed yield per plant by number of branches per plant *via* pod length (0.077) while negative indirect effect was exhibited by number of seeds per pod (-0.610) and days to first flowering (-0.492). The number of seeds per pod had maximum and positive indirect effect on seed yield per plant *via* number of branches per plant (1.002) followed by days to first flowering (0.196). Number of pods per plant showed negligible positive or negative indirect effect on seed yield per plant. Residual effect for treatment 4 was low (0.80081) and positive.

Table 4.15 Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in M<sub>3</sub> generation of cowpea for treatment 3 (225Gy + 0.25% EMS).

Characters	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Genetic correlation with seed yield per plant
Days to first flowering	<b>-0.458</b>	-0.003	0.186	-0.019	-0.003	-0.016	0.096	-0.011	-0.122	-0.353**
Days to maturity	-0.018	<b>-0.087</b>	0.042	-0.263	0.007	-0.024	-0.083	-0.062	0.024	-0.466**
Plant height (cm)	0.180	0.007	<b>-0.473</b>	0.121	0.028	0.011	0.065	-0.019	0.183	0.106
Number of branches per plant	0.021	0.054	-0.135	<b>0.425</b>	0.019	-0.109	0.021	-0.042	-0.129	0.126
Number of clusters per plant	-0.018	0.008	0.171	-0.105	<b>-0.079</b>	0.056	0.014	0.058	0.025	0.132
Number of pods per plant	0.021	0.006	-0.015	-0.133	-0.012	<b>0.348</b>	-0.062	0.032	-0.083	0.102
Pod length (cm)	-0.159	0.026	-0.111	0.033	-0.004	-0.079	<b>0.277</b>	-0.005	0.020	-0.002
Number of seeds Per pod	-0.059	-0.059	-0.102	0.197	0.050	-0.123	0.016	<b>-0.091</b>	0.081	-0.091
100-seeds weight (g)	-0.122	0.004	0.188	0.119	0.004	0.062	-0.012	0.016	<b>-0.460</b>	-0.199

\*, \*\* Significant at 5% and 1% levels, respectively. (Residual effect = 0.66960).

Table 4.16 Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in M<sub>3</sub> generation of cowpea for treatment 4 (250Gy + 0.25% EMS).

Characters	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Genetic correlation with seed yield per plant
Days to first flowering	<b>1.068</b>	0.006	-0.002	-0.596	-0.003	0.010	-0.338	-0.145	0.008	0.013
Days to maturity	0.528	<b>0.013</b>	-0.003	-0.513	0.030	0.002	-0.382	0.103	-0.021	-0.242
Plant height (cm)	-0.028	-0.005	<b>0.008</b>	0.307	-0.006	-0.010	-0.061	-0.261	0.052	-0.006
Number of branches per plant	-0.492	-0.005	0.002	<b>1.295</b>	0.013	-0.001	0.077	-0.610	-0.022	0.257*
Number of clusters per plant	0.002	-0.002	0.004	-0.115	<b>-0.151</b>	0.007	0.182	0.027	0.017	-0.031
Number of pods per plant	-0.084	-0.003	0.006	0.017	0.008	<b>-0.138</b>	-0.069	-0.052	0.022	-0.297*
Pod length (cm)	0.596	0.008	0.009	-0.165	0.045	-0.015	<b>-0.606</b>	-0.090	0.015	-0.211
Number of seeds per pod	0.196	-0.001	0.002	1.002	0.005	-0.009	-0.069	<b>-0.789</b>	0.024	0.362**
100-seeds weight (g)	0.062	-0.002	0.003	-0.197	-0.017	-0.021	-0.062	-0.130	<b>0.148</b>	-0.216

\*,\*\* Significant at 5% and 1% levels, respectively. (Residual effect = 0.80081).

**4.4.5 Path coefficient analysis for treatment 5 (275Gy + 0.25% EMS)**

The Table 4.17 revealed that seed yield per plant showed highly significant and positive correlation with 100-seeds weight ( $r_g=0.623$ ) followed by days to maturity ( $r_g=0.433$ ) and number of clusters per plant ( $r_g=0.350$ ) while, number of branches per plant ( $r_g=-0.741$ ) and plant height ( $r_g=-0.268$ ) had significant and negative correlation with seed yield per plant.

The highest positive direct effect on seed yield per plant was exhibited by number of seeds per pod (0.786) followed by days to maturity (0.418), followed by number of clusters per plant (0.406), followed by number of seeds per pod (0.053), followed by number of pods per plant (0.023) followed by number of branches per plant (0.008), however, negative direct effect on seed yield per plant were contributed through plant height (-0.352), followed by days to first flowering (-0.292) and pod length (-0.206).

Days to maturity had highest positive indirect effect on seed yield per plant *via* 100-seeds weight (0.113). Similarly plant height exhibited positive indirect effect *via* 100-seeds weight (0.288). Number of clusters per plant also showed positive indirect effect on seed yield per plant *via* plant height (0.069). The number of branches per plant had maximum positive indirect effect on seed yield per plant *via* number of clusters per plant (0.333) and showed negative indirect effect *via* 100-seeds weight (-0.801) followed by days to first flowering (-0.276) and pod length (-0.149). 100-seeds weight showed negligible positive or negative indirect effect on seed yield per plant.

Residual effect for treatment 4 was low (0.11995) and positive in path analysis.

**4.4.6 Path coefficient analysis for treatment 6 (300Gy + 0.25% EMS)**

Perusal of the Table 4.18 revealed that seed yield per plant showed highly significant and positive correlation with number of clusters per plant ( $r_g=0.363$ ). It was negatively and significantly correlated with pod length ( $r_g=-0.459$ ) and days to first flowering ( $r_g=-0.306$ ).

The highest positive direct effect on seed yield per plant was exhibited by plant height (0.483) followed by number of branches per plant (0.408), days to maturity (0.299), number of clusters of plant (0.186), however, negative direct effect on seed yield per plant were contributed through pod length (-0.964), followed by 100-seeds weight (-0.474), followed by days to first flowering (-0.451), followed by number of pods per plant (-0.281) and number of seeds per pod (-0.059).

Table 4.17 Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in M<sub>3</sub> generation of cowpea for treatment 5 (275Gy + 0.25% EMS).

Characters	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Genetic correlation with seed yield per plant
Days to first flowering	<b>-0.292</b>	0.120	-0.045	0.007	0.044	0.003	0.083	0.002	0.127	0.051
Days to maturity	-0.084	<b>0.418</b>	0.074	0.008	-0.055	-0.002	-0.023	-0.007	0.113	0.433**
Plant height (cm)	-0.037	-0.088	<b>-0.352</b>	-0.001	-0.079	0.009	-0.002	-0.004	0.288	-0.268*
Number of branches per plant	-0.276	0.003	0.076	<b>0.008</b>	0.333	-0.025	-0.149	0.089	-0.801	-0.741**
Number of clusters per plant	-0.031	-0.057	0.069	0.006	<b>0.406</b>	-0.004	0.018	-0.002	-0.053	0.350**
Number of pods per plant	-0.039	-0.052	-0.149	-0.009	-0.080	<b>0.023</b>	-0.038	-0.012	0.318	-0.040
Pod length (cm)	0.118	0.047	-0.004	0.006	-0.035	0.004	<b>-0.206</b>	0.007	0.057	-0.004
Number of seeds per pod	-0.013	-0.058	0.028	0.014	-0.019	-0.005	-0.029	<b>0.053</b>	-0.097	-0.127
100-seeds weight (g)	-0.047	0.060	-0.129	-0.008	-0.027	0.009	-0.015	-0.006	<b>0.786</b>	0.623**

\*,\*\* Significant at 5% and 1% levels, respectively. (Residual effect = 0.11995).

Table 4.18 Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in M<sub>3</sub> generation of cowpea for treatment 6 (300Gy + 0.25% EMS).

Characters	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Genetic correlation with seed yield per plant
Days to first flowering	<b>-0.451</b>	-0.074	-0.101	-0.129	0.025	-0.006	0.295	-0.003	0.133	-0.306*
Days to maturity	0.112	<b>0.299</b>	0.061	0.030	-0.018	-0.074	-0.081	-0.034	-0.098	0.196
Plant height (cm)	0.094	0.037	<b>0.483</b>	-0.035	-0.046	-0.118	-0.444	0.007	-0.021	-0.043
Number of branches per plant	0.143	0.022	-0.041	<b>0.408</b>	0.052	-0.120	-0.396	-0.025	0.100	0.142
Number of clusters per plant	-0.061	-0.029	-0.120	0.114	<b>0.186</b>	-0.104	-0.389	-0.024	0.067	0.363**
Number of pods per plant	-0.009	0.078	0.203	0.174	0.069	<b>-0.281</b>	-0.510	-0.046	0.111	0.201
Pod length (cm)	0.138	0.025	0.222	0.168	0.075	-0.149	<b>-0.964</b>	-0.011	0.036	-0.459**
Number of seeds per pod	-0.026	0.173	-0.064	0.175	0.078	-0.219	-0.184	<b>-0.059</b>	0.125	-0.002
100-seeds weight (g)	0.126	0.062	0.021	-0.086	-0.026	0.066	0.073	0.015	<b>-0.474</b>	-0.222

\*,\*\* Significant at 5% and 1% levels, respectively. (Residual effect = 0.22861).

The days to first flowering had maximum and positive indirect effect on seed yield per plant *via* pod length (0.295) followed by 100-seeds weight (0.133) while this trait exhibited negative indirect effect *via* number of branches per plant (-0.129) and plant height (-0.101). Similarly, number of clusters per plant showed positive indirect effect *via* number of branches per plant (0.114) and negative indirect effect *via* pod length (-0.389) and plant height (-0.120). Pod length exhibited maximum positive indirect effect on seed yield per plant *via* plant height (0.222) followed by number of branches per plant (0.168) and days to first flowering (0.138) whereas its negative indirect effect was through number of pods per plant (-0.149). Remaining traits exhibited negative or positive indirect effect with lower magnitude on seed yield per plant. Residual effect for treatment 6 was low (0.22861) and positive in path analysis.

#### 4.4.7 Path coefficient analysis for treatment 7 (400Gy + 0.25% EMS)

With reference to Table 4.19 revealed that seed yield per plant showed highly significant and positive correlation with 100-seeds weight ( $r_g=0.455$ ) followed by plant height ( $r_g=0.445$ ) and number of pods per plant ( $r_g=0.327$ ).

The highest positive direct effect on seed yield per plant was exhibited by number of pods per plant (1.169) followed by plant height (0.336) followed by pod length (0.167), followed by 100-seeds weight (0.132) and, however, negative direct effect on seed yield per plant were contributed through days to first flowering (-0.965), followed by day to maturity (-0.572) followed by number of clusters per plant (-0.522) and number of seeds per pod (-0.432).

Maximum positive indirect effect by plant height was exhibited on seed yield per plant *via* number of clusters per plant (0.144). Number of branches per plant exhibited positive indirect effect on seed yield per plant *via* number of seeds per pod (0.388) followed by 100-seeds weight (0.163), pod length (0.153) and number of pods per plant (0.109) while its negative indirect effect was exhibited *via* plant height (-0.355). Highest positive indirect effect was exhibited by 100-seeds weight on seed yield per plant *via* number of pods per plant (0.522) followed by number of seeds per plant (0.129) while showed negative indirect effect *via* days to first flowering (-0.316). Number pods per plant exhibited negligible positive indirect effect *via* 100-seeds weight (0.059) while its negative indirect effect was through days to first flowering (-0.563) and days to maturity (-0.219). Remaining traits exhibited negative or positive indirect effect with lower magnitude on seed yield per plant.

Residual effect for treatment 7 was low (0.3301) and positive in path analysis.

**4.4.8 Path coefficient analysis for treatment 8 (control)**

Perusal of the Table 4.20 revealed that seed yield per plant showed highly significant and positive correlation with number of clusters per plant ( $r_g=0.494$ ) followed by number of branches per plant ( $r_g=0.335$ ) and number of pods per plant ( $r_g=0.334$ ). It was negatively and significantly correlated with number of seeds per pod ( $r_g=-0.395$ ) followed by pod length ( $r_g=-0.333$ ), days to maturity ( $r_g=-0.286$ ) and days to first flowering ( $r_g=-0.280$ ).

The highest positive direct effect on seed yield per plant was exhibited by number of clusters per plant (3.688) followed by days to first flowering (2.889), pod length (1.266), plant height (0.899) and number of seeds per pod, however, negative direct effect on seed yield per plant were contributed through days to maturity (-1.541) followed by 100-seeds weight (-0.345), number of pods per plant (-0.263) and number of branches per plant (-0.229).

Days to first flowering exhibited negligible positive indirect effect on seed yield per plant *via* pod length (0.095) while it showed the highest negative indirect effect *via* number of clusters per plant (-2.813) followed by days to maturity (-0.437). Similarly, days to maturity showed positive indirect effect *via* days to first flowering (0.819) followed by number of clusters per plant (0.327) and plant height (0.202) whereas its negative indirect effect was exhibited *via* pod length (-0.174). The number of branches per plant showed positive indirect effect on seed yield per plant *via* pod length (0.522) and days to maturity (0.284). Number of clusters per plant had negative indirect effect *via* days to first flowering (-2.204) and pod length (-0.688). Highest positive indirect effect was exhibited by number of pods per plant on seed yield per plant *via* days to first flowering (0.918) followed by number of clusters per plant (0.252), plant height (0.238) and 100-seeds weight (0.136), its negative indirect effect was expressed *via* pod length (-0.605) and days to maturity (-0.308). The character pod length exhibited positive indirect effect on seed yield per plant *via* days to first flowering (0.218) and days to maturity (0.212), its negative indirect effect was highest *via* number of clusters per plant (-2.004). Number of seeds per pod exhibited positive indirect effect *via* pod length (0.268) on seed yield per plant and negative indirect effect *via* number of clusters per plant (-0.506) and days to first flowering (-0.204).

Residual effect for treatment 8 was low (0.32192) and positive in path analysis.

Table 4.19 Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in M<sub>3</sub> generation of cowpea for treatment 7 (400Gy + 0.25% EMS).

Characters	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Genetic correlation with seed yield per plant
Days to first flowering	<b>-0.965</b>	-0.016	0.003	-0.001	0.198	0.682	-0.017	0.031	0.043	-0.043
Days to maturity	-0.026	<b>-0.572</b>	0.024	0.002	-0.013	0.447	0.007	0.143	0.013	0.024
Plant height (cm)	-0.001	-0.041	<b>0.336</b>	-0.040	0.144	0.032	-0.045	0.079	-0.020	0.445**
Number of branches per plant	0.024	-0.037	-0.355	<b>0.038</b>	-0.151	0.109	0.153	0.388	0.163	0.334**
Number of clusters per plant	0.366	-0.015	-0.093	0.011	<b>-0.522</b>	0.155	0.037	0.101	0.007	0.048
Number of pods per plant	-0.563	-0.219	0.009	0.003	-0.069	<b>1.169</b>	-0.062	0.001	0.059	0.327*
Pod length (cm)	0.098	-0.024	-0.091	0.035	-0.116	-0.438	<b>0.167</b>	0.095	0.064	-0.209
Number of seeds per pod	0.069	0.189	-0.061	-0.034	0.122	-0.004	-0.036	<b>-0.432</b>	-0.039	-0.225
100-seeds weight (g)	-0.316	-0.060	-0.052	0.047	-0.029	0.522	0.081	0.129	<b>0.132</b>	0.455**

\*,\*\* Significant at 5% and 1% levels, respectively. (Residual effect = 0.33013) .

**Table 4.20** Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in M<sub>3</sub> generation of cowpea for treatment 8 (control).

Characters	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seeds weight (g)	Genetic correlation with seed yield per plant
<b>Days to first flowering</b>	<b>2.889</b>	-0.437	0.068	0.004	-2.813	-0.083	0.095	-0.016	0.014	-0.280*
<b>Days to maturity</b>	0.819	<b>-1.541</b>	0.202	0.042	0.327	-0.052	-0.174	0.022	0.068	-0.286*
<b>Plant height (cm)</b>	0.221	-0.351	<b>0.890</b>	-0.043	-0.765	-0.070	0.018	-0.035	-0.069	-0.206
<b>Number of branches per plant</b>	-0.050	0.284	0.169	<b>-0.229</b>	-0.145	-0.013	0.522	-0.014	-0.187	0.335**
<b>Number of clusters per plant</b>	-2.204	-0.136	-0.184	0.009	<b>3.688</b>	-0.018	-0.688	-0.032	0.061	0.494**
<b>Number of pods per plant</b>	0.918	-0.308	0.238	-0.011	0.252	<b>-0.263</b>	-0.605	-0.023	0.136	0.334**
<b>Pod length (cm)</b>	0.218	0.212	0.013	-0.094	-2.004	0.125	<b>1.266</b>	0.050	-0.121	-0.333**
<b>Number of seeds per pod</b>	-0.204	-0.148	-0.134	0.013	-0.506	0.026	0.268	<b>0.237</b>	0.052	-0.395**
<b>100-seeds weight (g)</b>	-0.117	0.304	0.177	-0.124	-0.657	0.104	0.444	-0.036	<b>-0.345</b>	-0.252

\*,\*\* Significant at 5% and 1% levels, respectively. (Residual effect = 0.32192).



# CHAPTER-V

## DISCUSSION

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Cowpea [*Vigna unguiculata* (L.) Walp.] is a short duration summer and rainy season crop. The crop species of cowpea possess substantial genetic variability in the stock available in the country.

Mutation breeding is one of the crop improvement programme which has been contributing significantly for increasing genetic resources and wide genetic variability for economically important traits and therefore, became a vital tool. Additionally, mutation breeding creates genetic variability, which was not available in wild germplasm. There are many examples in cross-pollinated species, which prove its efficiency as a substitute for conventional breeding methods. This programme was even tried in self-pollinated crops, where hybridization was less applicable. It was also true in case of certain pulses, where variations for more than one trait have been induced simultaneously. The material which are developed by mutation breeding has been commercialized on farmer's fields.

The progress of any breeding programme depends on the extent of variability present in a population. Therefore, an assessment of the genetic variability in the base population should be the first step in any breeding programme. It is well established fact that the growth and development of the plant on which seed yield is dependent, is determined jointly by the genetic makeup of the plant and the environment in which it is grown. Thus, the first and foremost step in this direction is to select most appropriate mutagen and its dose/concentration for their use in future breeding programme.

The amount of variability present in a population in respect of various quantitative characters is a pre-requisite for a plant breeder to commence any crop improvement programme. Heritability and genetic advance would help in deciding the appropriate selection intensity, whereas the genetic advance as percentage of mean predicts the gain that is likely to be achieved through selection.

Seed yield, being a complex and polygenic character, is influenced by various component traits. The effectiveness of selection for better genotype depends upon

magnitude and its direction of correlation between seed yield and yield contributing characters as well as association among various plant characters. Path coefficient analysis helps to avoid complications by measuring direct influence of one character upon other as well as permits the partitioning of a given correlation coefficient into its components of direct and indirect effects.

The present investigation was conducted by keeping in view the objectives like estimation of genetic variability parameters, correlation and path coefficient analysis in M<sub>3</sub> generation of cowpea for different quantitative characters. Efforts were made to know the extent of genetic variability, pattern of relationship among important yield components and useful selection criteria through combination of gamma rays and EMS mutagens in M<sub>3</sub> generation.

The obtained results have been discussed in the light of available literature and explanation wherever possible is provided under the following subheads:

- 5.1 Analysis of variance
- 5.2 Genetic variability parameters
- 5.3 Correlation coefficients
- 5.4 Path coefficient analysis

## **5.1 ANALYSIS OF VARIANCE**

The analysis of variance between families revealed that mean sum of squares between families were highly significant for all the characters studied. The Bartlett's test of homogeneity of error variance for all the families indicated that the error variance was homogenous for all characters except for number of clusters per plant, number of pods per plant and 100-seeds weight as showed by non-significance of chi-square values. The analysis of variance among all progenies within families indicated significant difference among 20 progenies means for all characters studied. Induction of sufficient variability through the mutagenic treatment is of immense importance for plant breeder and success of further breeding programme.

## **5.2 GENETIC VARIABILITY PARAMETERS**

Genetic variability is basic tool for crop improvement due to its wider scope for selection. Therefore, the effectiveness of selection depends upon the nature and

magnitude of genetic variability present in the experimental material and the extent of its heritability. The present experimental material showed wide range of variation for seed yield per plant, number of clusters per plant, number of branches per plant, plant height, pod length and number of seeds per pod as revealed by high values of coefficient of range. The phenotypic variation is not the precise criterion to estimate the amount of genetic variability present in the breeding population and is not comparable among various traits. The other genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance as expressed as percentage of mean are important to study the extent of genetic variability parameters more precisely.

### **5.2.1 Genotypic and Phenotypic coefficients of variation:**

The better index for measuring the genetic variation is genotypic coefficient of variation (GCV) as described by Burton (1952) for comparing the genetic variability present in experimental material. The estimates of genotypic and phenotypic coefficient of variability indicated that the values of phenotypic coefficient of variation were slightly higher than that of genotypic coefficient of variation for most of the traits, indicating less effect of environment on the expression of characters studied. Similar results have also been reported by Singh *et al.* (2013), Chattopadhyay *et al.* (2014); Nair and Mehta, (2014a) and Baranda *et al.* (2018).

Highest genotypic coefficient of variation and phenotypic coefficient of variation was observed for seed yield per plant in treatments 1, 2, 4 and 8 while treatments 5 and 6 showed high phenotypic coefficient of variation for number of branches per plant and seed yield per plant. High magnitude of genotypic coefficient of variation indicated the presence of wide variation for the characters under study to allow further genetic improvement by selection of the individual traits. High estimates of genotypic coefficient of variation in cowpea treated with various mutagens have been reported by Dhaka *et al.* (2013), Nair and Mehta (2014a) and Baranda *et al.* (2018) for seed yield per plant and number of branches per plant.

All treatments had moderate values for pod length, number of pods per plant and number of branches per plant while, treatments 3, 5, 6, 7 also showed moderate values for plant height, number of clusters per plant, number of seeds per pod and seed yield per plant. Rest of characters showed low phenotypic and genotypic coefficient of variation. Moderate GCV was reported in cowpea treated with various dose of

mutagens for number of branches per plant, plant height, number of clusters per plant and number of pods per plant by Dhaka *et al.* (2013) and Nair and Mehta (2014a), respectively. The findings of low PCV and GCV was reported by Baranda *et al.* (2018) for number of seeds per pod, days to first flowering and days to maturity while for days to first flowering was reported by Chattopadhyay *et al.* (2014).

### 5.2.2 Heritability

With the help of genotypic coefficient of variation alone, it is not possible to determine the extent of variation which is heritable. Thus, the knowledge of heritability of a character helps the plant breeders in predicting the genetic advance for any quantitative characters and aids in exercising necessary selection procedure. Burton (1952) suggested that genotypic coefficient of variation together with heritability estimate would give the best picture expected for selection.

All mutagenic treatments showed very high to high heritability (broad sense) for days to first flowering, days to maturity, plant height, number of clusters per plant, number of pods per plant, pod length, 100 seed weight and seed yield per plant. The moderate heritability results showed by number of branches per plant and number of seeds per pod. Considering the mutagenic effect of various treatments, the treatment 4 (250Gy + 0.25% EMS) expressed maximum heritability for days to first flowering, plant height, number of clusters per plant, 100-seeds weight and seed yield per plant followed by treatment 1 for days to first flowering, number of clusters per plant, 100-seeds weight and seed yield per plant and treatment 6 for plant height, number of clusters per plant and 100-seeds weight. Overall treatment 4 expressed considerable high heritability estimates for maximum characters under study.

The high heritability values for days to first flowering, plant height, number of clusters per plant, 100-seeds weight and seed yield per plant indicated that heritability may be due to higher mutagenic effect of treatment 4 (250Gy + 0.25% EMS) on these traits. High heritability for the above traits which were controlled by polygenes might be useful to the plant breeders for making effective selection.

High magnitude of heritability estimates in cowpea has been reported for days to first flowering (Chattopadhyay *et al.*, 2014), plant height (Nair and Mehta, 2014a; Baranda *et al.*, 2018), 100 seed weight (Baranda *et al.*, 2018) and seed yield per plant (Chattopadhyay *et al.*, 2014; Baranda *et al.*, 2018). On the contrary, high to moderate

heritability estimates were also reported for number of branches per plant by Nair and Mehta, (2014a) and Baranda *et al.* (2018), number of pods per plant by Chattopadhyay *et al.*, (2014), number of seeds per pod by Baranda *et al.* (2018) and pod length by Nair and Mehta (2014a).

### 5.2.3 Genetic advance expressed as percentage of mean

The shift in gene frequency under selection pressure towards desirable side is termed as genetic advance. Johnson *et al.* (1955) suggested that the heritability estimate along with genetic advance is more useful than the heritability alone in predicting the resultant effect of selection. Both the parameters are also useful in designing breeding programme. Heritability in broad sense and genetic advance as percentage of mean are direct selection parameters that provide index of transmissibility of traits which gives indication about the effectiveness of selection in improving the characters. The genetic advance is the further estimation of expected gain resulting from selection pressure in breeding material.

High genetic advance expressed as percentage of mean for seed yield per plant was expressed by all the treatments except treatment 3, followed by pod length, number of pods per plant and plant height. There was low genetic advance expressed as percentage of mean for days to first flowering, days to maturity, number of branches per plant, number of seeds per pod and 100-seeds weight by all the mutagenic treatments.

Looking to the mutagenic effect of individual treatment, the treatment 4 (250Gy + 0.25% EMS) and treatment 6 (300Gy +0.25% EMS) expressed high genetic advance expressed as percentage of mean for plant height, number of clusters per plant, number of pods per plant, pod length and seed yield per plant followed by treatment 5 (275Gy + 0.25% EMS) for plant height, number of clusters per plant, number of pods per plant and seed yield per plant. The remaining treatments showed variable effects on different character.

High values of genetic advance expressed as percentage of mean have been reported in cowpea for plant height (Baranda *et al.*, 2018), number of seeds per pod (Chattopadhyay *et al.*, 2014), pod length (Nair and Mehta, 2014a and Chattopadhyay *et al.*, 2014) and seed yield per plant (Dhaka *et al.*, 2013, Nair and Mehta, 2014a, Chattopadhyay *et al.*, 2014, Baranda *et al.*, 2018).

In the present study, treatment 4 (250Gy + 0.25% EMS) and treatment 6 (300Gy +0.25% EMS) showed high estimates of heritability coupled with high to moderate genetic advance as percentage of mean for days to first flowering, plant height, number of clusters per plant, number of pods per plant, pod length, 100-seeds weight and seed yield per plant which may be attributed to the preponderance of additive gene action and possess high selective value. Thus, selection pressure could profitably be applied on these characters for their rationale improvement. Similar results were reported by Dhaka *et al.* (2013) and Baranda *et al.* (2018) for plant height, Dhaka *et al.* (2013) and Chattopadhyay *et al.* (2014) for number of pods per plant, Chattopadhyay *et al.* (2014) for pod length and Dhaka *et al.* (2013) and Baranda *et al.* (2018) for seed yield per plant. Moderate estimates of heritability coupled with low genetic advance as percentage of mean was expressed by number of branches per plant and number of seeds per pod may be inferred that these traits were regulated by non-additive gene action and presence of high genotype x environment interaction.

For the trait days to maturity had major environmental variation leading to low heritability and low expected genetic advance may be result in little gain through simple selection.

### **5.3 CORRELATION COEFFICIENTS**

At genetic level, negative correlation arises from repulsion linkage of gene (s) controlling X and Y traits. Conversely, a positive correlation occurs due to coupling phase of linkage. However, both types (directions) of correlation may also stem from pleiotropy, *i.e.* developmental correlation (character differences which are influenced by same developmental or metabolic pathway controlled by the same genes). However, a transient genetic correlation may be due to linkage disequilibrium rather than pleiotropy. No correlation ( $r = 0$ ) indicates that genes concerned are located far apart on the same chromosome or they are located on different chromosome. However, nature (*i.e.* direction) of correlation can often be altered by selection and hybridization.

The seed yield is complex and polygenic character, depend on number of component characters. Therefore, the study of relationship among yield contributing characters and their association with seed yield is immense important to provide information for exercising selection pressure in relation to yield attributes for genetic improvement of seed yield.

In plant breeding programme, to improve the yield per plant, it is necessary to collect the detailed information regarding the association of various plant characters with yield per plant and among themselves. The mutagenic treatment wise correlation coefficients were estimated among pair of characters to find out association of seed yield per plant and its component at genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) levels.

The correlation is the overall or net effect of the segregating genes. Some of the genes may increase both the characters causing the positive correlation between the traits, while the others may increase the one and decrease the other causing the negative correlation. Thus, to accumulate optimum combination of yield contributing characters in a single genotype, it is essential to know the implication of the interrelationship of various plant characters.

In the present investigation, most of the character pairs recorded higher values of genotypic correlations than their corresponding phenotypic correlations. Such high amount of genotypic correlations could result due to masking or modifying effect of environments on the association of characters. This indicated that though there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environmental factors. The occurrence of higher estimates of genotypic correlations than the corresponding phenotypic correlations between seed yield and yield components in cowpea has also been reported by Santos *et al.* (2014), Sharma *et al.* (2016a), Sharma *et al.* (2016b) and Manohara *et al.* (2019).

In the present investigation, seed yield per plant had significant and positive correlation with number of branches per plant and number of pods per plant in treatments 1, 2, 7 and 8 at both genotypic and phenotypic levels while, treatments 1 and 4 also showed positive correlation with number of seeds per plant at genotypic level followed by treatment 5 with days to maturity, number of clusters per plant and 100-seeds weight at both levels, treatment 7 with plant height and 100-seeds weight at genotypic level and treatment 8 with number of clusters per plant at both levels indicating that these attributes were more influencing the seed yield in cowpea. Therefore, these traits were important for bringing genetic improvement in seed yield. The positive genotypic association in cowpea has been reported between seed yield per plant with number of branches per plant (Sharma *et al.*, 2016b, Srinivas *et al.*, 2017 and

Kana and Kwon, 2019), number of clusters per plant (Sharma *et al.*, 2016a, Sharma *et al.*, 2016b, Srinivas *et al.*, 2017, Baranda *et al.*, 2018), number of pods per plant (Manggoel *et al.*, 2012, Chattopadhyay *et al.*, 2014, Santos *et al.*, 2014, Sharma *et al.*, 2016a, Sharma *et al.*, 2016b, Nair *et al.*, 2017, Srinivas *et al.*, 2017, Kana and Kwon, 2019 and Walle *et al.*, 2018), number of seeds per pod (Chattopadhyay *et al.*, 2014, Sharma *et al.*, 2016a, Lopes *et al.*, 2017, Srinivas *et al.*, 2017, Kana and Kwon, 2019 and Walle *et al.*, 2018) and 100 seed weight (Manggoel *et al.*, 2012, Sharma *et al.*, 2016a, Sharma *et al.*, 2016b, Srinivas *et al.*, 2017, Baranda *et al.*, 2018, Kana and Kwon, 2019 and Nandini and Duddukur, 2019).

The present results on correlation coefficients among different mutagenic treatments revealed that treatment 1 (100Gy + 0.25% EMS) and treatment 5 (275Gy + 0.25% EMS) has more effect on seed yield by having more number of traits in association followed by treatment 7 (400Gy + 0.25% EMS). Besides these, number of branches per plant and number of pods per plant were the most important traits to contribute towards higher seed yield per plant. The interrelationship among seed yield components would help in increasing the seed yield. Therefore, more emphasis should be given to the mutagenic treatment which has more number of traits in association with seed yield per plant. Thereby treatments 1, 5 and 7 may be recommended mutagenic treatments for achieving higher seed yield in cowpea.

#### **5.4 PATH COEFFICIENT ANALYSIS**

The coefficients of phenotypic and genotypic correlations quantify the associations in magnitude and direction; nevertheless, they are not sufficient for expressing the direct and indirect effects, while path analysis allows a clearer interpretation of the direct effect of one variable on another, and of the interference that other variables have on this association.

Seed yield, a polygenic trait is influenced by various components directly as well as indirectly *via* other traits, which create a complex situation before a breeder for making selection. Therefore path coefficient analysis could provide a more realistic picture of the interrelationship, as it considers direct as well as indirect effects of the variable by partitioning the correlation coefficient.

The genotypic path coefficient was analyzed for different traits for different mutagenic treatments. The result discussed onward had significant and positive

genotypic correlation with seed yield per plant. Mutagenic effect of treatment 1 exhibited high to moderate and positive direct effect on seed yield per plant for number of seeds per pod, number of branches per plant and number of pods per plant whereas, in treatment 2 direct effect was observed for number of branches per plant, number of pods per plant and number of seeds per pod. The highest direct effect on seed yield was expressed only by number of branches per plant in treatment 4 while, in treatment 5 the traits days to maturity, number of clusters per plant and 100-seeds weight exhibited positive direct effect on seed yield per plant. Only number of clusters per plant had positive direct effect on seed yield per plant in treatment 6 while in case of treatment 7, the traits plant height, number of pods per plant and 100-seeds weight exhibited positive direct effect on seed yield per plant. There was positive direct effect on seed yield per plant by treatment 8 (control) for days to first flowering, number of clusters per plant, pod length and number of seeds per pod. Similar kinds of results were also reported for days to maturity (Santos *et al.*, 2014 and Walle *et al.*, 2018), plant height (Patel *et al.*, 2016, Baranda *et al.*, 2018 and Walle *et al.*, 2018), number of branches per plant (Sharma *et al.*, 2016b and Srinivas *et al.*, 2017), number of clusters per plant (Srinivas *et al.*, 2017 and Nandini and Duddukur, 2019), number of pods per plant (Sharma *et al.*, 2016a, Sharma *et al.*, 2016b, Nair *et al.*, 2017 and Nandini and Duddukur, 2019), number of seeds per pod (Srinivas *et al.*, 2017 and Kana and Kwon, 2019) and 100 seed weight (Manggoel *et al.*, 2012, Sharma *et al.*, 2016b, Baranda *et al.*, 2018 and Kana and Kwon, 2019).

From the forgoing discussion it was clear that treatment 1 (100Gy + 0.25% EMS) and treatment 5 (275Gy + 0.25% EMS) had the maximum mutagenic effect on number of branches per plant, number of pods per plant and 100-seeds weight which resulted as main yield contributing characters.

## CHAPTER-VI

### SUMMARY AND CONCLUSIONS

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The present investigation entitled “Estimation of genetic variability induced through combination of gamma rays and EMS mutagens in M<sub>3</sub> generation of cowpea [*Vigna unguiculata* (L.) Walp.]” was conducted to assess the genetic variability, correlation coefficient and path coefficient analysis in M<sub>3</sub> generation of cowpea treated with combination of gamma rays and EMS mutagens at different dose/concentration for 10 quantitative characters viz., days to first flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100-seeds weight and seed yield per plant. The experimental material of the present investigation comprised of seeds treated with 7 different mutagenic dose/concentration and control. The basic seeds were exposed to 7 different doses of gamma rays at Bhabha Atomic Research Centre (BARC), Trombay, Mumbai and there after seeds were treated with 0.25% EMS for each physical mutagenic treatment during 2017-18 and M<sub>1</sub> and M<sub>2</sub> generations were advanced. The M<sub>2</sub> derived M<sub>3</sub> seeds of cowpea variety Gujarat Cowpea 5 (GC-5) were obtained from Professor and Head of Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh. The present study was conducted at Main Oilseed Research Station, Junagadh Agricultural University, Junagadh in Compact Family Block Design with three replications during *kharif* 2019. The observations were recorded on ten randomly selected plants from each progeny and each replication. The data were analyzed at computer cell of Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh.

**The salient features of the findings are as under:**

1. The analysis of variance revealed that mean sum of squares between families (mutagens) and among the progenies within the families (dose/concentration) were found highly significant for all the characters studied which indicated the presence of sufficient amount of variability between the families and among the progenies within the family.

## Summary and Conclusions

2. The test of homogeneity of error variance indicated that the error variance was homogenous for all the characters except for number of clusters per plant, number of pods per plant and 100-seeds weight.
3. Maximum phenotypic range of variation was recorded for seed yield per plant followed by number of clusters per plant, number of branches per plant, plant height, pod length and number of seeds per pod. The low phenotypic range of variation was observed for 100-seeds weight, number of pods per plant, days to first flowering and days to maturity.
4. The estimates of genotypic and phenotypic coefficient of variation in all the mutagenic treatments indicated that the values of phenotypic coefficient of variation were higher than that of genotypic coefficient of variation for most of the traits, indicating the effect of environment on the expression of characters studied.
5. The highest genotypic as well as phenotypic coefficient of variation was observed for seed yield per plant in treatments 1, 2 and 4, while for number of branches per plant only phenotypic coefficient of variation for treatments 3, 4, 5, 6 and 7. This indicated the presence of wide genetic variation for these characters in respective mutagenic treatment.
6. High heritability estimates were observed for days to first flowering, plant height, number of clusters per plant, 100-seeds weight and seed yield per plant in treatment 4 (250Gy + 0.25% EMS) indicated that this treatment showed higher mutagenic effect on these traits suggesting the presence of sufficient amount of heritable variation.
7. Highest estimates of genetic advance expressed as percentage of mean were found for plant height, number of clusters per plant, number of pods per plant, pod length and seed yield per plant in treatments 4 and 6. Remaining treatments had moderate to low genetic advance expressed as percentage of mean for characters studied.
8. High heritability coupled with high to moderate genetic advance expressed as percentage of mean were observed in treatment 4 (250Gy + 0.25% EMS) and treatment 6 (300Gy + 0.25% EMS) for days to first flowering, plant height, number of clusters per plant, number of pods per plant, pod length, 100-seeds weight and seed yield per plant suggesting preponderance of additive gene

## **Summary and Conclusions**

action and simple selection of these characters may be rewarding in case of induced mutagenesis.

9. Higher values of genotypic correlations than their corresponding phenotypic correlations were recorded by most of the character pairs. This indicated that there was high degree of association between two variables at genotypic level and its phenotypic expression was deflated by the influence of environmental factors.
10. Highly significant and positive genotypic and phenotypic correlations in treatments 1, 5 and 7 were expressed for seed yield per plant with number of branches per plant, number of pods per plant, number of seeds per pod and 100-seeds weight which could be the major yield determining traits that are to be selected for simultaneous improvement for seed yield.
11. The highly significant and positive correlation and genotypic path coefficient analysis revealed that the number of branches per plant, number of pods per plant and 100-seeds weight exhibited high and positive correlation as well as direct effects on seed yield per plant in treatments 1 and 5. Therefore, these traits could be used as selection criteria for improving seed yield in cowpea treated with respective mutagenic treatments.
12. The genotypic residual effect was observed in low magnitude for all the mutagenic treatments studied suggesting that the majority of the yield attributes have been included in the study of path analysis.

## **CONCLUSION**

It can be concluded from the present findings that, additive gene action was operating for days to first flowering, plant height, number of clusters per plant, number of pods per plant, pod length and 100-seeds weight for mutagenic treatments 4 (250Gy + 0.25% EMS) and 6 (300Gy + 0.25% EMS) indicating simple selection will be rewarding for improvement of these traits. Correlation and path coefficient analysis revealed that number of branches per plant, number of pods per plant and 100-seeds weight had positive and significant association with seed yield per plant as well as positive and direct effect on seed yield per plant under treatments 1 and 5. Therefore, due weightage should be given to these traits for simultaneous improvement in cowpea using the mutagenic treatments 1 (100Gy + 0.25% EMS) and 5 (275Gy + 0.25% EMS).

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## APPENDIX-I

Mean weekly meteorological data recorded during crop growth period of *kharif* 2019  
at meteorology department, JAU, Junagadh

Month	Std. Weak No.	Temperature (°C)		Relative Humidity (%)		Rainfall (mm)	Rainy Days
		Max.	Min.	Max.	Min.		
July 2019	31	28.9	25.5	96	95	213.3	6
Aug 2019	32	30.6	25.3	96	92	180.6	4
	33	32.4	24.8	96	84	22.9	3
	34	30.9	25.5	90	73	3.9	0
	35	31.1	25.4	96	88	49.6	4
Sept 2019	36	29.8	25.3	94	86	248.0	7
	37	32.6	25.1	96	85	180.5	4
	38	31.0	24.3	89	77	24.6	2
	39	32.5	23.9	93	84	196.2	6
Oct 2019	40	34.9	23.4	87	65	36.8	2
	41	35.2	22.7	80	49	0.0	0
	42	32.6	24.8	77	43	1.0	0
	43	34.0	23.7	64	52	0.0	0
	44	33.3	22.0	80	54	4.4	1

## APPENDIX-II

The mean values of 8 treatments in M<sub>3</sub> generation of cowpea variety GC-5 treated with gamma rays and EMS for all the 10 quantitative characters along with mean, standard error of mean (S.Em), critical difference (C.D.), coefficient of variation (C.V.) and range.

Sr. No.	Treatments	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
1	Treatment 1 (100Gy + 0.25% EMS)	48.70	65.67	93.10	4.20	7.13	10.57	9.13	9.73	8.48	11.35
2		48.60	64.33	116.07	4.70	7.27	9.87	5.73	9.47	7.39	21.60
3		48.90	68.00	105.53	4.13	7.73	12.77	10.67	11.63	8.12	14.39
4		49.07	66.67	123.13	4.73	6.13	8.43	11.43	8.83	8.36	11.37
5		50.60	65.33	104.53	3.57	7.40	8.25	11.60	8.43	8.61	9.78
6		48.43	66.67	100.90	3.43	7.60	8.07	10.83	8.27	9.38	8.03
7		49.03	66.67	115.03	4.50	6.60	8.93	10.17	8.17	8.66	9.91
8		49.83	65.33	94.83	5.23	6.93	8.03	10.23	9.03	8.43	11.18
9		46.60	63.33	103.45	4.47	7.07	9.30	10.23	9.37	6.56	9.21
10		49.73	64.33	103.38	4.73	6.97	10.03	11.23	9.63	8.64	22.27
11		47.47	65.67	111.07	5.00	6.87	7.50	10.90	7.47	8.58	6.52
12		49.43	67.33	100.43	4.23	7.53	11.17	9.67	11.40	8.40	14.11
13		48.00	65.67	98.70	5.93	7.00	9.83	11.90	8.43	8.59	14.15
14		50.47	67.33	104.77	4.63	8.30	11.90	10.00	10.37	9.55	10.33
15		49.83	67.67	81.90	4.57	8.27	10.67	10.70	8.90	8.52	11.07
16		49.77	65.33	109.35	5.53	7.63	10.60	10.77	9.20	8.46	20.72
17		47.77	66.67	98.50	4.90	7.17	11.00	8.50	9.33	9.34	8.97
18		48.33	64.33	102.83	4.03	6.87	9.17	10.17	9.93	8.34	14.47
19		48.40	66.67	94.23	5.10	7.53	9.80	10.90	9.37	9.48	13.91
20		51.70	66.67	91.43	5.37	7.23	7.97	9.87	8.30	8.47	11.95
<b>Mean</b>		49.03	65.98	102.66	4.65	7.26	9.69	10.23	9.26	8.52	12.76
<b>S.Em ±</b>		0.10	0.13	0.91	0.06	0.04	0.26	0.15	0.20	0.03	0.20
<b>C.D. at 5%</b>		0.19	0.27	1.84	0.13	0.08	0.52	0.30	0.40	0.06	0.40
<b>C.V. (%)</b>		1.07	1.11	4.85	8.08	3.18	14.72	8.07	11.78	1.96	8.50
<b>Range</b>		46.6-51.7	63.3-68	81.9-123.1	3.4-5.9	6.1-8.3	7.5-12.7	5.7-11.9	7.4-11.6	6.5-9.5	6.5-22.2

Sr. No.	Treatments	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
21	Treatment 2 (200Gy + 0.25% EMS)	54.37	65.33	89.03	4.03	6.20	14.37	9.03	6.20	8.37	10.80
22		53.47	66.33	94.60	3.47	6.70	15.43	10.70	6.80	8.38	7.35
23		49.93	65.67	95.23	4.20	7.53	14.83	9.17	7.73	8.40	6.27
24		52.60	67.33	103.27	3.53	7.33	16.70	11.63	9.00	9.23	9.92
25		54.37	67.33	103.47	4.53	6.17	12.03	10.40	7.17	8.28	7.30
26		52.80	66.33	121.83	3.77	7.43	10.77	10.13	8.60	9.28	7.15
27		54.37	64.00	98.70	2.50	6.53	12.03	11.90	8.53	7.37	8.23
28		54.03	64.67	84.93	4.03	7.23	15.57	5.53	7.23	8.43	8.30
29		53.23	67.67	92.50	3.90	7.03	15.90	11.03	7.17	9.43	10.30
30		52.77	64.33	74.77	4.10	6.57	14.77	10.67	8.50	9.17	12.23
31		53.67	66.67	88.57	3.70	6.87	15.50	10.63	8.07	8.34	7.28
32		51.83	64.67	126.87	4.17	6.53	15.47	10.57	7.43	8.30	6.42
33		56.10	64.33	95.00	3.93	6.87	14.70	9.73	7.87	9.19	6.41
34		54.93	67.33	79.10	3.47	6.83	10.83	8.63	10.27	8.41	5.63
35		56.03	64.67	91.80	3.97	6.37	13.77	10.43	6.80	8.19	8.19
36		53.60	63.67	91.93	3.63	7.10	14.13	12.23	6.73	8.44	7.42
37		52.33	64.67	99.90	4.13	6.80	13.10	8.13	6.87	8.36	9.28
38		52.03	66.67	93.73	4.27	8.13	13.23	10.30	8.47	8.41	7.68
39		52.43	67.33	121.40	3.87	7.67	15.40	12.10	6.90	8.33	11.34
40		50.80	65.33	110.46	3.67	5.53	13.43	10.40	8.68	8.40	9.62
<b>Mean</b>		53.29	65.72	97.85	3.84	6.87	14.10	10.17	7.75	8.54	8.36
<b>S.Em ±</b>		0.14	0.14	1.34	0.06	0.06	0.22	0.17	0.20	0.02	0.21
<b>C.D. at 5%</b>		0.28	0.28	2.72	0.12	0.13	0.45	0.34	0.41	0.05	0.43
<b>C.V. (%)</b>		1.44	1.17	7.52	8.12	5.07	8.66	9.07	14.37	1.52	13.94
<b>Range</b>		49.9-56.1	63.6-67.6	74.7-126.8	2.5-4.5	5.5-8.1	10.7-16.7	5.5-12.2	6.2-10.2	7.3-9.4	5.6-12.2

Sr. No.	Treatments	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
41	Treatment 3 (300Gy + 0.25% EMS)	53.83	64.67	67.03	3.07	11.50	16.27	9.83	7.87	9.48	8.88
42		54.20	65.67	98.33	2.87	11.30	11.87	10.33	7.37	8.56	7.15
43		51.83	67.67	77.53	2.67	10.13	13.60	6.57	8.17	9.40	8.30
44		52.50	66.33	100.47	2.50	10.87	11.87	11.33	6.93	9.05	6.65
45		51.00	63.33	128.63	3.23	9.80	13.57	8.67	7.83	8.39	11.34
46		50.90	66.00	120.60	2.73	11.03	15.23	10.33	7.77	9.35	10.15
47		51.57	64.67	109.53	3.07	9.70	13.27	11.37	8.57	8.41	9.15
48		51.53	66.33	110.73	2.97	10.90	13.23	11.30	8.30	9.04	9.95
49		51.77	65.00	114.97	3.17	8.80	10.33	11.47	8.60	9.55	7.99
50		53.03	66.33	135.03	2.70	8.30	12.57	10.73	10.47	8.79	6.98
51		51.17	67.33	121.33	2.67	9.70	17.10	8.67	8.07	8.40	7.85
52		51.17	66.67	109.80	2.57	9.80	12.30	6.43	8.80	9.01	8.24
53		50.37	66.33	112.57	2.67	11.80	10.33	10.30	8.57	7.35	9.76
54		50.37	68.00	122.20	1.80	10.07	14.57	9.57	9.67	8.38	6.79
55		53.97	65.33	120.03	1.60	10.13	14.27	11.93	8.33	8.85	8.30
56		51.57	67.33	106.30	3.07	9.07	12.00	10.10	10.97	8.83	8.79
57		54.07	67.67	96.87	2.20	8.30	11.27	10.77	10.70	8.51	9.18
58		52.33	66.33	97.13	2.50	9.07	11.43	9.37	8.77	8.73	7.93
59		53.77	67.33	99.10	2.93	11.70	11.70	10.27	10.50	9.07	8.36
60		50.67	64.33	96.10	3.57	10.30	11.67	10.53	8.33	8.91	8.23
<b>Mean</b>		52.08	66.13	107.22	2.73	10.11	12.92	9.99	8.73	8.80	8.50
<b>S.Em ±</b>		0.14	0.14	1.35	0.08	0.10	0.17	0.16	0.20	0.04	0.18
<b>C.D. at 5%</b>		0.28	0.28	2.73	0.15	0.20	0.35	0.33	0.41	0.08	0.36
<b>C.V. (%)</b>		1.44	1.13	6.88	15.11	5.33	7.28	8.84	12.59	2.32	11.60
<b>Range</b>		50.3-54.2	63.3-68	67-135	1.6-3.5	8.3-11.8	10.3-17.1	6.4-11.9	6.9-10.9	7.3-9.5	6.6-11.3

Sr. No.	Treatments	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
61	Treatment 4 (400Gy + 0.25% EMS)	49.67	65.67	77.37	1.77	7.40	14.70	10.73	7.53	6.60	8.45
62		48.90	62.00	116.80	2.83	9.27	14.07	6.37	7.87	6.78	10.46
63		50.53	64.33	116.40	2.73	7.60	13.70	11.17	9.73	6.62	12.33
64		50.20	66.00	118.77	1.70	6.90	14.20	9.93	7.33	8.51	8.92
65		50.47	67.00	104.70	2.40	7.70	15.77	9.63	10.13	7.13	7.46
66		49.60	63.67	87.67	2.60	6.93	14.70	8.27	8.17	7.32	13.81
67		47.60	66.33	106.03	2.80	7.03	15.70	10.23	7.87	6.59	8.01
68		49.37	66.00	70.90	2.80	6.50	14.27	9.87	7.70	6.37	7.57
69		50.57	66.67	112.20	2.63	7.23	17.83	11.20	7.87	6.88	11.00
70		48.67	66.00	98.93	2.93	6.43	16.27	10.57	8.80	6.48	10.45
71		50.83	67.33	92.90	1.80	6.77	12.83	8.90	7.23	5.57	7.90
72		50.87	63.67	120.90	2.77	5.43	15.57	9.70	9.40	6.66	11.62
73		50.53	66.33	100.50	2.00	7.17	14.13	10.67	8.03	5.84	16.77
74		50.30	64.67	130.20	2.47	7.50	17.22	11.13	7.70	6.32	7.59
75		49.67	64.33	121.10	3.10	6.93	9.83	10.77	8.47	6.64	11.87
76		50.83	66.33	91.50	1.97	6.13	16.23	9.73	7.80	5.74	11.23
77		50.27	67.33	104.50	2.33	6.47	11.57	11.23	7.47	6.35	8.49
78	45.33	63.33	110.77	3.00	6.17	13.87	6.60	8.17	6.06	13.56	
79	52.07	67.67	101.80	3.07	7.00	11.73	9.97	9.07	6.56	13.80	
80	49.80	66.33	87.70	2.67	8.30	12.77	8.90	7.90	5.54	12.76	
<b>Mean</b>		49.80	65.55	103.55	2.52	7.04	14.35	9.78	8.21	6.53	10.70
<b>S.Em ±</b>		0.12	0.16	1.33	0.07	0.07	0.25	0.16	0.15	0.06	0.21
<b>C.D. at 5%</b>		0.24	0.32	2.70	0.14	0.13	0.51	0.32	0.29	0.11	0.43
<b>C.V. (%)</b>		1.31	1.31	7.05	15.21	5.09	9.57	8.84	9.71	4.69	10.96
<b>Range</b>		45.3-52	62-67.6	70.9-130.2	1.7-3.1	5.4-9.2	9.8-17.8	6.3-11.2	7.2-10.1	5.5-8.5	7.4-16.7

Sr. No.	Treatments	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
81	Treatment 5 (500Gy + 0.25% EMS)	46.67	66.67	81.13	4.33	5.63	14.73	11.13	7.37	13.34	8.57
82		47.03	67.67	116.63	3.80	6.20	17.37	9.90	6.99	14.72	8.74
83		47.20	67.67	111.10	3.93	4.67	13.13	11.27	9.47	14.50	8.85
84		46.60	67.33	108.27	2.67	5.93	15.00	9.50	7.10	15.33	12.66
85		48.10	67.33	109.63	3.43	6.30	14.20	9.67	8.57	11.92	7.02
86		46.80	66.67	115.27	3.63	6.57	12.93	10.53	7.93	15.37	13.54
87		48.07	65.33	107.27	3.20	5.50	18.43	10.17	7.83	15.80	10.27
88		46.53	66.67	105.53	2.53	8.00	16.93	9.90	7.50	15.51	11.60
89		46.83	65.33	103.60	3.63	5.97	10.70	7.37	7.67	13.56	8.96
90		48.40	65.67	106.17	2.63	7.60	17.13	10.13	9.80	14.65	12.24
91		46.23	63.67	113.73	3.57	6.17	17.70	9.83	7.13	13.77	8.85
92		48.00	65.67	135.27	3.23	4.43	18.23	10.67	7.70	14.73	7.24
93		46.77	63.33	142.37	3.97	7.07	15.83	9.87	7.63	14.60	6.43
94		49.73	66.33	137.87	3.63	5.37	18.77	9.67	7.47	15.83	10.09
95		48.20	66.33	109.80	4.47	8.17	12.07	10.50	8.27	13.73	9.74
96		49.90	67.67	113.83	3.50	6.00	17.70	6.83	7.17	14.50	10.12
97		50.07	64.67	100.37	3.90	7.27	12.50	7.97	8.27	14.51	9.04
98		49.23	67.33	106.73	3.87	7.20	17.57	10.90	7.27	14.72	9.70
99		46.47	62.33	108.70	3.33	6.60	17.57	10.13	7.20	13.42	7.93
100		46.57	64.33	113.07	3.37	5.63	16.03	9.43	10.83	14.48	7.52
<b>Mean</b>		47.67	65.90	112.32	3.53	6.31	15.73	9.77	7.96	14.45	9.46
<b>S.Em ±</b>		0.12	0.16	1.34	0.07	0.09	0.23	0.13	0.17	0.05	0.22
<b>C.D. at 5%</b>		0.25	0.32	2.71	0.14	0.18	0.47	0.26	0.34	0.10	0.44
<b>C.V. (%)</b>		1.42	1.32	6.53	10.66	7.76	8.02	7.27	11.56	1.82	12.59
<b>Range</b>		46.2-50	62.3-67.6	81.1-142.3	2.5-4.4	4.4-8.1	10.7-18.7	6.8-11.2	6.9-10.8	11.9-15.8	6.4-13.5

Sr. No.	Treatments	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
101	Treatment 6 (600Gy + 0.25% EMS)	53.17	67.67	101.60	3.13	8.03	13.20	9.80	9.90	10.72	9.79
102		55.23	63.67	106.13	2.77	8.10	11.93	8.77	6.87	12.74	7.32
103		52.13	64.67	82.40	2.53	6.43	9.57	5.40	7.00	12.60	10.09
104		55.33	66.67	114.90	1.57	6.27	9.70	6.40	6.60	12.69	6.79
105		54.30	67.33	111.70	2.87	9.37	12.60	9.37	8.90	12.58	6.31
106		55.70	63.33	111.20	2.37	8.43	12.80	10.70	7.57	10.51	6.99
107		55.67	64.33	107.23	2.53	6.67	8.50	6.37	6.83	10.52	9.81
108		52.87	66.33	73.97	1.93	8.83	8.03	10.03	6.73	12.60	6.84
109		52.00	67.33	103.67	2.63	7.30	11.63	9.13	7.83	12.58	7.45
110		52.37	65.67	101.40	2.67	7.10	10.00	10.57	7.03	12.96	7.94
111		54.83	66.67	97.43	2.97	6.40	10.53	10.27	7.07	10.32	7.71
112		52.10	64.67	114.93	3.03	7.93	10.97	10.60	7.17	11.57	8.75
113		51.53	66.67	127.60	2.03	4.37	11.50	8.90	7.17	12.41	8.92
114		51.03	67.00	146.60	2.93	8.10	12.00	10.87	6.93	11.64	11.47
115		51.83	64.33	133.02	2.33	6.17	8.77	9.83	6.97	12.49	7.49
116		53.53	66.33	137.57	2.67	8.17	11.60	10.57	7.23	12.17	7.20
117		54.57	67.33	106.80	2.73	5.40	9.97	5.90	7.43	11.95	11.46
118		52.77	65.33	135.40	2.67	5.90	11.07	9.97	7.00	11.52	8.81
119		53.73	67.00	151.43	2.57	6.27	12.47	11.80	7.23	12.67	6.17
120		54.23	66.00	115.03	1.83	6.17	9.20	9.67	7.70	13.50	9.83
<b>Mean</b>		53.45	65.92	114.00	2.54	7.07	10.80	9.25	7.36	12.04	8.36
<b>S.Em ±</b>		0.13	0.13	1.34	0.06	0.09	0.16	0.18	0.15	0.06	0.20
<b>C.D. at 5%</b>		0.27	0.26	2.71	0.13	0.17	0.33	0.37	0.30	0.12	0.40
<b>C.V. (%)</b>		1.34	1.05	6.42	13.33	6.65	8.28	10.88	10.94	2.71	13.00
<b>Range</b>		51-55.7	63.3-67.6	73.9-151.4	1.5-3.1	4.3-9.3	8-13.2	5.4-11.8	6.6-9.9	10.3-13.5	6.1-11.4

Sr. No.	Treatments	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
121	Treatment 7 (700Gy + 0.25% EMS)	56.47	68.20	113.43	2.93	7.50	10.90	10.50	6.67	11.56	7.71
122		56.73	66.17	88.88	2.27	7.83	11.83	8.47	10.97	10.71	6.99
123		56.17	65.67	115.02	3.17	9.10	12.50	10.00	7.43	12.59	9.19
124		56.97	67.17	123.77	2.37	9.47	13.90	10.67	8.57	11.88	10.68
125		56.83	66.57	117.50	2.97	6.93	13.53	10.60	7.33	13.55	12.28
126		57.57	64.73	121.83	2.93	8.07	11.93	10.33	7.23	13.40	8.63
127		57.77	67.63	126.85	2.53	7.90	16.13	9.77	7.30	12.93	8.89
128		58.10	63.30	112.93	2.33	6.33	15.00	9.23	12.53	12.65	9.41
129		57.03	67.03	117.63	2.93	8.10	14.70	10.87	9.10	12.91	8.93
130		58.77	65.90	88.12	2.77	7.93	14.80	10.77	7.77	13.50	9.20
131		55.93	65.20	120.50	3.10	7.90	11.73	10.33	9.80	11.47	8.42
132		57.83	63.77	138.40	2.47	6.67	11.97	6.83	7.83	10.59	10.49
133		58.50	65.00	127.82	2.30	7.13	13.07	10.97	7.97	11.78	6.75
134		58.00	67.30	109.00	3.20	7.17	12.67	10.50	7.67	12.88	7.65
135		58.73	67.60	116.70	2.23	6.80	14.27	10.80	8.33	12.85	8.88
136		57.40	62.80	100.63	3.13	9.27	13.87	10.50	7.70	13.52	9.85
137		57.70	65.10	94.23	2.57	8.37	12.80	10.93	8.50	12.02	7.63
138		57.33	66.87	125.40	3.13	7.10	12.63	10.57	9.20	13.18	10.50
139		58.57	68.17	123.22	2.57	8.23	18.13	7.43	8.20	12.49	9.33
140		57.83	68.23	110.67	2.73	7.60	17.37	8.60	7.92	12.87	9.91
<b>Mean</b>		57.51	66.12	114.63	2.73	7.77	13.69	9.93	8.40	12.47	9.07
<b>S.Em ±</b>		0.08	0.13	1.34	0.06	0.09	0.19	0.16	0.16	0.05	0.20
<b>C.D. at 5%</b>		0.16	0.27	2.71	0.12	0.17	0.39	0.32	0.33	0.11	0.40
<b>C.V. (%)</b>		0.75	1.11	6.40	12.20	6.03	7.65	8.85	10.74	2.31	11.89
<b>Range</b>		55.9-58.7	62.8-68.2	88.1-138.4	2.2-3.2	6.3-9.4	10.9-18.1	6.8-10.9	6.6-12.5	10.5-13.5	6.7-12.28

Sr. No.	Treatments	Days to first flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
141	Treatment 8 (control)	57.23	67.43	80.07	2.67	5.57	12.73	10.80	6.83	7.39	12.28
142		57.47	63.80	76.70	3.30	5.20	14.27	9.87	6.57	6.63	10.41
143		57.90	65.10	86.30	2.40	4.30	11.77	10.47	6.87	7.57	5.24
144		58.50	66.83	74.20	2.93	5.40	13.00	9.97	7.43	7.46	6.64
145		57.90	68.10	87.30	2.63	4.77	12.63	10.97	7.17	5.51	7.96
146		56.97	63.57	66.13	2.67	4.87	9.47	10.67	7.73	7.77	7.65
147		57.33	64.80	103.97	2.73	4.73	11.40	10.53	6.63	7.40	7.08
148		56.60	66.60	80.30	2.90	4.90	11.77	10.60	7.03	7.52	7.33
149		57.57	68.10	93.00	2.93	5.13	13.87	7.90	7.37	7.62	7.73
150		58.33	65.13	85.77	2.67	4.13	14.03	10.73	6.80	7.59	11.67
151		57.27	67.03	82.63	2.13	6.03	14.73	5.37	6.67	5.57	12.80
152		56.43	61.93	89.43	2.77	5.17	13.03	11.10	6.23	7.55	11.09
153		57.33	66.93	96.07	3.10	5.07	12.50	10.60	6.10	7.60	8.61
154		56.53	66.10	95.03	2.70	4.90	13.83	11.33	8.67	6.68	6.95
155		57.77	64.80	87.40	2.37	4.70	12.97	10.17	6.73	7.61	5.62
156		57.97	66.57	93.07	3.17	4.87	13.07	10.43	6.70	7.72	8.30
157		56.67	67.97	74.63	1.73	5.40	12.53	10.03	6.47	6.41	7.40
158		57.20	64.27	78.67	2.73	5.07	11.53	10.63	6.77	6.88	10.98
159		57.60	67.27	98.30	2.73	5.13	12.73	9.33	6.00	7.83	7.87
160		54.40	64.77	83.60	3.17	7.03	11.63	9.47	6.97	7.67	11.03
<b>Mean</b>		57.25	65.86	85.63	2.72	5.12	12.68	10.05	6.89	7.20	8.73
<b>S.Em ±</b>		0.10	0.16	1.33	0.06	0.05	0.08	0.16	0.13	0.03	0.20
<b>C.D. at 5%</b>		0.20	0.32	2.70	0.13	0.11	0.17	0.32	0.26	0.06	0.40
<b>C.V. (%)</b>		0.92	1.33	8.54	12.47	5.82	3.64	8.66	10.30	2.27	12.48
<b>Range</b>		54.4-58.5	61.9-68.1	66.1-103.9	1.7-3.3	4.1-7	9.4-14.7	5.3-11.3	6.0-8.6	5.5-7.8	5.2-12.8

