Journal of Plant Genomics
ISSN: 0976-8823 & E-ISSN: 0976-8831, Volume 2, Issue 1, 2012, pp.-28-33.
Available online at http://www.bioinfo.in/contents.php?id=78

INDUCTION AND ASSESSMENT OF GENETIC VARIABILITY FOR YIELD AND YIELD CONTRIBUTING TRAITS OF CHICKPEA [*Cicer arietinum* L.]

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Received: August 19, 2012; Accepted: September 03, 2012

Abstract- Genetic improvement for higher production and better quality has remained pivotal to agriculture. Lack of sufficient genetic variability for economically important traits is one of the reasons attributed for slow advancement in chickpea. Improvement in either single or few economic traits and quality characters can be achieved with the help of induced mutations within the shortest possible time. An experiment was conducted to evaluate the extent of biological damage in M_1 and M_2 generations along with genetic variability for yield and yield contributing traits in M_3 and M_4 generations of chickpea following mutagenesis with EMS and SA. The breeding behavior of the mutants was studied through M_1-M_4 generations. All the mutagenic treatments brought about dose dependent diminution in seed germination, pollen fertility and seedling growth in M_1 and M_2 generations. The reduction was more prominent in M_1 than in M_2 generation, indicating that some sort of recovery mechanism must be operating in the superseding period. A significant increase in mean values for pod bearing branches per plant, pods per plant, 100-seed weight (g) and total plant yield (g) was noticed in both M_3 and M_4 generations. Moreover, the magnitude of genotypic coefficient of variation, heritability and genetic advance for yield and its contributing components were recorded to be higher in the mutagenized population. Increase in mean values in conjunction with an augment in genetic variability advocate further possibilities of selecting more promising lines with high yield and genetic potential. The mutants isolated can be utilized in future as suitable genetic source material in breeding, genetic and functional genomics research.

Keywords- Chickpea, chemical mutagens, biological damage, genetic variability, yield components

Abbreviations- EMS- ethylmethane sulphonate, SA- sodium azide, HZ- hydrazine hydrate, NMU- N-Nitroso-N-methylurea, RCBD- randomized complete block design, LSD- least significant difference, SE- Standard error, PCV- phenotypic coefficient of variation, GCV- genotypic coefficient of variation, h^2- heritability, GA- genetic advance

Citation: Wani M.R., et al. (2012) Induction and Assessment of Genetic Variability for Yield and Yield Contributing Traits of Chickpea [*Cicer arietinum* L.]. Journal of Plant Genomics, ISSN: 0976-8823 & E-ISSN: 0976-8831, Volume 2, Issue 1, pp.-28-32.

Introduction

Pulses, well known as grain legumes belonging to family Fabaceae, are cherished for their opulence in protein which makes them indispensable along with cereals in daily human diet. Pulses due to their high genetic potential to thrive well under varied environmental conditions, capacity of soil fertility restoration and soil ameliorative properties have become the most important component of the sustainable agriculture. India has the pride of being the world's principal producer of pulses contributing nearly 13-15 million tonnes to the global production [41].

Chickpea (*Cicer arietinum* L.) is a self pollinated crop with natural cross pollination ranging between 0-1percent [37]. It is an annual legume which is used mainly for human dietary consumption in India. Being a winter season crop, it requires a cool climate for its optimal growth, high temperature for maturity and performs well on sandy or loam soils having adequate drainage system. It normally grows under rainfed environmental conditions; nevertheless furnish fine proceeds in irrigated conditions as well. The soil chosen for its cultivation should preferably be neutral in reaction and free from excessive soluble salts. Chickpea is classified as "Kabuli type" or "Desi type" based primarily on seed size and color. Kabuli type chickpea seed is bold and has a thin and usually white seed coat, while Desi type seed is less than half the size of kabuli type and has a thicker seed coat ranging brown to yellow in color [17]. Moreover, chickpea is well known for its use in cosmetics and herbal medicine. Its protein digestibility is the utmost among the dry edible legumes. In India, chickpea was grown over an area of 8.26 million hectares with the production of 6.20 million tonnes in 2009. The average yield of 751 kg/ha is low and is not sufficient to meet the growing demand [17]. Due to lack of ample natural variability, conventional methods of plant breeding had a narrow scope in the upgrading of chickpea. Micke [28] advocated that mutation approach was superior to other methods of crop improvement especially in those cases where the required amount of variation could be produced hastily.

Mutation breeding is a well functioning branch of plant breeding supplementing to conventional methods in a favorable manner [10]. It combines quite a few advantages in plant improvement by up-

grading an explicit character without altering the original genetic makeup of the cultivar. In that sense, it provides a speedy method to improve the crop varieties, without resorting to hybridization and back crossing. One of the chief advantages of mutation breeding is that it can give rise to many diverse mutant alleles with different degree of trait modification. In contrast, transposon or T-DNA mutagenesis generally leads to loss of function through gene disruption [6]. Therefore, conventional mutagenesis is still preferred for crop improvement.

Chemical mutagenesis is stared as an effective and imperative tool in improving the yield and quality traits of crop plants. The triumph of the breeder in opting genotypes possessing higher yield and growth traits depends principally on the subsistence and exploitation of genetic variability to the fullest extent. The role of mutation breeding in increasing the genetic variability for quantitative traits in various crop plants have been proved beyond doubt by a number of scientists [3,12,23,24,32,43,48].

Sodium azide (NaN_3) is well recognized for its high mutagenic effect in numerous crops. It is an excellent chemical mutagen with high water solubility and low toxicity to biological materials as compared to alkylating agents that are frequently used for the induction of mutations in crop plants [2,21]. The mutagenicity of azide compound is mediated through the production of an organic metabolite which creeps into the nucleus, interacts with DNA and creates point mutations in the genome.

Keeping in view the economic and nutritional significance of chickpea, the present study is aimed at understanding the genetic basis of yield and yield components in *Cicer arietinum* about which information is little scanty.

Materials and Methods

A field experiment was conducted during winter (Rabi) season of 2004, 2005, 2006 and 2007 at the University Agricultural Farm, Aligarh Muslim University, Aligarh, India. Uniform and healthy seeds of chickpea (*Cicer arietinum* L.) var. Avrodhi were presoaked in distilled water for 9 hours, prior to treatment with chemical mutagens viz., 0.1%, 0.2% ethylmethane sulphonate (EMS) and 0.01%, 0.02% sodium azide (SA) for 6 hours. The healthy, non-dormant and untreated (no mutagen applied) seeds soaked in distilled water only for 15 hours were sown as control. The solution of EMS was prepared in phosphate buffer of pH 7, whereas SA solution was prepared in phosphate buffer attuned to pH 3. Chemically treated seeds were thoroughly washed in running tap water to eliminate the residue mutagens from the seed surface.

One hundred seeds for every treatment and control were sown in the field in a randomized complete block design (RCBD) to raise M_1 generation. The distance between the seeds in a row and between the rows was kept as 30 cm and 60 cm respectively. Seeds harvested from individual M_1 plants were sown as M_2 families in three replicates in the field. For raising M_3 generation, such 10 M_2 progenies were selected which showed significant deviation in mean values in the positive direction from the control mean values, particularly for the yield and its associated components. Seeds from each selected M_2 progeny were bulked by taking an equal amount of seeds from each M_2 progeny and thoroughly mixed. A random sample of this bulk was sown to obtain M_3 progeny. Progenies of each M_3 selection were grown again as families in M_4 generation. Data collected for pod bearing branches per plant (counted at maturity as the number of branches which bore more than one pod), pods per plant (number of pods borne on a whole plant), 100-seed weight (weight in grams of a random sample of 100 seeds from each plant) and total plant yield (weight in grams of total number of seeds harvested per plant) of the mutants isolated in M_3 and M_4 generations were subjected to statistical analysis in order to assess the extent of induced variation. The significance of difference between the means of treated and control population was tested by using least significant difference (LSD) estimated from the error mean square and tabulated't' values at 5% and 1% levels of significance.

Components of Variance

Analysis of variance was done to find out the variation between the families and within the families. The components of variance considered were;

- Within-families variation in the control and treated material which was an estimate of environmental variation,
- Between-families variation which was an estimate of the between families genetic variation.

Genotypic Variance ($\sigma^2 g$)

The genotypic variance ($\sigma^2 g$) was estimated by the following formula:

$$\sigma^2 g = \frac{(MS_{Bf} - MS_e)}{N}$$

Where, MS_{Bf} and MS_e = Mean sum of squares for between families and within families or error, respectively

N=Number of replications

Genotypic Coefficient of Variation (GCV)

$$GCV(\%) = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Phenotypic Variance ($\sigma^2 p$)

Phenotypic variance was estimated by summing the estimated genotypic variance ($\sigma^2 g$) and the environmental variance (MS_e or $\sigma^2 e$)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Phenotypic Coefficient of Variation (PCV)

$$PCV(\%) = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Heritability (h^2)

The broad-sense heritability (h^2) was estimated by the formula suggested by Johnson, et al. [13].

$$h^2(\%) = \frac{\sigma^2 g}{\sigma^2 t} \times 100$$

Where, $\sigma^2 g$ = induced genotypic variance and

$\sigma^2 t$ = is the total phenotypic variance ($\sigma^2 t = \sigma^2 g + \sigma^2 e$) calculated from the treated populations.

Genetic Advance (GA)

The estimate of genetic advance (GA) at 1% selection intensity was computed by the following formula:

$$GA = k.\ \sigma p.\ h^2$$

$$GA\ (\%\ of\ \bar{X}) = \frac{GA}{\bar{X}} \times 100$$

σp= phenotypic standard deviation of the mean performance of treated populations.
h^2= heritability (broad- sense).
K= 2.64, constant for 1% selection intensity.

Twenty five seeds from each treatment and control were spread over moist cotton in petri-plates and kept in BOD incubator at 27±1°C temperature in order to determine the percentage of seed germination and seedling growth. After ten days of sowing the seeds in petri-plates, germination counts and growth observations were recorded on shoot and root length. Pollen fertility was determined by staining the pollen grains with 1% of acetocarmine solution. For this purpose, 15 M_1 and M_2 plants at random were selected from each treatment and control and finally 10 young flower buds from each plant were used for microscopic analysis. Pollen grains which took stain and had a regular outline were considered as fertile, while shrunken, empty and unstained ones as sterile. The following formula was used to calculate the percentage of inhibition in seed germination or reduction in pollen fertility.

$$\text{Percent injury} = \frac{\text{Control} - \text{Treated}}{\text{Control}} \times 100$$

Results and Discussion

In the present study, the dose dependent reduction in various biological parameters viz., seed germination, pollen fertility and seedling growth was noticed with increasing concentrations of EMS and SA in M_1 and M_2 generations of chickpea. The inhibition in seed germination was recorded maximum 14.28% with 0.02% SA in M_1 generation [Table-1] [Fig-1A]. The seed germination percentage too decreased in M_2, but it was rather less as compared to M_1 generation. The reduction in seed germination might have arisen due to impediment or inhibition of physiological and biological processes including enzymatic activity [26], hormonal disproportion [7] and hampering of mitotic process [1]. Azide ion plays an imperative role in causing mutations by interacting with enzymes as well as DNA within the cell. These azide anions are sturdy inhibitors of cytochrome oxidase which in turn inhibits oxidative phosphorylation process [44]. In addition, it is a potent inhibitor of the proton pump [22] and alters the mitochondrial membrane potential [49]. These effects caused by NaN_3 together may hinder ATP biosynthesis resulting in decreased availability of ATP molecules which may slow down the germination rate and reduce the germination percentage. Reduced seed germination in the present investigation, may be the result of altered enzymatic activity.

Varying degree of pollen sterility has been observed in different concentrations of both the mutagens under study. Maximum reduction in pollen fertility was 13.03% with 0.02% SA in M_1 generation [Table-1] [Fig-1B]. The reduction in pollen fertility was found to be more in M_1 than in M_2 generation. This indicates that some sort of recuperation mechanism must be operational in between these two generations. The higher degree of pollen sterility was reported to be associated with asynapsis or desynapsis [25]. In most cases, meiotic aberrations are responsible for pollen sterility [18,27,29,39] because meiosis is more prone to any conceivable type of disturbances [20]. High degree of pollen sterility has been reported in rice after treatments with SA, gamma rays, EMS and HZ [34]. Besides chromosomal anomalies, some physiological changes may possibly have caused pollen sterility.

In M_1 generation, the range of percentage injury in seedling growth was 13.72% to 22.99% in EMS treatments, whereas it ranged from 15.26% to 25.84% in SA treatments. The seedling growth also showed a declining trend in M_2, but it was pretty less as compared to M_1 generation [Table-1] [Fig-1C]. The inhibition in seedling growth was elucidated due to auxin obliteration and change in ascorbic acid content [46], destruction of apical meristems [30], transitory deferral of cell division [8] and reduction in the level of amylase activity [33]. Moreover, the suppression in seedling growth may be the consequence of gross injury caused at cellular level either due to gene controlled biochemical processes or acute chromosomal aberrations or both [4].

Table 1- Effects of EMS and SA on seed germination, seedling growth and pollen fertility in M_1 and M_2 generations of chickpea var. Avrodhi

Treatment	Percent Seed germination	Percent inhibition	Seedling growth (cm) Mean±S.E.	Percent injury	Pollen fertility (%)	Percent reduction
M_1 generation						
Control	98	-	28.05±0.20	-	97.16	-
0.1% EMS	92	6.12	24.20±0.43	13.72	90.5	6.85
0.2% EMS	86	12.24	21.60±0.39	22.99	86.2	11.28
0.01% SA	90	8.16	23.70±0.42	15.51	88.3	9.12
0.02% SA	84	14.28	20.80±0.45	25.84	84.5	13.03
M_2 generation						
Control	98	-	28.35±0.22	-	97.3	-
0.1% EMS	94	4.08	25.90±0.46	8.64	91.6	5.85
0.2% EMS	90	8.16	23.10±0.37	18.52	88.8	8.73
0.01% SA	92	6.12	24.80±0.36	12.52	89.1	8.42
0.02% SA	89	9.18	21.70±0.40	23.45	86.4	11.2

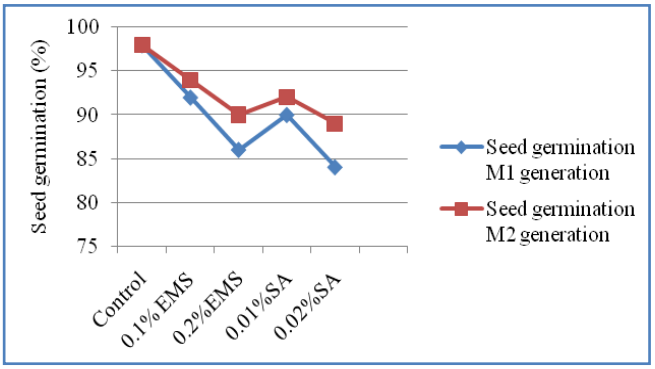

Fig. 1A- Effects of EMS and SA on seed germination in M_1 and M_2 generations of Chickpea

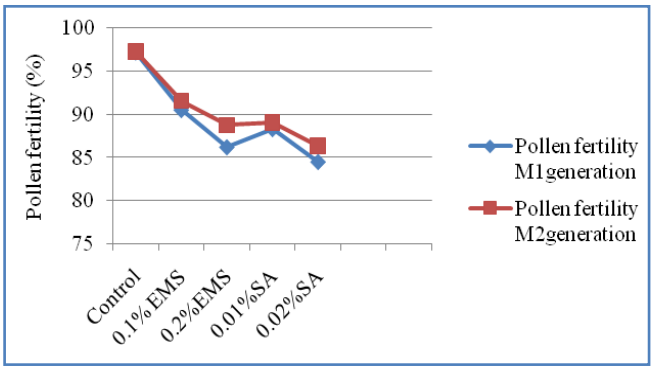

Fig. 1B- Effects of EMS and SA on pollen fertility in M_1 and M_2 generations of Chickpea

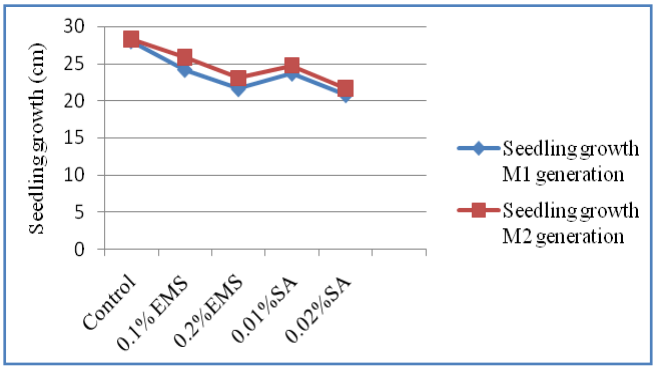

Fig. 1C- Effects of EMS and SA on seedling growth in M_1 and M_2 generations of Chickpea

Mutations affecting quantitative characters can be inferred by the estimation of mean and genetic parameters viz., genotypic coefficient of variation, heritability and genetic advance in the mutagen treated population [16]. In the recent past, there have been a number of efforts to assess the mutagen induced genetic variability for quantitative traits in different crop plants such as *Cajanus cajan* [42], *Vigna unguiculata* [11], *Vigna mungo* [40], *Lathyrus sativus* [47], *Lens culinaris* [41] and *Vigna radiata* [19,48]. In the current investigation, there was a considerable increase in the mean pod bearing branches per plant in all the mutagen treatments over the control in both M_3 and M_4 generations [Table-2] [Table-3]. Mean number of pod bearing branches were recorded higher in M_4 than in M_3 generation. Singh and Chaturvedi [38] showed increase in mean values of number of primary branches in *Lathyrus sativus* from M_2 to M_3 using NMU as mutagen. The EMS treatments were more effectual in increasing the mean values than SA in both the generations. The highest coefficient of phenotypic (18.07%) and genotypic (16.98%) variability was recorded with 0.1% EMS treatment, whereas the highest heritability estimate (94.12%) was observed with 0.02% SA in M_4 generation [Table-3]. The expected genetic advance was more distinct in EMS treated population as compared to SA treated one in both M_3 and M_4 generations.

The mean values of the number of pods per plant in treated population differed significantly from the control in both M_3 and M_4 generations. EMS treatments were found to be more effective than SA treatments. In M_4, significantly higher mean value (12.20 pods per plant) was noted with 0.2% EMS treatment. EMS at 0.2% concentration gave the maximum values of genetic parameters in both the generations [Table-2] [Table-3]. The increase in variability for number of pods per plant following mutagenesis has been reported in *Lathyrus sativus* [47] and *Vigna mungo* [40]. In this study, the variability in the treated population was much higher than the control for all the traits, namely pod bearing branches per plant, pods per plant, 100-seed weight and seed yield per plant. The degree of genetic variability available for selection can play an important role in overcoming the yield barriers. The increase in the number of pods in the present study was obviously due to an increase in the number of flowers. Similar boost in the number of pods have been also reported by Tickoo and Chandra [45] in mungbean.

The weight of 100 seeds is a dependable index of yielding ability in pulses. Although the mean 100 seed weight showed a slight positive shift, yet the difference was significant over the control in both M_3 and M_4 generations [Table-2] [Table-3]. These results are in compliance to the previous findings of Scossiroli [36] and Khan [16]. However, no significant enhancement in grain weight was reported by Potdukhe, et al. [31] in durum wheat subsequent to treatment with gamma rays. The grain yield of a crop is a complex character and is the multiplicative end product of many yield components. The data on seed yield per plant presented in [Table-2] and [Table-3], show that there was a significant increase in mean values for each treatment against the control in both M_3 and M_4 generations. The highest coefficient of genotypic variation, heritability and genetic advance were observed in EMS treatments. Increase in mean values of various yield attributing traits may be the outcome of rigorous selection of normal looking plants in M_2, which led to the confiscation of anomalous plants and also due to changes induced at genetic level. Gaul [9] recommended that the selection process should be deferred until M_3 or later generations following mutagenesis. In this study, the selection of progenies on the basis of desirable mean and variance in early generation was useful, leading to the requisite enhancement of yield and its components in subsequent (M_3 and M_4) generations.

Table 2- Estimates of mean values ($\bar{X}$), shift in $\bar{X}$ and genetic parameters for various quantitative traits in M_3 generation of chickpea var. Avrodhi.

Treatment	Mean±S.E.	Shift in $\bar{X}$	PCV (%)	GCV (%)	h^2 (%)	GA (% of $\bar{X}$)
Number of pod bearing branches						
Control	11.35±0.08	-	2.90	2.08	10.58	3.59
0.1% EMS	13.84±0.12	+2.49	5.82	4.45	58.46	8.85
0.2% EMS	14.93±0.13	+3.58	5.62	4.05	51.77	8.60
0.01% SA	13.54±0.14	+2.19	6.13	4.51	46.37	7.51
0.02% SA	14.50±0.12	+3.15	5.78	4.26	54.28	8.19
LSD at 5%		1.37				
LSD at 1%		2.07				
Number of pods per plant						
Control	50.14±0.27	-	3.41	1.73	25.68	2.31
0.1% EMS	56.67±0.52	+6.53	7.73	6.47	69.81	14.24
0.2% EMS	58.77±0.56	+8.63	8.80	7.41	70.52	15.88
0.01% SA	55.80±0.59	+5.66	8.22	6.75	68.80	14.79
0.02% SA	56.27±0.58	+6.13	8.28	6.61	63.73	13.92
LSD at 5%		2.22				
LSD at 1%		3.18				
100-seed weight(g)						
Control	21.94±0.14	-	3.52	1.43	11.70	2.01
0.1% EMS	23.25±0.19	+1.31	7.42	6.18	69.23	13.55
0.2% EMS	23.60±0.24	+1.66	7.29	5.06	48.15	9.23
0.01% SA	23.01±0.21	+1.07	7.02	5.22	55.23	10.19
0.02% SA	23.18±0.23	+1.24	7.27	5.86	64.79	12.38
LSD at 5%		0.37				
LSD at 1%		0.51				
Total plant yield (g)						
Control	28.12±0.16	-	2.98	1.55	27.90	5.66
0.1% EMS	32.67±0.27	+4.55	7.01	6.88	74.37	11.41
0.2% EMS	33.76±0.29	+5.64	7.80	6.56	62.99	11.26
0.01% SA	32.16±0.25	+4.04	6.42	4.74	54.33	9.19
0.02% SA	31.70±0.23	+3.58	6.51	4.81	57.36	9.78
LSD at 5%		0.67				
LSD at 1%		1.01				

In mutagenic treatments, high genotypic variance indicates better chances for selection to be successful. The estimates of phenotypic coefficient of variation in general, were higher than the estimates of genotypic coefficient of variation for all the characters studied, which suggested that the apparent variation is not only due to the genotypes but also due to the influence of environment. The genotypic coefficient of variation measures the range of genetic variability revealed by the particular trait. However, with the help of geno-

typic coefficient of variation alone, it may not be feasible to ascertain the amount of heritable variation and the relative degree to which a trait is transmitted from parent to offspring. In order to know the breeding utility of this variability and selection value of various quantitative traits, the estimates of genotypic coefficient of variation and heritability are essential [14] since they indicate the degree of stability to the environmental fluctuations and potential transmissibility of a trait from generation to generation. The data, in general, indicate a relatively higher estimated heritability (broad sense) for various yield attributing traits in M_4 generation. The increased heritability values in M_4, in comparison to M_3 generation, may be due to an increased homozygosity of the genes involved and indicates that the induced variability in mutant population has been fixed by selection. These findings are in harmony with those of Sarkar [35] and Borojevic [5]. The estimate of heritability acts as a predictive instrument in expressing the reliability of phenotypic values. Therefore, its ultimate value depends on the magnitude of all the components of variance. High heritability estimates indicate the presence of large number of fixable additive factors. Kaul and Kumar [15] acquired low heritability values for grain yield in rice. The discrepancy in the results could be due to the fact that heritability is a property not only of a character but also of the population and the environment to which the genotypes are subjected to. The high estimates of heritability in the quantitative traits has been found to be useful from the view point of plant breeding, as it enables the selection to be based on phenotypic performance.

Table 3- Estimates of mean values ($\bar{X}$), shift in $\bar{X}$ and genetic parameters for various quantitative traits in M_4 generation of chickpea var. Avrodhi

Treatment	Mean±S.E.	Shift in $\bar{X}$	PCV (%)	GCV (%)	h² (%)	GA (% of $\bar{X}$)
Number of pod bearing branches						
Control	11.43±0.10	-	9.50	4.20	13.50	4.85
0.1% EMS	16.03±0.27	+4.60	18.07	16.98	88.31	41.16
0.2% EMS	17.10±0.29	+5.67	17.23	16.22	88.70	40.26
0.01% SA	15.10±0.24	+3.67	15.82	14.79	87.39	36.35
0.02% SA	16.01±0.22	+4.58	15.24	14.69	94.12	37.82
LSD at 5%		1.67				
LSD at 1%		2.73				
Number of pods per plant						
Control	50.07±0.29	-	3.80	2.18	32.78	3.28
0.1% EMS	60.40±0.57	+10.33	10.49	10.18	93.34	26.01
0.2% EMS	62.27±0.95	+12.20	16.73	16.17	94.48	41.23
0.01% SA	59.27±0.62	+9.20	11.35	10.95	93.08	27.88
0.02% SA	60.32±0.65	+10.25	11.77	11.35	92.85	28.84
LSD at 5%		3.12				
LSD at 1%		3.98				
100-seed weight(g)						
Control	21.90±0.15	-	3.92	2.56	24.89	4.65
0.1% EMS	23.50±0.24	+1.60	6.01	5.77	67.84	10.74
0.2% EMS	23.85±0.26	+1.95	10.85	10.30	89.95	25.74
0.01% SA	23.25±0.23	+1.35	10.35	9.85	90.67	24.68
0.02% SA	23.45±0.24	+1.55	10.96	9.92	82.09	23.71
LSD at 5%		0.43				
LSD at 1%		0.75				
Total plant yield (g)						
Control	28.07±0.29	-	6.78	3.63	32.90	5.72
0.1% EMS	34.40±0.60	+6.33	19.83	18.64	93.88	47.65
0.2% EMS	35.74±0.61	+7.67	19.41	18.33	94.93	46.47
0.01% SA	34.14±0.56	+6.07	19.12	18.05	92.32	45.28
0.02% SA	34.04±0.59	+5.97	17.14	16.75	90.32	40.98
LSD at 5%		1.07				
LSD at 1%		1.78				

Genetic advance offer the degree of stability and genetic progress for a particular trait under an appropriate selection system and as a result carries much significance in self pollinated crops like chickpea. Heritability estimates along with genetic advance are usually more helpful than the heritability value alone in predicting the resultant effect of selecting the preeminent individuals [13]. High heritability along with high genetic advance as percent of mean were recorded for all the yield contributing traits in M_4 generation, indicating that these traits are governed by additive gene action and sustained selection in upcoming generations will be extremely responsive.

Conclusion

Induced mutations have the ability to increase the rate of domestication of many underexploited species of legume plants that may be potentially useful as the source of food, forage and industrial raw material. The results reported in this study, resolutely demonstrated the usefulness and the effective potential of the induced mutational approaches in genetic improvement of chickpea for recovering superior mutant plant types possessing desirable plant architecture associated with high yield. Furthermore, it is evident that the significant increase in mean values for pod bearing branches per plant, pods per plant and seed yield per plant was induced among the mutant lines in M_3 and M_4 generations. The degree of genotypic coefficient of variation, heritability and genetic advance for yield and yield components were also recorded to be higher in the treated population. The bump up in pod bearing branches and pods per plant played a significant role in boosting the seed yield in both the generations. The increase in mean values coupled with an increase in genetic variability for yield contributing traits suggest further possibilities of selecting more promising lines with high yield potential. The stability of genetic variability should be analyzed in subsequent generations and genes for important traits could be cloned and exploited in transgenic technique of chickpea.

Acknowledgement

The authors are indebted to the Chairman, Department of Botany, Aligarh Muslim University, Aligarh, India for providing necessary infrastructural support for carrying out hasslefree research experiments.

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