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Original Paper

Performance evaluation of induced mutant lines of black gram (*Vigna mungo* (L.) Hepper)

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Present investigation was carried out to explore the possibility of inducing genetic variability for yield and yield contributing traits in well-adapted variety PU-19 of black gram (*Vigna mungo* (L.) Hepper) following mutagenesis with methyl methane sulfonate (MMS), sodium azide (SA) and hydrazine hydrate (HZ). A considerable increase in mean values for fertile branches per plant, pods per plant and total plant yield was noticed among the mutant lines in M_4 and M_5 generations. Estimates of genotypic coefficient of variation, heritability and genetic advance for yield and yield components were also recorded to be higher compared to control. MMS followed by SA and HZ showed highest mutagenic potential for improving total plant yield of black gram var. PU-19. Treatment concentration 0.3% was found to be most effective in generating significant increase in total plant yield of black gram var. PU-19. The increased genetic variability for yield and yield components indicates the ample scope of selection for superior mutants in subsequent generations due to preponderance of additive gene action.

Keywords: black gram, mutagenesis, chemical mutagens, genetic variability, yield components

1 Introduction

Grain legumes, commonly known as pulses, occupy a pivotal position in meeting the protein needs of masses in developing countries like India. These have proved to be nutrient dense food stuffs especially the source of vegetable proteins. Besides nutritional values, pulse crops are endowed with unique property of maintaining and restoring soil fertility through biological nitrogen fixation (Dewanjee and Sarkar, 2017). The cultivation of pulse crops is preferred in rainfed areas of the country having poor management conditions prevailing with high biotic and abiotic stresses. In spite of constraints like unfavourable environment, non-availability of quality seeds, poor post-harvest management and inadequate market, the country has raised the annual pulse production from 8.41 to 16.35 million tonnes attributable to area expansion from 19.09 million ha in 1951 to 24.91 million ha during 2015–2016 and filled a yield gap from 441 to 656 kg ha^{-1} (Annual Report, 2016–2017). With population growth, the demand for food and feed is consistently growing, while natural resources are limited. Erratic rainfalls, sudden and severe drought conditions even deteriorate the crop production conditions (Auti, 2012).

Low yield arising from susceptibility of crops to diseases and pests and the absence of an effective mechanism to ensure remunerative returns have further forced the farmers to grow pulses on marginal lands. Development of high yielding and disease resistant varieties is the basic need of the time. Use of induced mutagenesis in breeding programmes for developing superior varieties has been used extensively for developing new crop

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cultivars and for changing the plant traits. During the past five decades, more than 3200 varieties have been released worldwide either as direct mutants or from their progenies (FAO/IAEA). Improvement of best available varieties by inducing mutations in one or two major traits without altering the basic genotypic and phenotypic design of the crop has been the background objective of mutation breeding (Ahloowalia et al., 2004; Shu et al., 2012; Mba, 2013; Tomlekova et al., 2014; Laskar et al., 2015; Raina et al., 2019).Genetic variability is one of the pre-requisites for crop improvement. The genetic variability in most of the pulse crops including black gram has been greatly reduced over the years due to natural selection under low level of management. Considering the several reported works in various crops (Giri et al., 2010; Dewanjee and Sarkar, 2017; Laskar and Khan, 2017; Wani, 2018; Laskar et al., 2018; Goyal et al., 2019; Raina et al., 2020), it is now quite clear that induced micro-mutations bring about significant genetic variability in the mutagen treated population(s). Micro-mutations basically create variability in quantitatively inherited traits in plants, which necessitates plant breeder's keen attention towards their utilization for improving complex trait(s) including yield.

The modes of action of different mutation causing agents are different (Laskar et al., 2019); hence wide variations can be observed in the resultant mutations induced in the crop population(s) exposed to different mutagens and their concentrations/doses. In general, chemical mutagens cause single base-pair (bp) changes or single-nucleotide polymorphisms (SNPs) while physical mutagens cause deletions or translocations in the exposed genome(s) (Sikora et al., 2011).In practice, multiple mutagens are used for inducing mutation(s) in target crop genotype(s) in a single experiment to amplify the scope of inducing wide range of desirable mutation(s). As reviewed by Laskar et al. (2019), among the various chemomutagens, alkylating agents like methyl methane sulphonate (MMS) are the most potent and commonly used category of chemical mutagens, which mediate through alkylation of DNA at various sites that result into micro-mutation(s) in the exposed genotype(s), useful for improvement of economically important quantitative trait(s).Sodium azide (SA) creates point mutation(s) in the targeted genome through the interaction between organic metabolite of azide and DNA, which is highly dependent on acidic pH. Hydrazine hydrates directly reacts to cause loss of the pyrimidines from DNA, G : C–A : T transitions and intermediate radical reactions, which results into wide variations in the subjected genotype(s). Mutagenecity of these highly potent chemomutagens was utilized in the present investigation to broaden the genetic variations induced in the desirable quantitative traits of black gram var. PU-19.

Black gram [*Vigna mungo* (L.)Hepper], commonly called as urdbean, is an important legume crop of India. It belongs to family Leguminosae and sub-family Papilionaceae with Indian subcontinent as the centre of its origin. It is considered to be domesticated from its wild progenitor *Vigna mungo* var. *silvestris* (Gill et al., 2017). Urdbean possesses deep penetrating root system which enables it to utilize the limited available moisture content more efficiently than many other competitive crops and contribute substantially to the loosening of the soil. Due to this reason, farmers choose to grow urdbean under highly diversified conditions. Moreover, urdbean is an excellent source of high-quality dietary protein with good digestibility and contributes a major portion of lysine in vegetarian diets of most of the Asian population (Gill et al., 2017). As per the MoA&FW (2020), around 80 recommended black gram varieties are under cultivation at present in India. Black gram var. PU-19, used in this experiment, was developed by pedigree method of selection from the cross between UPU-1 X UPU-2 (MoA&FW, 2020). Among the several breeding strategies, mutation breeding has been successfully implemented in creating 8 mutant varieties in India till now (MVD, 2020). Keeping in view the economic and nutritional importance of black gram, the present investigation was carried out to estimate the improvement of yield and yield contributing traits in M_4 and M_5 generations of black gram var. PU-19 following mutagenesis with MMS, SA and HZ.

2 Materials and methods

Uniform and healthy seeds of black gram (*Vigna mungo* (L.) Hepper) var. PU-19 were pre-soaked in distilled water for 9 hours, prior to treatment with chemical mutagens viz., 0.1–0.4% of methyl methane sulphonate (MMS) and 0.01–0.04% of sodium azide (SA) and hydrazine hydrate (HZ) for 6 hours. The untreated seeds soaked in distilled water for 15 hours were sown as control. Initially, the concentrations of chemical treatments were determined based on preliminary germination and survival test, where inhibition above 50% was considered lethal. The solutions of MMS and HZ were prepared in phosphate buffer of pH 7, whereas SA solution was prepared in phosphate buffer adjusted to pH 3. All the chemically treated seeds were thoroughly washed in running tap water to get rid of the remaining mutagens from seed surface. The experiment was carried out at the Agriculture Farm, Aligarh Muslim University, Aligarh, India. The site of present study viz., Aligarh, is located in the north-western part of Uttar Pradesh, India and extends from 27° 29′ to 28° 11′ North latitudes and 77° 29′ to 78° 38′ East longitudes. Aligarh

has the characteristic semi-arid and subtropical climate with hot dry summers (~35 °C) and cold winters (~15 °C) with average rainfall of about 847.30 mm. 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 at 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 mean values of control, 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 for seed yield trait were grown again as families in M_4 generation. Similar procedure was adopted to raise M_5 generation. The mutagenised populations were allowed to advance in subsequent generations based on yield statistics from M_2 onwards to narrow down the selection and attain yield stability. Finally, quantitative evaluations of yield traits were done at M_4 and M_5 generations to ascertain the yield performance of significantly stable mutant lines. Data collected for fertile 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) and total plant yield (weight in grams of total number of seeds harvested per plant) of the mutant lines isolated in M_4 and M_5 generations were subjected to statistical analysis in order to assess the extent of induced variation. Analysis of variance was done according to Singh and Chaudhary (1985) to find out the variance between the families and within the families. The components of variance considered were:

1. within-family variation in the control and in the treated material which was an estimate of environmental variation;
2. between–families variation which was an estimate of 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*):

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

Phenotypic Variance ($\sigma^2 p$) – 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*):

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

Heritability (h^2) – It is the ratio of genotypic variance to the total phenotypic variance. The broad-sense heritability (h^2) was estimated by the formula suggested by Johnson et al. (1955).

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

where:

$\sigma^2 g$ – induced genotypic variance

$\sigma^2 t$ – total phenotypic variance ($\sigma^2 t = \sigma^2 g + \sigma^2 e$) calculated from the treated population

Genetic Advance (*GA*) – the estimates of genetic advance (*GA*) with 1% selection intensity were based on the formula given below:

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

where:

h^2 – broad sense heritability

σp – phenotypic standard deviation of the mean performance of treated population

K – 2.64, constant for 1% selection intensity

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

Critical Difference (*CD*) – between the means of treated and control population was estimated from the error mean square and tabulated '*t*' value at 5% level of significance:

$$CD \text{ at } 5\% (p = 0.05)\ level = \sqrt{\frac{2\ MS_e}{r}}\ (t - \text{value at } 5\% \text{ level})$$

3 Results and discussion

In present investigation, a wide range of mutant phenotypes with altered characteristic affecting different plant parts were induced in the mutagenized populations of the black gram var. PU-19. The induced mutations for detectable phenotypes in yield attributing traits like branches and pods at different growth phases of plants were categorically inspected throughout the M_2 and M_3 season. Quantitative analysis of this induced phenotypic diversity facilitated the selection of desirable mutant progenies for advancement into subsequent generations from M_2 onwards and allowed up to M_5 generation for attainment of trait stability.The data recorded on fertile branches per plant, pods per plant and total plant yield is presented in Tables 1–3. It is clear from the data that mean values increased significantly for yield and yield

Table 1 Estimates of mean values ($\bar{X}$), shift in $\bar{X}$ and genetic parameters for fertile branches per plant in M_4 and M_5 generations of urdbean var. PU-19

Treatment	Mean ±S.E.	Shift in $\bar{X}$	*PCV* (%)	*GCV* (%)	h^2 (%)	GA (% of)
M_4 generation						
Control	6.26 ±0.12	–	12.12	7.14	18.24	6.10
0.1% MMS	6.62 ±0.22	+0.36	26.34	18.15	36.76	20.50
0.2% MMS	7.39 ±0.14	+1.13	28.20	20.19	40.92	24.20
0.3% MMS	7.62 ±0.17	+1.36	30.15	21.12	41.86	21.90
0.4% MMS	6.34 ±0.20	+0.08	21.10	16.86	38.72	16.22
CD (p = 0.05)	–	0.63	–	–	–	–
0.01% SA	6.36 ±0.16	+0.10	16.80	11.20	22.20	14.20
0.02% SA	7.10 ±0.21	+0.84	22.20	16.71	34.74	18.82
0.03% SA	7.27 ±0.18	+1.01	24.62	17.62	38.90	20.62
0.04% SA	6.42 ±0.19	+0.16	19.50	13.50	32.10	16.86
CD (p = 0.05)	–	0.73	–	–	–	–
0.01% HZ	6.35 ±0.13	+0.09	18.76	11.07	19.76	10.25
0.02% HZ	6.96 ±0.20	+0.70	20.92	16.95	30.26	16.77
0.03% HZ	7.15 ±0.16	+0.89	21.72	16.20	32.92	17.20
0.04% HZ	6.38 ±0.14	+0.12	18.82	11.60	21.76	14.90
CD (p = 0.05)	–	0.59	–	–	–	–
M_5 generation						
Control	6.30 ±0.18	–	11.50	6.86	22.11	8.11
0.1% MMS	7.10 ±0.28	+0.80	27.32	19.23	64.20	28.50
0.2% MMS	7.90 ±0.22	+1.60	29.27	21.09	72.66	30.17
0.3% MMS	8.10 ±0.26	+1.80	32.21	22.23	78.15	32.25
0.4% MMS	6.90 ±0.19	+0.60	22.76	17.76	62.11	27.12
CD (p = 0.05)	–	0.51	–	–	–	–
0.01% SA	6.95 ±0.25	+0.65	17.53	13.15	60.50	27.23
0.02% SA	7.35 ±0.18	+1.05	24.12	18.11	67.76	28.76
0.03% SA	7.70 ±0.16	+1.40	27.29	18.62	69.24	30.02
0.04% SA	6.82 ±0.21	+0.52	22.15	14.26	59.67	24.62
CD (p =0.05)	–	0.44	–	–	–	–
0.01% HZ	6.85 ±0.23	+0.55	20.12	12.25	58.21	25.95
0.02% HZ	7.25 ±0.26	+0.95	21.92	17.34	63.25	26.32
0.03% HZ	7.48 ±0.16	+1.18	22.13	17.96	66.21	28.71
0.04% HZ	6.78 ±0.24	+0.48	19.76	13.07	57.15	23.92
CD (p = 0.05)	–	0.39	–	–	–	–

*CD (p = 0.05) mean Critical Difference at 5% level of significance

Table 2 Estimates of mean values ($\bar{X}$), shift in $\bar{X}$ and genetic parameters for pods per plant in M_4 and M_5 generations of urdbean var. PU-19

Treatment	Mean ±S.E.	Shift in $\bar{X}$	*PCV* (%)	*GCV* (%)	h^2 (%)	*GA* (% of $\bar{X}$)
M_4 generation						
Control	31.50 ±0.20	–	6.14	3.12	20.12	4.20
0.1% MMS	33.20 ±0.18	+1.70	10.20	7.25	28.96	9.25
0.2% MMS	34.10 ±0.26	+2.60	12.16	8.16	43.20	12.66
0.3% MMS	35.07 ±0.21	+3.57	14.18	8.97	44.70	14.20
0.4% MMS	33.60 ±0.27	+2.10	9.76	6.20	32.15	10.15
CD ($p = 0.05$)	–	1.37	–	–	–	–
0.01% SA	32.60 ±0.32	+1.10	9.25	6.36	34.10	10.66
0.02% SA	33.45 ±0.34	+1.95	10.96	7.61	38.76	11.50
0.03% SA	34.30 ±0.26	+2.80	11.92	7.92	36.96	12.10
0.04% SA	33.30 ±0.22	+1.80	8.86	5.36	30.15	9.76
CD ($p = 0.05$)		1.05				
0.01% HZ	32.40 ±0.28	+0.90	8.74	6.26	30.98	10.15
0.02% HZ	33.30 ±0.31	+1.80	10.32	6.91	35.70	10.97
0.03% HZ	34.15 ±0.22	+2.65	10.76	7.15	32.89	11.23
0.04% HZ	32.70 ±0.27	+1.20	7.96	5.22	28.20	8.64
CD ($p = 0.05$)	–	1.12	–	–	–	–
M_5 generation						
Control	31.65 ±0.18	–	5.50	2.90	21.07	3.98
0.1% MMS	33.60 ±0.26	+1.95	12.20	8.34	60.12	15.12
0.2% MMS	35.15 ±0.31	+3.50	14.11	9.16	64.23	17.11
0.3% MMS	35.95 ±0.34	+4.30	16.22	11.11	66.11	18.22
0.4% MMS	34.70 ±0.22	+3.05	10.13	7.86	55.14	16.25
CD ($p = 0.05$)	–	1.63	–	–	–	–
0.01% SA	33.15 ±0.27	+1.50	11.25	7.32	56.20	15.95
0.02% SA	34.55 ±0.30	+2.90	13.26	9.92	58.11	16.62
0.03% SA	35.60 ±0.34	+3.95	14.92	10.07	61.50	17.02
0.04% SA	33.95 ±0.26	+2.30	9.98	7.12	53.52	13.92
CD ($p = 0.05$)	–	1.33	–	–	–	–
0.01% HZ	33.25 ±0.24	+1.60	10.72	6.62	54.70	14.07
0.02% HZ	34.41 ±0.29	+2.76	11.90	8.84	56.90	14.98
0.03% HZ	35.05 ±0.35	+3.40	12.61	8.98	59.26	15.86
0.04% HZ	33.60 ±0.23	+1.95	8.84	5.58	51.55	11.68
CD ($p = 0.05$)	–	1.12	–	–	–	–

*CD ($p = 0.05$) mean Critical Difference at 5% level of significance

contributing traits under study. Higher values of mean for number of fertile branches, number of pods and total plant yield were recorded at 0.3% MMS treatment in both M_4 and M_5 generations. The comparative analysis of different mutagen treatment conditions for total plant yield showed that MMS concentrations 0.3% followed by 0.2% provided highest increase in both M_4 and M_5 generations (Figure 1 and Figure 2). Overall, in the present investigation MMS followed by SA and HZ generated maximum positive shift in mean plant yield with respect to control value of black gram var. PU-19. In mutagenesis programmes, substantial changes in mean values indicate random occurrence of mutations in quantitative traits. However, the shift in mean values in the positive direction indicates that more positive mutations have occurred for these traits. The increase in

Table 3 Estimates of mean values ($\bar{X}$), shift in $\bar{X}$ and genetic parameters for total plant yield (g) in M_4 and M_5 generations of urdbean var. PU-19

Treatment	Mean ±S.E.	Shift in $\bar{X}$	*PCV* (%)	*GCV* (%)	h^2 (%)	*GA*(% of $\bar{X}$)
M_4 generation						
Control	7.86 ±0.10	–	6.88	2.98	25.52	5.38
0.1% MMS	8.56 ±0.14	+0.70	10.32	6.36	42.20	16.11
0.2% MMS	9.54 ±0.21	+1.68	14.66	9.25	46.70	18.92
0.3% MMS	10.34 ±0.24	+2.48	16.25	9.67	52.11	20.12
0.4% MMS	8.76 ±0.16	+0.90	9.20	6.20	38.86	16.27
CD ($p = 0.05$)	–	0.58	–	–	–	–
0.01% SA	8.81 ±0.22	+0.95	9.37	6.53	30.67	15.50
0.02% SA	9.21 ±0.25	+1.35	11.15	7.15	38.92	16.73
0.03% SA	9.76 ±0.17	+1.90	12.11	7.66	39.25	17.91
0.04% SA	8.66 ±0.20	+0.80	8.86	6.33	36.66	15.07
CD ($p = 0.05$)	–	0.44	–	–	–	–
0.01% HZ	8.41 ±0.13	+0.55	8.29	5.92	34.23	13.81
0.02% HZ	9.06 ±0.16	+1.20	10.92	6.71	36.12	15.36
0.03% HZ	9.56 ±0.20	+1.70	11.09	6.92	35.34	16.02
0.04% HZ	8.48 ±0.12	+0.62	7.98	5.23	28.96	11.61
CD ($p = 0.05$)	–	0.38	–	–	–	–
M_5 generation						
Control	7.80 ±0.15	-	5.90	2.70	26.11	6.12
0.1% MMS	9.06 ±0.20	+1.26	12.12	7.20	63.12	20.34
0.2% MMS	10.60 ±0.18	+2.80	15.27	10.11	66.44	22.11
0.3% MMS	11.60 ±0.29	+3.80	17.21	11.19	68.70	23.54
0.4% MMS	9.30 ±0.31	+1.50	12.12	7.85	59.53	21.90
CD ($p = 0.05$)	–	0.98	–	–	–	–
0.01% SA	9.40 ±0.26	+1.60	10.52	7.71	60.44	19.76
0.02% SA	10.10 ±0.30	+2.30	12.34	8.12	63.77	21.34
0.03% SA	10.50 ±0.22	+2.70	13.31	8.66	66.55	22.55
0.04% SA	9.40 ±0.27	+1.60	10.32	7.54	58.77	19.13
CD ($p = 0.05$)	–	0.88	–	–	–	–
0.01% HZ	8.95 ±0.18	+1.15	10.15	6.12	59.33	18.55
0.02% HZ	9.70 ±0.23	+1.90	11.26	7.23	60.11	20.07
0.03% HZ	10.15 ±0.31	+2.35	12.15	7.92	63.07	20.96
0.04% HZ	9.02 ±0.25	+1.22	8.11	6.61	53.55	18.82
CD ($p = 0.05$)	–	0.95	–	–	–	–

*CD ($p = 0.05$) mean Critical Difference at 5% level of significance

mean plant yield, in the present study, may be attributed to the increased number of flowers, fertile branches and pods. A high degree of correlation between these traits was earlier reported by Khan et al. (2004) in mungbean and Khan and Wani (2005) in chickpea. Increase in mean was much prominent in M_5 as compared to M_4 generation. The increased mean seed yield in M_5 over M_4 and control population could be attributed to effective selection adopted for various yield contributing traits in M_4 generation. Bhatia and Swaminathan (1962) while working with wheat concluded that the mean of the irradiated population shows relatively decreasing trend compared to control if selection was not applied with regard to a specific character. The selection of progenies on the basis of superior mean and greater variance in M_4 was found highly useful in this study which had led to

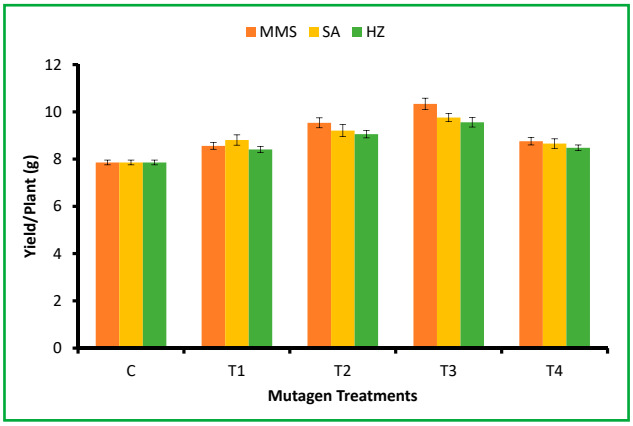

Figure 1 Comparative representation of yield/plant (g) at different mutagen treatment conditions in M_4 generation of urdbean var. PU-19
MMS – 0.1% (T1), 0.2% (T2), 0.3% (T3), 0.4% (T4) and SA; HZ– 0.01% (T1), 0.02% (T2), 0.03% (T3), 0.04% (T4)

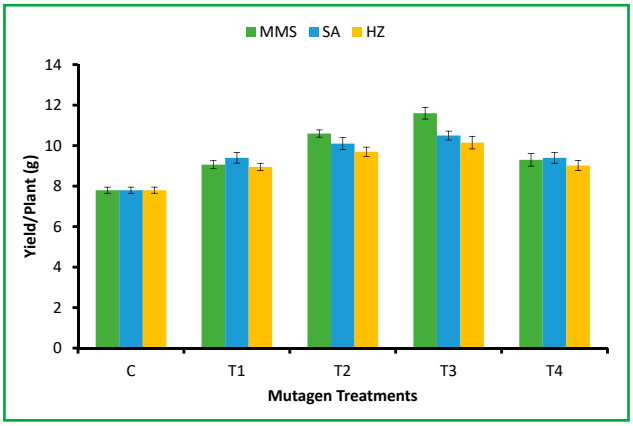

Figure 2 Comparative representation of yield/plant (g) at different mutagen treatment conditions in M_5 generation of urdbean var. PU-19
MMS – 0.1% (T1), 0.2% (T2), 0.3% (T3), 0.4% (T4) and SA; HZ – 0.01% (T1), 0.02% (T2), 0.03% (T3), 0.04% (T4).

increased mean seed yield in M_5 generation. Waghmare and Mehra (2000) achieved considerably increased mean seed yield in M_3 generation after gamma rays and EMS treatments in *Lathyrus sativus*.

Estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance are indispensable in indicating the degree of stability to environmental impacts and the probable trait transmission from parent to offspring (Wani, 2007). In the present study, the genetic parameters like genotypic coefficient of variation, heritability and genetic advance showed an increase over the control in all the treatments. The PCV estimates were higher than the GCV estimates for all the traits of yield, indicating the fair influence of environmental fluctuations on these traits. High heritability estimates for different traits have been found useful for selecting suitable types based on their phenotypic performance. The data, in general, indicates a relatively higher heritability estimates for yield and yield attributes in M_5 generation. Increased heritability values in M_5 in comparison to M_4 generation may be due increased homozygosity of the genes involved. Johnson et al. (1955) advocated that heritability estimates along with genetic advance are usually more helpful than the heritability value alone in predicting the effect of selection. Genetic advance is indicative of genetic progress for a particular trait under suitable selection procedure (Kaul and Garg, 1982), thus carries much significance in self-pollinated crops. The results are in conformity with the reports of Singh et al. (2001) and Raut et al. (2004) in mungbean and chickpea. The higher values of heritability and genetic advance suggest that the variability so evolved could be effectively exploited for the improvement of urdbean crop.

4 Conclusion

The findings of the study suggest that preliminary assessment on induced diversity in genetically complex trait like yield could effectively be done by applying statistical tools on quantitative traits of the crop. The high GCV together with high heritability and genetic advance observed in the selected mutant lines compared to parent genotype confirms the substantial potential for improving yield trait through further selection in the urdbean var. PU-19. Therefore, the high yielding mutant lines screened from the mutagenized populations could be used directly in urdbean breeding program for generating elite mutant cultivars or through hybridization for obtaining desirable segregants in the subsequent generations.

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