Original Research Article

Effect of mutation on seed yield per plant and chlorophyll content in M_3 generation of green gram [*Vigna radiata* (L.) R. Wilczek]

ABSTRACT

Aims: Mutation breeding used to induce quantitative variability in M_3 generation of green gram of two excellent variety GM-4 and Meha with a view to study effect various mutagen and for the estimation of genetic variability parameters like GCV, PCV, Heritability and Genetic advance percent of mean for characters like as seed yield per plant and chlorophyll content.

Place and Duration of Study: The Field experiment was conducted at Instructional Farm, COA, Junagadh Agricultural University, Junagadh during the *Summer*-2015.

Methodology: The experimental material consisted of M_2 derived M_3 seeds which consists of sixty-six M3 progeny lines (64 mutant + 2 controls). The progeny lines were selected on the basis of yield and its associated characters from M_2 generation.

Results: The analysis of variance between family revealed that families differed significantly for chlorophyll content while non-significant for seed yield per plant. GCV and PCV were higher in all the mutagenic family with respect to control for both the characters as well as for both the variety. For both characters, phenotypic coefficient of variation was higher than genotypic coefficient of variation indicating that there was environmental influence on these traits. Heritability exhibited higher in all the mutagenic families and also higher genetic advance was observed. The combined results for heritability showed that the high estimates of heritability and genetic advance were scored for seeds per plant indicating that these characters were under the control of additive genetic effects.

Conclusion: Mutagenic progenies with additive gene effect can be selected for improvement of desirable traits in mungbean.

Keywords: *Key words: Mutation, GCV, PCV, GM-4, Meha, Variability*

1. INTRODUCTION

Green gram [*Vigna radiata* (L.) R. Wilczek] (2n= 2x= 22) is third important pulse after chickpea and Pigeon pea. It is a self-pollinated crop and is an important grain legume of the tropical area and southeast Asia. The worldwide green gram area is around 7.3 million ha with 721 kg/ha yield on average. It is also largely produced by other countries including China, Kenya, Thailand, Tanzania, and Indonesia (R. Nair and Schreinemachers, 2020). The intensifying of this crop is also expanding to non-traditional cultivation horizons primarily because of its shorter growth period and life cycle, great nourishing value, less resource needs, soil ameliorating assets, and extreme global necessity. In India, it is cultivated in Maharashtra, Andhra Pradesh, Rajasthan, Orissa, Karnataka, and Uttar Pradesh. Green

gram contributes 18.07 % of total pulses area and 11.48 % of total pulses production in India. Area, production, and productivity of green gram in India are 34.4 lakh ha, 14 lakh tons and 406.98 kg/ha respectively (iipr.res.in, 2014-15). Among the wide array of pulse cultivation in India, mung bean holds a highly valuable legume crop because of its wider adoptability, low water requirement, ability to improve soil fertility, high protein content and digestibility (Shil and Bandopanhya, 2007). Selection of superior parents exhibiting better heritability and genetic advance for various characters is an essential prerequisite for any yield improvement programme. The knowledge of genetic variability existing within the different parameters contributing to the yield is an important criterion for yield enhancement but in highly self- pollinating crops like green gram, natural variation is narrow resulting in limited selection opportunity. The efficacy of selection depends upon the magnitude of genetic variability for yield and yield contributing traits in the breeding material. Although there are many beneficial aspects, few qualities in product have reduced the speed of breeding programs in yield context (Lambrides and Godwin, 2007). This knowledge of heritability and genetic advance directs the plant breeders to choose exceptional parents to begin an efficient and successful breeding program (Raturi et al., 2015).

Mung is an important crop as it contains more digestible proteins than the other pulses. Pulse is defined as the split cotyledons of dry legume seeds boiled in excess of water, softened, macerated, and used as a soup. It is an excellent source of high-quality protein in the diet of low-income group in developing countries. Mung is generally eaten as complete seed or splits, gram flour, or as germinated sprouts, forming an vital resource of dietetic protein (Nair et al., 2019). Sprouted seeds of mungbean possess essential amino acids like thiamine, niacin, and ascorbic acid (Itoh et al., 2006). When it is allowed to sprout, ascorbic acid (vitamin C) is synthesized, and amount of riboflavin and thiamine are also increased. It contains 24 per cent proteins with all essential amino acids. It is consumed in a variety of ways Sprouted whole beans are used in South Indian diet for preparing curry and a Savory dish and halwa Sprouted beans are widely used as fresh vegetables in Chinese and Japanese foods. Sometimes it is also used as green manuring crop and fodder crop as well. In view of low input requirement and short duration, its cultivation is quite economic. Due to its short maturity, it can be accommodated well in multiple and relay cropping systems compared to other crops, particularly the cereals. Mungbean yield performance ranges between 2.5-3.0 t/ha although there is reduction in production which is staggering low at 0.5 t/ha (Nair *et al*., 2019). The mutations through Gamma rays have been exploited majorly for the improvement in characteristics of several crops (Songsri et al., 2011). Various genetic variations which are stable can be created by mutations as a tool and also used in various experiments.

2. MATERIAL AND METHODS

The Field experiment was conducted at Instructional Farm, COA, Junagadh Agricultural University, Junagadh during the Summer-2015. The experimental material consisted of M2 derived M3 seeds which consists of sixty-six M3 progeny lines (64 mutant + 2 controls). The progeny lines were selected on the basis of yield and its associated characters from M2 generation. Each progeny line is an individual's plant seed. M2 generation consists of two base varieties (GM-4 and meha) and two base mutagens (gamma rays and EMS) which present in Table 1.

Both the mutagens with four levels viz, (gamma rays: 200, 400, 600, 800 Gy and EMS: 0.15, 0.20, 0.25, 0.30 %). From each mutagenic family [Sixteen families (GM-4; 200, 400, 600, 800 Gy and 0.15, 0.20, 0.25, 0.30 %) and (Meha;200, 400, 600, 800 Gy and 0.15, 0.20, 0.25, 0.30 %)] four progeny lines were selected, which leads to sixty-four mutagenic progeny lines in M3 generation. The M3 generation was grown with three replications of randomized block design. Biometric observations were recorded, and individual plant data were used for statistical analysis in order to asses extends of induced variation. Study

carried out for various character which are days to flowering, days to maturity, plant height, numbers of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, seed yield per plant, test weight and chlorophyll content. Significant differences were identified using the least significance difference estimated from the error mean square and tabulated values at the 5% level of significance. The analysis of variance for M3 generation was carried out for Compact Family Block Design as per analysis suggested by Panse and Sukhatme (1978). Parameters estimated were the phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), broad-sense heritability (h2) and expected genetic advance (GA). The estimate of the expected genetic advance as percentage of the mean values were assumed and computed by the formula (Johnson et al., 1955) Heritability in broad sense was calculated by the following formula suggested by Allard (1960). Phenotypic variation and Genotypic variation calculated by the formula suggested by (Burton and DeVane, 1953). Treatment detail listed in below Table 2.

3. RESULTS AND DISCUSSION

Experimental carried out to study the effect of mutation of M2 derived M3 seeds for various characters. M2 generation consists of two base varieties (GM-4 and meha) and two base mutagens (gamma rays and EMS). From each mutagenic family [Sixteen families (GM-4; 200, 400, 600, 800 Gy and 0.15, 0.20, 0.25, 0.30 %) and (Meha;200, 400, 600, 800 Gy and 0.15, 0.20, 0.25, 0.30 %)] four progeny lines were selected, which leads to sixty-four mutagenic progeny lines in M3 generation. The analysis of variance between family revealed that families differed significantly for chlorophyll content while non-significant for seed yield per plant. The analysis of variance in M3 generation for progeny within family indicated significant difference for chlorophyll content. However, few progenies were found to be significant for seed yield per plant (Family 3, 13 and 15). Both the characters were found homogeneous for environmental variation, leads to failure of Bartlett's test and failure of comparison among families and progenies. Therefore, simple RBD was used to identify the best progeny line, analysis of variance revealed significant difference for various characters whereas characters seed yield per plant were found to be non-significant while chlorophyll content found significant (Table 3 and 4).

In M3 generation, family mean of different mutagenic treatments were in positive direction for seed yield per plant. This indicated accumulation of positive gene. However, rest of the character like chlorophyll content had mean values in both the directions. Most of the mutagenic treatments had wide range as compared to their respective control for seed yield per plant and chlorophyll content. This expended range of variation for different measurements generated in progenies of M3 generation could be attributed to substantial changes in the genetic background comprising modifies complexes during mutation process. Wide genotypic and phenotypic difference was observed which indicates that there was significance influence of environment. All the mutagenic treatments show its superiority over control in phenotypic range, GCV, PCV, heritability and genetic advance (Table 5 and 6).

In case of seed yield per plant for GM-4 variety the maximum phenotypic range was observed in 200 Gy gamma rays treatments (1.0-16.7) as compared to control (3.9-8.2). In majority of mutagenic families means shifted toward higher side. Higher PCV, GCV and genetic advance were observed in all mutagenic families as compared to control. Highest heritability (56.9 %) and highest genetic advance (44.2 %) were observed in family-3. The PCV is higher than GCV indicates significant influence of environment. While in case of Meha Phenotypic range was higher in all the mutagenic treatments as compared to control. Highest phenotypic range was observed in 400 Gy gamma rays' treatment (1.7-14.3) (Table 5).

Treatment means was higher in all mutagenic treatment, indicating shifting of means of positive direction. PCV and GCV were higher in all the mutagenic family with respect to control. The PCV is higher than the GCV indicates significant influence of environment. Heritability exhibited higher in all the mutagenic families. Higher genetic advance was observed in family-15 (65.2 %).

For chlorophyll content phenotypic range was observed higher in all the mutagenic treatment as compared to controls in both the varieties. Less genotypic and phenotypic difference indicates that there is less influence of environment. During study of GM-4 variety Phenotypic ranges in all the mutagenic families were greater than control (17.0-21.5). The maximum phenotypic range was observed in 0.25 % EMS treatment (19.9-46.6). The PCV and GCV values were higher in all the mutagenic treatments as compared to control. The high range PCV (20.39 %), GCV (20 17 %), heritability (97.9 %) and genetic advance (41.1 %) were observed in 0.30 % EMS (Table 6).

While in case of meha variety the maximum range was recorded for 0.30 % EMS treatment (12.2-38.8) as compared to control (20.0-30.0). The highest phenotypic mean observed in 800 Gy gamma rays' treatment (31.42) followed by 0.15 % EMS treatment (29.80) as compared to control mean (25.80). Value of PCV and GCV were higher in all the mutagenic treatments except 600 Gy gamma rays and 20 % EMS as compared to control. The higher value of PCV (30.04 %), GCV (29.40 %) and genetic advance (59.3 %) were observed in family-16 and heritability (98.0 %) observed in family-8 as compared to control.GM-4 control showed plants with low (< 20) to moderate (20-30) chlorophyll content. Whereas majority of GM-4 mutants were in moderate to higher category. However, majority of meha control plants were in moderate class interval. Whereas its mutant was more or less equally distributed in moderate and high-class interval.

When comparing 66 progeny lines it was observed that found to be significant for these characters. For chlorophyll content, progeny line 39 (42.1) was significantly higher than the control and at par with progeny-13 (39.3), progeny line 31 (40.2) and progeny line-46 (40.4). All the mutagenic families of meha had showed increase in frequency of plants with seed yield more than seven, as compared to control which have all the plants with seed yield less than seven grams per plant (Fig 1 and 2).

GM-4 control showed plants with low (< 20) to moderate (20-30) chlorophyll content. Whereas majority of GM-4 mutants were in moderate to higher category. However, majority of meha control plants were in moderate class interval. Whereas its mutant was more or less equally distributed in moderate and high-class interval (Fig 3). Environmental influence was high for both the character. Genetic parameters such as heritability & genetic advance increased many folds in almost all characters, as compared to control. The phenotypic and genotypic coefficients of variation increased in all the mutagenic treatments for both of character.

Various genetic variations which are stable can be created by mutations as a tool and also used in various experiments. The effectiveness of mutagen is measured by its ability to induce chlorophyll mutations. A large spectrum of mutations affecting chlorophyll development is observed in M2 and M3 generation. Also, the overall frequency of chlorophyll mutations has been found to be higher in electron beam treated population in comparison to gamma rays treated population (Souframanien et al., 2020). In addition, there are a wide range of morpho, physiological, biochemical, molecular, biotic-abiotic stress tolerant and biofortified impactful mutants identified by various researchers all over the nation and world. The scoring of chlorophyll mutation frequency in M2 on wards generation is one of the most reliable measures for evaluating the mutagenic induced genetic alterations of the mutagen treatments used on the plant ideotype (Chaturvedi and Singh, 1990). Chlorophyll deficient

chimers in M1 generation and their segregation in M2 and M3 generations are often observed in a mutagenized population. In present study also there was wide range of phenotypic variation was observed between treated and control families which is in agreement with earlier findings of Souframanien et al., (2016), Ramchander et al., (2018), Tamilzharasi et al., (2019) and Devi et al., (2020) in black gram.

For seed yield per plant also there was significant shift was observed from M2 to M3 in comparison to controls. Through there is environmental influence as values of PCV were high but breeders will never neglect importance of mutagenic variants they are finding. Some of the noteworthy mutagenic studies fall in alignment with our findings were also reported by Vaishali Mori (2015), Ahir et al., 2018), Wani et al. (2018) in green gram; Bara et al. (2012) in chickpea and Priyanka et al., (2021) in horse gram. Lavanya et al., (2011), Kozgar et al., (2011) and Majhi P. K. and Mogali S. C. (2020) reported significant effect of EMS and gamma rays on yield and yield related traits in green gram. Majority of mutant varieties (64 %) were developed by the gamma rays (Ahloowalia et al. 2004). The M3 is considered to be the most crucial stage for selection to commence, as M3=F3. This ostensibly saves the experiment of his considerable resources because a great deal of (unnecessary) load (of unproductive plants) is shed right in the M3 generation itself. The varieties released in these crops comprise direct mutants or mutant derivatives through inter-mutant or cultivar-mutant hybridizations. Many of the mutants released in India are very popular among farming communities and have contributed substantially in elevating their economic status.

4. CONCLUSION

Effect of mutation in M3 generation of green gram observed that the analysis of variance between family revealed that families differed significantly for chlorophyll content while non-significant for seed yield per plant. The analysis of variance in M3 generation for progeny within family indicated significant difference for chlorophyll content characters showed presence of diversity so the mutagenic families shaving presence in wide range of class intervals as compared to controls. Phenotypic coefficient of variation was higher than genotypic coefficient of variation indicating that there was environmental influence on these traits. In M3 generation, family mean of different mutagenic treatments were in positive direction for seed yield per plant. This indicated accumulation of positive gene. However, rest of the character chlorophyll content had mean values in both the directions. Both the variety GM-4 and Meha which treated by various mutagen exhibit significant difference and exhibited more diversity as compared to control so the outcome of the present investigation can be used directly as a variety or parental lines for future hybridization programme, as majority of progeny lines showed homogeneity for most of the characters and induced mutagenesis plays an important role in improvement of crops like green gram.

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TABLE 1: TREATMENT DETAILS.

Physical Mutagen			Chemical Mutagen		
Variety	**M_3 families**	**Progeny Lines**	**Variety**	**M_3 families**	**Progeny Lines**
GM-4	**T1 (200Gy) Gamma ray**	L-1	**GM-4**	**T_9 (0.15%) EMS (Ethyl**	L-33
		L-2			L-34

	Family-1	L-3		**Methane Sulfonate) Family-9**	L-35
		L-4			L-36
	T2 (400Gy) Gamma ray Family-2	L-5		**T_{10} (0.20%) EMS (Ethyl Methane Sulfonate) Family-10**	L-37
		L-6			L-38
		L-7			L-39
		L-8			L-40
	T3 (600Gy) Gamma ray Family-3	L-9		**T_{11} (0.25%) EMS (Ethyl Methane Sulfonate) Family-11**	L-41
		L-10			L-42
		L-11			L-43
		L-12			L-44
	T4 (800Gy) Gamma ray Family-4	L-13		**T_{12} (0.30%) EMS (Ethyl Methane Sulfonate) Family-12**	L-45
		L-14			L-46
		L-15			L-47
		L-16			L-48
Meha	**T5 (200Gy) Gamma ray Family-5**	L-17	**Meha**	**T_{13} (0.15%) EMS (Ethyl Methane Sulfonate) Family-13**	L-49
		L-18			L-50
		L-19			L-51
		L-20			L-52
	T_6 (400Gy) Gamma ray Family-6	L-21		**T_{14} (0.20%) EMS (Ethyl Methane Sulfonate) Family-14**	L-53
		L-22			L-54
		L-23			L-55
		L-24			L-56
	T_7 (600Gy) Gamma ray Family-7	L-25		**T_{15} (0.25%) EMS (Ethyl Methane Sulfonate) Family-15**	L-57
		L-26			L-58
		L-27			L-59
		L-28			L-60
	T_8 (800Gy) Gamma ray Family-8	L-29		**T_{16} (0.30%) EMS (Ethyl Methane Sulfonate) Family-16**	L-61
		L-30			L-62
		L-31			L-63
		L-32			L-64
CONTROL					
	T_{17} CONTROL Family-17	L-65		**T_{18} CONTROL Family-18**	**L-66**

Table 2: Two base mutagens (gamma rays and EMS) used in the study with mode of action and levels.

Mutagen	Source	Mode of action	Level (Gy and %)

a. Physical Mutagen Gamma Rays	Seeds were treated with ^{60}CO gamma cell 2.8 kR per minute at Bhabha Atomic Research Center, Trombay, Bombay.	Ionization	200, 400, 600 and 800
b. Chemical Mutagen Ethyl Methane Sulphonate (EMS) $C_2H_5OSO_2CH_3$	HI-Media; Bombay Chemical	Alkylation	0.15, 0.20, 0.25 and 0.30 %

Table 3: Analysis of variance (mean square) between families for different characters in M_3 generation of green gram

Source	Mean sum of square			
	Between Family		Among Family	
	Families	Error	Progenies	Error
d.f	17	17	65	65
1. Days to flowering	6.50**	0.82	8.32*	2.28
2. Days to maturity	27.86**	0.38	31.87*	1.85
3. Plant height	24.16**	3.93	49.00*	8.12
4. Number of primary branches per plant	0.10*	0.05	0.19*	0.12
5. Number of clusters per plant	2.74	3.11	7.42	6.70
6. Number of pods per cluster	0.04*	0.02	0.10*	0.05
7. Number of pods per plant	28.77	23.55	69.82	54.41
8. Pod length	0.16**	0.04	0.23*	0.08
9. Number of seeds per pod	0.45**	0.07	0.84*	0.26
10. Seed yield per plant	**2.51**	**2.01**	**5.53**	3.95
11. Test weight	0.12**	0.04	0.33*	0.10
12. Chlorophyll content	**57.18****	0.44	**86.09***	2.65

** = significant at p=0.01, * = significant at p=0.05

Table 4: General ANOVA (control vs. treated) in M3 generation of green gram for seed yield per plant and chlorophyll content.

Sources of variation		Seed yield per plant	Chlorophyll content
	d.f	**MS**	**MS**

Replication	2	**47.3****	**49.1****
Entries over sample	343	**7.4****	**97.3****
AMONG CONTROL	29	3.8	**43.8****
AMONG MUTANTS	313	**7.6****	**91.1****
Control vs. Mutants	1	**29.0***	**3609.0****
Sampling Error	686	5.26	10.20

Fig.1:- Comparision of GM-4 and Meha variety controlled plant with mutagenic plant

Control plant GM-4

Mutagenic plant GM-4

Control plant Meha

Mutagenic plant Meha

234 **Table 5: Phenotypic range, mean, phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation, heritability and genetic advance for seed yield per plant in M_3 generation of variety GM-4 and Meha.**

Treatment	Phenotypic range	Mean	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	H^2 (BS)	GA (%)
GM-4								
T_1 (Family-1) 200Gy Gamma Rays	1.0-16.7	6.21	6.0	0.9	39.55	14.92	14.2	11.6
T_2 (Family-2) 400Gy Gamma Rays	0.6-10.7	5.65	-	-	-	-	-	-
T_3 (Family-3) 600Gy Gamma Rays	0.8-9.5	4.63	3.1	1.7	37.74	28.46	56.9	44.2
T_4 (Family-4) 800Gy Gamma Rays	0.6-10.1	4.49	-	-	-	-	-	-
T_9 (Family-9) 0.15% EMS	0.6-11.7	4.36	-	-	-	-	-	-
T_{10} (Family-10) 0.20% EMS	1.8-13.0	6.02	4.0	1.8	33.07	22.48	46.2	31.5
T_{11} (Family-11) 0.25% EMS	0.6-10.3	5.69	1.6	0.6	21.98	13.86	39.8	18.0
T_{12} (Family-12) 0.30% EMS	1.5-13.5	6.01	6.4	2.5	41.94	26.46	39.8	34.4
T_{17} (Family-17) Control	3.9-8.2	5.79	0.009	0.002	1.62	0.81	25.0	0.8
Meha								
T_5 (Family-5) 200Gy Gamma Rays	0.9-10.0	4.77	-	-	-	-	-	-
T_6 (Family-6) 400Gy Gamma Rays	1.7-14.3	6.03	-	-	-	-	-	-
T_7 (Family-7) 600Gy Gamma Rays	4.1-14.3	6.94	-	-	-	-	-	-
T_8 (Family-8) 800Gy Gamma Rays	0.3-8.9	4.36	2.0	0.8	32.60	20.55	39.8	26.7
T_{13} (Family-13) 0.15% EMS	1.3-11.7	6.06	3.0	1.9	28.60	22.64	62.7	36.9
T_{14} (Family-14) 0.20% EMS	1.3-10.1	6.05	2.5	0.7	26.40	13.55	26.3	14.3
T_{15} (Family-15) 0.25% EMS	0.8-10.3	3.91	4.0	2.5	51.40	40.33	61.5	65.2
T_{16} (Family-16) 0.30% EMS	1.1-14.0	6.28	-	-	-	-	-	-
T_{18} (Family-18) Control	2.6-5.0	3.85	0.004	0.001	1.70	0.97	32.4	1.1

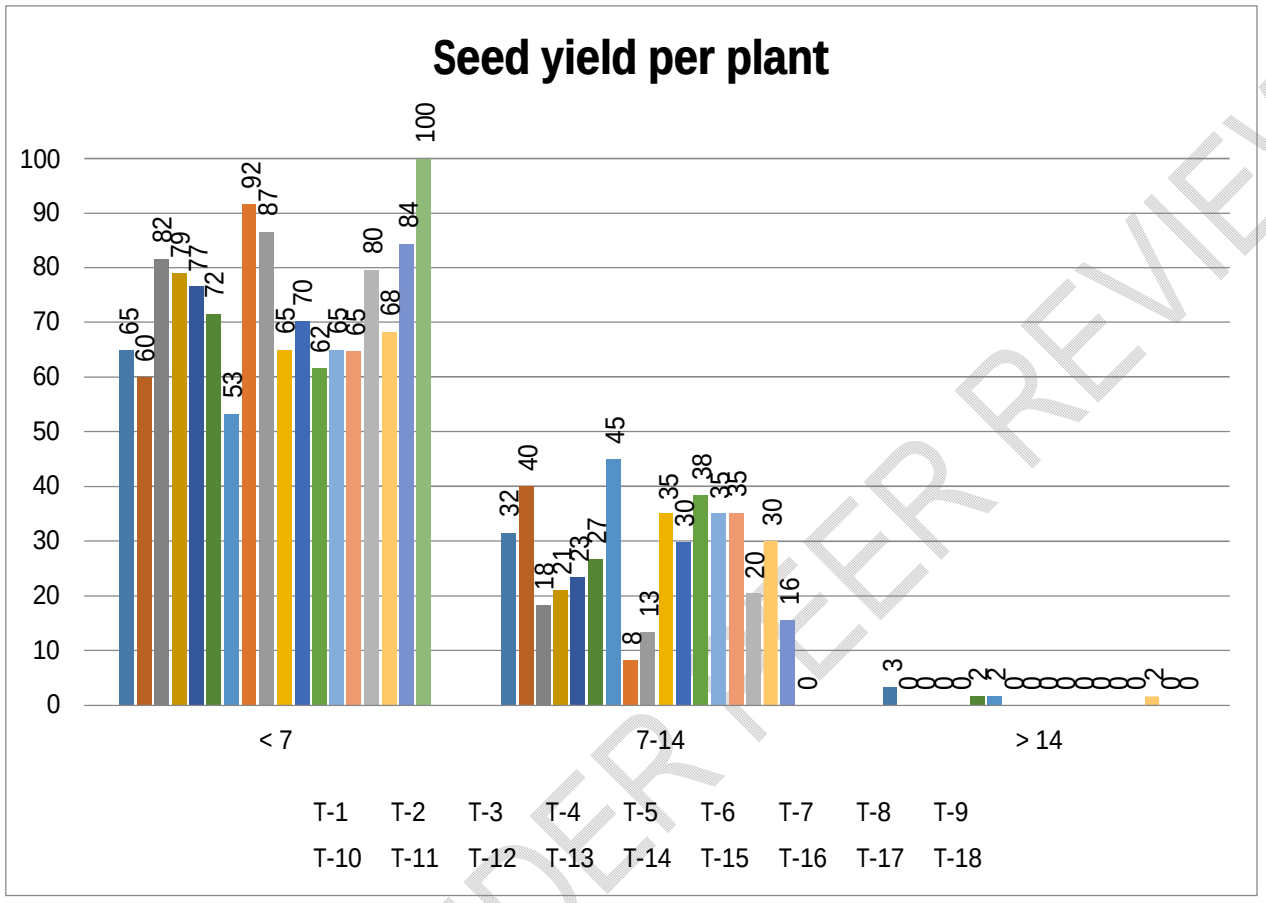
235 - Estimation of variance were negative

Table 6: Phenotypic range, mean, phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation, heritability and genetic advance for chlorophyll content in M_3 generation of variety GM-4 and Meha.

Treatment	Phenotypic range	Mean	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	H^2 (BS)	GA (%)
GM-4								
T_1 (Family-1) 200Gy Gamma Rays	17.3-39.7	29.24	35.0	33.7	20.24	19.84	96.1	40.1
T_2 (Family-2) 400Gy Gamma Rays	26.2-42.8	35.95	8.1	1.8	7.94	3.69	21.6	3.5
T_3 (Family-3) 600Gy Gamma Rays	26.0-39.3	32.88	2.9	1.6	5.21	3.80	53.0	5.7
T_4 (Family-4) 800Gy Gamma Rays	23.3-44.7	33.68	18.9	13.6	12.91	10.94	71.8	19.1
T_9 (Family-9) 0.15% EMS	22.2-38.2	29.36	3.0	0.2	5.93	1.60	7.3	0.9
T_{10} (Family-10) 0.20% EMS	22.2-43.2	29.34	13.2	11.2	12.93	11.40	84.7	21.6
T_{11} (Family-11) 0.25% EMS	19.9-46.6	34.07	55.3	47.1	21.83	20.15	85.2	38.3
T_{12} (Family-12) 0.30% EMS	23.2-43.7	32.95	45.1	44.2	20.39	20.17	97.9	41.1
T_{17} (Family-17) Control	17-21.5	19.19	0.2	0.1	2.40	1.20	24.9	1.2
Meha								
T_5 (Family-5) 200Gy Gamma Rays	18.8-38.0	29.07	14.0	11.8	12.89	11.82	84.2	22.3
T_6 (Family-6) 400Gy Gamma Rays	17.6-36.4	26.01	14.0	10.4	14.39	12.39	74.2	22.0
T_7 (Family-7) 600Gy Gamma Rays	15.7-30.7	23.33	2.6	1.3	6.86	4.95	52.1	7.4
T_8 (Family-8) 800Gy Gamma Rays	22.0-44.6	31.42	35.9	35.2	19.08	18.88	98.0	38.5
T_{13} (Family-13) 0.15% EMS	17.5-38.2	29.80	11.1	9.8	11.17	10.50	88.4	20.3
T_{14} (Family-14) 0.20% EMS	20.3-32.7	25.86	4.1	1.6	7.79	4.84	38.6	6.2
T_{15} (Family-15) 0.25% EMS	19.8-32.8	25.73	-	-	-	-	-	-
T_{16} (Family-16) 0.30% EMS	12.2-38.8	23.25	48.8	46.7	30.04	29.40	95.8	59.3
T_{18} (Family-18) Control	20.0-30.0	25.80	1.6	0.5	4.96	2.84	32.8	3.4

- Estimation of variance were negative

FIG. 2 FREQUENCY DISTRIBUTION (%) OF DIFFERENT MUTAGENIC TREATMENTS ON SEED YIELD PER PLANT.



Where,

T_1 – 200 Gy gamma rays GM-4

T_2 – 400 Gy gamma rays GM-4

T_3 – 600 Gy gamma rays GM-4

T_4 – 800 Gy gamma rays GM-4

T_9 – 0.15 % EMS GM-4

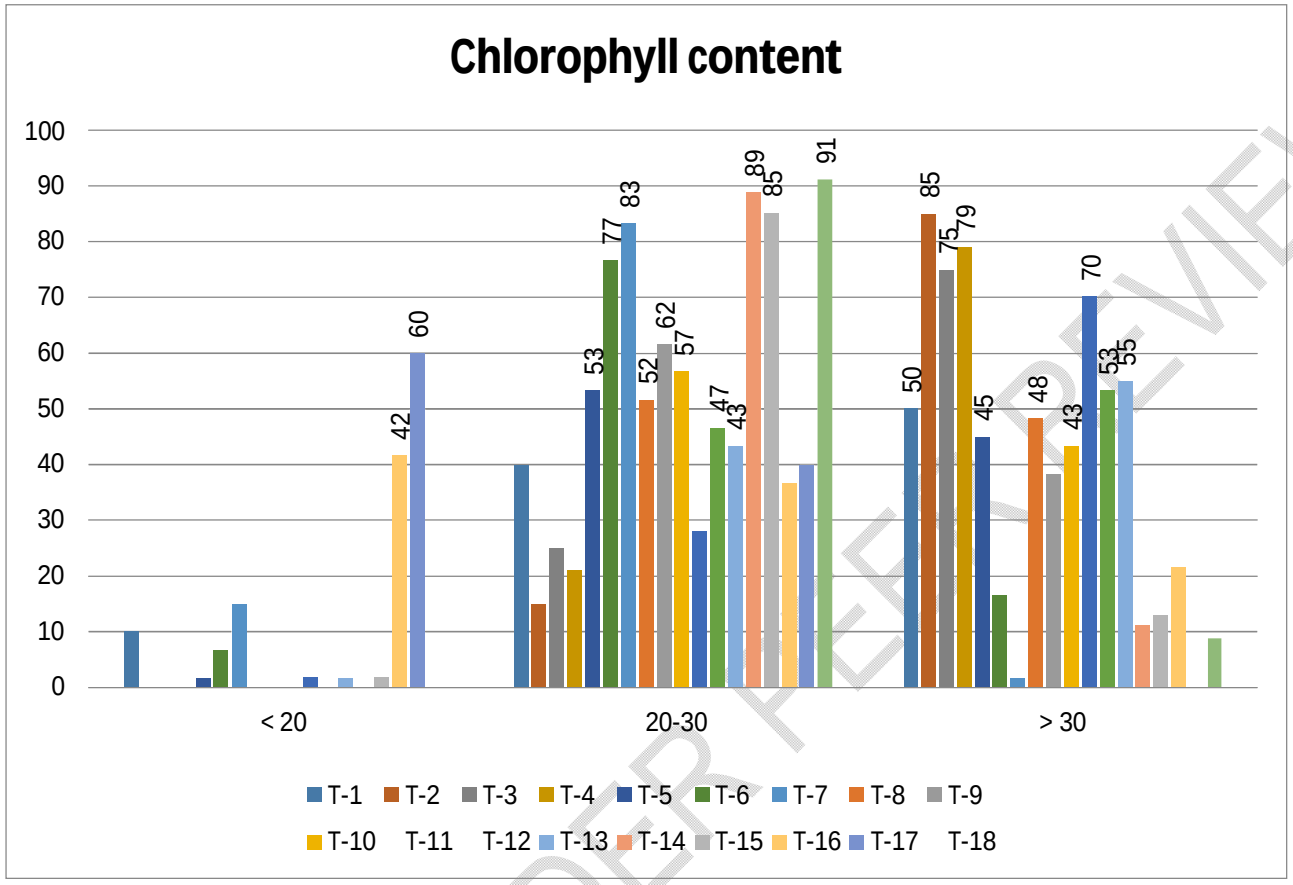
T_{10} – 0.20 % EMS GM-4

T_{11} – 0.25 % EMS GM-4

T_{12} – 0.30 % EMS GM-4

T_{17} – GM-4 control

Fig. 3 Frequency distribution (%) of different mutagenic treatments on chlorophyll content.



Where,

T_1 – 200 Gy gamma rays GM-4

T_2 – 400 Gy gamma rays GM-4

T_3 – 600 Gy gamma rays GM-4

T_4 – 800 Gy gamma rays GM-4

T_9 – 0.15 % EMS GM-4

T_{10} – 0.20 % EMS GM-4

T_{11} – 0.25 % EMS GM-4

T12 – 0.30 % EMS GM-4

T_{17} – GM-4 control