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Identification of early maturing high yielding mutants in Black gram [*Vigna Mungo* (L.) Hepper]

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ABSTRACT

Present study was carried out for identifying early maturing high yielding mutants in black gram [*Vigna Mungo* (L.) Hepper]" in a mutant population generated by using EMS, DMS and their post treatment with respective modifiers IAA and GA on in the background of black gram variety Barkha. The experiment was carried out in compact family block design during *Kharif,* 2005 at Experimental field of Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, Udaipur. Use of EMS 0.4 + 3 x 10^{-3} M IAA induced early maturity with higher yield and also induced variability for other yield contributing traits. On the basis of yield parameters, eight progenies identified as high yielder and eighteen progenies were earlier in maturity than control. Genetic variability parameters viz., GCV, PCV, heritability and genetic advance exhibited high values for yield and yield contributing traits for family derived from use of 0.4% EMS 0.4 and DMS 0.04 with modifiers.

Key words: Ethylmethane sulphonate (EMS), Dimethyl sulphonate (DMS), Indol Acetic Acid (IAA) and Gibberellic Acid (GA), GCV, PCV, Heritability and Genetic advance

Black gram is the fourth important pulse crop in India, which occupies about 12% of the total pulse area and contributing about 8%t to the total pulse production. In spite of its high nutritional value, its productivity is very low due to several reasons including force maturity due to terminal stress. Barkha variety of black gram is well adapted to the climatic conditions of southern Rajasthan. It is liked by the farmers due to its bold, black shining grains but it is late in maturity and faces terminal drought. This strongly thrust the importance of inducing earliness in the background of this well adopted variety. 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. The practical utility of induced mutations for the improvement of quantitatively inherited characters in urd bean is well recognized.

Therefore, present investigation is carried out to induce genetic variability in black gram through mutation breeding by using chemicals mutagens like Ethylmethane sulphonate (EMS) and Dimethyl sulphonate (DMS) and their modifiers viz., Indol Acetic Acid (IAA) and Gibberellic Acid (GA) in order to isolate early maturing and high yielding genotype with shining bold grains.

MATERIALS AND METHODS

In present study, seed of Barkha variety was used for mutation. It was treated with chemical mutagens like Etylmethane sulphonate (EMS), Dimethyle sulphonate (DMS) and their combinations with different plant growth regulators like Indol Acitic Acid (IAA) and Gibberellic acid (GA). The following combinations of mutagens and growth regulators were used. (i) Control (ii) EMS 0.4 per cent (iii) EMS 0.6 per cent (iv) DMS 0.04 per cent (v) DMS 0.06 per cent (vi) EMS 0.4 + 3 x 10^{-3} M IAA (vii) EMS 0.4 + 3 x 10^{-4} M IAA (viii) EMS 0.6 + 3 x 10^{-3} M IAA (ix) EMS 0.6 + 3 x 10^{-4} M IAA (x) DMS 0.04 + 3 x 10^{-3} M GA (xi) DMS 0.04 + 3 x 10^{-4} M GA. Normal appearing competitive ten M_1 plants (progenies) from each selected treatment (families) as below were advanced to M_2 generation.

Experimental Methodology

Normal appearing M_1 generation plants from each treatment (), which exhibited relatively high fertility, were selected to advance in M_2 generation. The M_2 generation was raised in compact family block design with three replications. Each treatment was taken as family and within treatment the individual plant progeny was taken as progenies. All the progenies within family were randomized; likewise the family blocks were also randomized. Progenies were sown in single row plot of three meter length and distance between plant to plant and row to row () was maintained as 30 x 10 cm.

Procedure of Observations

Observations were recorded on ten randomly selected plants in each progeny of all the families except days to 50 per cent flowering and days 75 per cent maturity, which were recorded on plot basis.

Statistical methods

The analysis of variance for each of the family was done separately according to Panse and Sukhatme (1978). The components of variance and their expectations are given as following.

Analysis of variance for differences between families and within families (between progenies)

Source	d.f.	S.S.	M.S.	EMS
Replication	r – 1	SSr	MSr	
Families	n –1	SSn	MSn	$\sigma^2_e + rp\sigma^2_F$
Progenies	p - 1	SSp	MSp	$\sigma^2_e + r\sigma^2_P$
Error		SSe	MSe	σ^2_e
Total (T)		SS(T)		

Where,

r, n, p = replications, families, progenies in a family and error, respectively

(i) Critical difference for difference between families :

$$CD = \sqrt{\frac{2\,MSe}{Pr}} \times t \text{ value at 5\% level of significance of error d. f.}$$

(ii) Critical difference for differences between progenies within family :

$$CD = \sqrt{\frac{2\,MSe}{r}} \times t \text{ value at 5\% level of significance of error d. f.}$$

(iii) Coefficient of variation

$$CV = \frac{\sqrt{MSe}}{\bar{X}} \times 100$$

Variability parameters:

Following genetic variability parameters calculated in all those families, which revealed significant progeny differences.

(i) Genotypic Coefficient of Variation (GCV) :- The magnitude of genetic variation existing in a character was worked out by the formula given by Burton (1952).

$$GCV = \frac{\sqrt{V_g}}{\bar{X}} \times 100$$

Where,

$$V_g = \frac{MSp - MSe}{r}$$

Where,

V_g = Genotypic variance

X = Mean of the character under study

MSp = Mean square due to progenies

MSe = Error variance

r = Number of replications.

(ii) Phenotypic Coefficient of Variation (PCV) :- The magnitude of phenotypic variation existing in a character was estimated by using the formula suggested by Burton (1952).

$$PCV = \frac{\sqrt{Vph}}{\bar{X}} \times 100$$

$$V_{ph} = V_g + MSe$$

Where,

V_{ph} = Phenotypic variance

X = Mean of the character under study

V_g = Genotypic variance

MSe = Error variance

(iii) Heritability:- Heritability in broad sense was estimated by using following formula proposed by Burton and Davane (1953), Jhonson *et al.* (1955) and Hanson *et al.* (1956).

$$H = \frac{V_g}{V_{ph}} \times 100$$

Where,

V_g = Genotypic variance

V_{ph} = Phenotypic variance

(iv) Genetic gain:- It is the genetic advance expressed as per cent of mean :

$$\text{Genetic gain} = \frac{GA \times 100}{\bar{X}}$$

Where genetic advance (GA) was estimated using the formula suggested by Robinson *et al.* (1949), Johnson *et al* (1955).

$$GA = k[V_g/V_{ph}] \times \sqrt{V_{ph}}$$

Where,

V_g = Genotypic variance

V_{ph} = Phenotypic variance

X = Mean of the character under study

K = Selection differential (constant) at 5 % selection intensity (Allard, 1960) i.e. 2.06

Result and Discussion

Analysis of variance revealed that highly significant differences existed between the families for all the traits (Table1).

(i) Days to 50 per cent flowering: Progenies differences were significant in all the families except control and EMS 0.6 per cent (Table 1). On the basis of mean family EMS 0.4 +3 x 10^{-4} M IAA (37.77) was significantly earlier in flowering than control (38.53). Maximum range for days to 50 per cent flowering was recorded in family EMS 0.4 + 3 x 10^{-3} M IAA (35.67-41.00) against the control (38.33-39.00) (Table 2). Maximum coefficient of variation was observed in family EMS 0.4 + 3 x 10^{-3} M IAA (7.70) than control (1.26).

Table 1: Mean squares for different characters in Barkha variety of black gram in M2 generation

Sources	Days to 50 per cent flowering	Days to 75 per cent maturity	Plant height	Number of branches per plant	Number of pods per plant	100 seed weight	Seed yield per plant	Biological yield	Harvest index	Seed Protein content
Replication	0.91	0.371	1.97 *	0.08**	0.65	0.010	0.02	0.27**	0.39 *	0.19
Between Family	4.60**	2.39**	68.14**	1.92**	17.11**	0.19**	0.98**	66.90**	65.27**	8.27**
Within Family										
Control	0.24	0.60	0.39	0.05	0.04	0.01	0.01	0.15	0.12	0.14
EMS 0.4 per cent	3.65**	6.85**	12.07**	0.46**	9.30**	0.05	0.22**	7.42**	6.22**	2.44**
EMS 0.6 per cent	0.83	2.52**	18.11**	0.16**	0.87	0.02	0.02	17.06**	5.37**	1.05**
DMS 0.04 per cent	1.87 *	6.37**	10.64**	0.13**	0.72	0.05	0.07**	18.32**	4.68**	2.12**
DMS 0.06 per cent	2.74**	8.85**	19.60**	0.17**	0.83	0.03	0.02	9.16**	3.07**	2.18**
EMS 0. 4 + 3 x 10^{-3} M IAA	8.67**	15.20**	12.22**	0.09**	7.90**	0.02	0.10**	12.95**	10.17**	2.95**
EMS 0. 4 + 3 x 10^{-4} M IAA	6.89**	11.93**	27.90**	0.21**	3.99**	0.03	0.20**	11.04**	10.11**	0.91**
EMS 0.6 + 3 x 10^{-3} M IAA	8.21**	9.66**	17.01**	0.33**	2.13**	0.02	0.10**	11.99**	4.16**	2.52**
EMS 0.6 + 3 x 10^{-4} M IAA	5.70**	10.16**	17.48**	0.52**	1.54**	0.04	0.03**	15.20**	7.43**	3.04**
DMS 0.04 + 3 x 10^{-3} M GA	2.37**	8.13**	15.22**	0.48**	5.19**	0.06	0.12**	15.62**	10.18**	0.26
DMS 0.04 + 3 x 10^{-4} M GA	2.00 *	2.90**	9.79**	0.67**	2.52**	0.03	0.12**	13.99**	6.01**	0.80**
Error	0.86	0.51	1.15	0.03	0.55	0.03	0.01	0.12	0.24	0.17

*, ** Significant at 5% and 1% level of significance, respectively

(ii) **Days to 75 per cent maturity:** Progeny differences were significant in all the families except control (Table 1). Family EMS 0.4 + 3 x 10^{-3} M IAA (78.83) and family EMS 0.4 + 3 x 10^{-4} M IAA (78.90) were significantly earlier in maturity than control (79.77). Highest range for days to 75 per cent maturity was observed in family EMS 0.6 + 3 X 10^{-3} M IAA (76.00 – 82.33) against control (79.00–80.33). Coefficient of variation in control was 0.97 per cent, which increased to 4.95 in family EMS 0.4 + 3 X 10^{-3} M IAA (Table 2). Eighteen progenies exhibited early maturity than control. The variability parameters recorded for all the families were low in magnitude except EMS 0.4 + 3 X 10^{-3} M IAA (GCV = 2.69, PCV = 2.74, Heritability = 96.59, Genetic gain = 5.45) (Table 3).

(iii) **Plant height (cm):** Progeny differences were significant in all the families except control (Table 1). Maximum plant height was observed in family EMS 0.4 +3 x 10^{-3} (28.60) than control (27.40). Wide range was observed in family DMS 0.06 per cent (20.14-32.12) than control (26.93-27.86). Coefficient of variation in control was 2.29 per cent, which increased in all the families. Highest coefficient of variation was observed in family EMS 0.4 + 3 x 10^{-4} M IAA (18.91) (Table 2). Thirty four progenies exhibited significant increase in plant height than control in all the mutagenic families.

(iv) **Number of primary branches per plant:** Progeny differences were significant in all the families except control (Table 1). Maximum number of primary branches per plant was observed in family EMS 0.4 + 3 x 10^{-3} M IAA (2.80) than control (2.56). Highest range for this trait was observed in family DMS 0.04 + 3 x 10^{-3} MGA (1.87-3.14) as compared to (2.36 - 2.69) control (Table 2). Coefficient of variation was maximum in family DMS 0.04 +3 x 10^{-4} M GA (37.08). Higher number of primary branches per plant was observed in twenty seven progenies over all the families.

(v) **Number of pods per plant:** Statistically significant differences between progeny were recorded in all the families except control, EMS 0.6 per cent, DMS 0.04 per cent and DMS 0.06 per cent (Table 1). None of the families exhibited positive shift in number of pods per plant as compared to control (15.86). Wide range for number of pods per plant was observed in family DMS 0.04 + 3 x 10^{-3} M GA (13.60 - 18.23) against control (15.67 - 16.03). Coefficient of variation was 1.20 percent in control. It was increased at all the mutagenic treatments and highest in family EMS 0.4 per cent (19.40) (Table 2). Among all the families six progenies exhibited higher number of pods per plant than control.

(vi) **100-seed weight (g):** No significant differences between progenies were observed for 100-seed yield than control (4.37). Coefficient of variation was 1.82 per cent in control and it was increased in all the families. Range for seed yield per plant was observed narrow in all the families than control (Table 2). None of the progeny was found superior than control for 100-seed weight.

(vii) **Seed yield per plant (g):** Progeny differences were found significant in all the families except control, EMS 0.6 per cent and DMS 0.06 per cent (Table 1). Grain yield was higher in two families viz., EMS 0.4 per cent (3.78) and family EMS 0.4 + 3 x 10^{-3} M IAA (3.70) than control (3.60). Coefficient of variation was 1.96 per cent in control which increased in all the mutagenic treatment and it ranged from 1.96 per cent (control) to 12.64 per cent (EMS 0.4 + 3 x 10^{-4} M IAA). Wide range for seed yield per plant was observed in

Table 2 : Mean, range and coefficient of variation for different characters in Barkha variety of black gram in M2 generation.

Families		Days to 50 pre cent flowering	Days to 75 per cent maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	100 seed weight (g)	Seed yield per plant (g)	Biological yield per plant (g)	Harvest index (%)	Seed Protein content (%)
Control	M	38.53	79.77	27.40	2.56	15.86	4.37	3.60	16.39	18.03	24.45
	R	38.33-39.00	79.0-80.33	26.93-27.86	2.36-2.69	15.67-16.03	4.29-4.46	3.53-3.65	16.08-17.17	17.10-18.49	24.07-24.88
	CV	1.26	0.97	2.29	8.38	1.20	1.82	1.96	4.53	4.35	2.72
EMS 0.4 per cent	M	38.50	79.70	27.53	2.59	15.72	4.30	3.78	18.38	17.13	24.67
	R	35.67-39.33	76.33-81.67	22.67-29.68	1.94-3.08	14.10-19.17	4.09-4.46	3.52-4.34	16.30-21.20	15.48-19.33	23.14-26.07
	CV	4.96	3.28	12.62	26.25	19.40	5.31	12.50	14.82	14.55	6.34
EMS 0.6 per cent	M	39.20	80.67	24.39	2.12	14.21	4.21	3.26	21.40	13.34	23.88
	R	38.33-40.00	79.33-82.00	20.76-28.04	1.83-2.54	13.07-15.00	4.03-4.36	3.14-3.39	17.97-24.20	11.67-15.15	23.07-25.10
	CV	2.32	1.97	17.45	18.68	6.56	3.73	4.48	19.30	17.37	4.29
DMS 0.04 per cent	M	38.80	80.43	25.46	2.26	14.81	4.24	3.36	18.87	15.22	24.30
	R	37.33-40.00	77.67-82.67	22.25-28.09	1.94-2.58	13.77-15.53	4.00-4.37	3.20-3.65	16.83-20.97	13.00-16.85	23.15-26.03
	CV	3.52	3.14	12.81	15.84	5.74	5.47	8.12	22.69	14.21	5.99
DMS 0.06 per cent	M	39.00	80.70	24.15	1.90	13.70	4.18	3.27	21.53	13.24	24.24
	R	38.00-40.67	78.33-83.33	20.14-32.12	1.59-2.31	12.79-14.33	4.05-4.39	3.16-3.44	18.83-24.83	11.99-14.63	23.35-26.28
	CV	4.24	3.69	18.33	21.80	6.64	4.01	4.51	14.06	13.24	6.08
EMS 0. 4 + 3 x 10^{-3} M IAA	M	38.23	78.83	28.60	2.80	15.84	4.37	3.70	20.54	15.42	24.19
	R	35.67-41.00	76.00-82.00	25.56-32.29	2.54-3.09	14.10-18.73	4.25-4.45	3.53-4.07	17.80-24.23	13.25-18.60	23.11-26.22
	CV	7.70	4.95	12.22	10.65	17.74	2.92	8.50	20.35	20.68	7.10
EMS 0. 4 + 3 x 10^{-4} M IAA	M	37.77	78.90	27.93	2.58	15.97	4.28	3.51	20.03	15.02	23.62
	R	35.33-39.67	75.67-81.00	23.64-32.74	2.22-2.30	14.90-18.13	4.14-4.42	3.32-3.94	17.67-23.23	12.49-18.23	23.00-24.22
	CV	6.95	4.38	18.91	17.78	12.51	3.86	12.64	16.59	21.16	4.03
EMS 0.6 + 3 x 10^{-3} M IAA	M	38.60	79.70	27.91	2.37	14.56	4.23	3.35	20.71	13.99	24.94
	R	35.00-40.67	76.00-82.33	23.90-31.12	1.89-2.84	13.53-16.47	4.03-4.33	3.21-3.71	17.90-23.50	12.21-15.55	23.14-26.11
	CV	7.42	3.90	14.78	24.11	10.03	3.55	9.46	16.72	14.58	6.36
EMS 0.6 + 3 x 10^{-4} M IAA	M	38.67	79.47	27.87	2.43	14.59	4.39	3.27	19.75	14.35	24.78
	R	37.00-41.00	76.67-82.33	23.80-30.19	1.74-2.85	13.37-15.60	4.11-4.46	3.15-3.54	17.47-24.23	11.62-16.69	23.24-26.51
	CV	6.18	4.01	15.00	29.58	8.51	4.35	5.63	19.75	18.99	7.04
DMS 0.04 + 3 x 10^{-3} M GA	M	38.43	79.27	27.38	2.38	14.76	4.16	3.42	20.67	14.33	23.34
	R	36.33-39.67	76.00-81.67	23.88-29.95	1.87-3.14	13.60-18.23	3.95-4.41	3.21-3.93	17.90-23.67	12.05-17.53	23.11-24.00
	CV	4.01	3.60	14.25	29.09	15.42	5.78	10.05	19.13	22.26	2.20
DMS 0.04 + 3 x 10^{-4} M GA	M	38.23	79.53	26.77	2.20	14.80	4.26	3.39	19.67	14.81	23.57
	R	37.33-39.67	77.67-81.00	23.52-29.48	1.75-2.89	13.80-16.90	4.08-4.40	3.23-3.91	17.07-23.83	12.38-16.34	23.00-24.11
	CV	3.70	2.14	11.69	37.08	10.72	3.75	10.25	19.02	16.56	3.80
X		38.54	79.72	26.85	2.38	14.98	4.27	3.45	19.81	14.99	24.18
Se		0.169	0.131	0.196	0.031	0.135	0.032	0.021	0.062	0.089	0.076
CD 5%		0.471	0.364	0.546	0.086	0.376	0.088	0.059	0.174	0.248	0.212
CD 1%		0.621	0.480	0.720	0.113	0.496	0.117	0.078	0.229	0.327	0.279
CV		2.399	0.897	3.995	7.088	4.928	4.068	3.351	1.723	3.252	1.718

all the families than control (3.53 - 3.65) (Table 2). In all the families only eight progenies were statistically superior for grains yield per plant than control. Maximum value of variability parameters was observed in family EMS 0.4 + 3 x 10^{-4} M IAA (GCV = 6.86, PCV = 7.06, Heritability = 94.46 and Genetic gain = 13.73) followed by family DMS 0.04 + 3 x 10^{-3} M GA (GCV=5.44, PCV = 5.63, Heritability = 93.39 and Genetic gain = 10.83) (Table 3).

(viii) **Biological yield per plant (g):** For biological yield per plant progenies differences were significant in all the families except control (Table 1). Biological yield was significantly higher in all the families than control (16.39). Highest biological yield was observed in family DMS 0.06 per cent (21.53). Increase in range was observed in all the families than control (16.08-17.17). Higher coefficient of variation was observed in all the treatments than control (4.53). Maximum coefficient of variation (22.69) was observed in DMS 0.04 per cent (Table 2). Among all the families thirty five progenies were superior for biological yield per plant over control.

(ix) **Harvest index (%):** For harvest index progeny differences were significant in all the families except control (Table 1). None of the family exhibited significant increase in harvest index than control (18.03), though increased in range was exhibited by all the families. Highest coefficient of variation was observed in DMS 0.04 + 3 x 10^{-3} M GA (22.26) than control (4.35) (Table 2). One progeny among all the families was found superior than control.

(x) **Seed Protein content (%):** Significant progeny differences were observed in all the families except control and DMS 0.04 + 3 x 10^{-3} M GA (Table 1). Seed Protein content was significantly higher in family EMS 0.4 per cent (24.67), EMS 0.6 + 3 x 10^{-3} M IAA (24.94) and EMS 0.6 + 3 x 10^{-4} M IAA (24.78) than control (24.45). Narrow range for protein content was observed in all the families. Coefficient of variation was highest in EMS 0.4 + 3 x 10^{-3} M IAA (7.10) than control (2.72) (Table 2). Ten progenies among all the families were significantly superior to control for protein content.

Analysis of variance of M_2 generation revealed significant inter-family differences for all the traits. This included that different loci/genes have been affected in the progenies in respect of all traits (Mahala *et al.*, 1999). Progeny differences were significant in all most all the families for all the traits except 100-seed weight.

The mean values of different characters shifted either to positive or negative direction from the control due to mutagenic treatments. EMS 0.4 + 3 x 10^{-3} M IAA treatment exhibited early maturity with higher number of primary branches per plant, plant height and seed yield. EMS 0.4 per cent was also efficient treatment for seed yield and seed protein content. High estimate of coefficient of variation with increased range for most of the traits indicate induction of polygenic mutants. Similar observations were recorded by Prema Manapure *et al.* (1998) and Solanki and Joshi (2000).

The coefficient of variation and range were higher in all the families as compared to their respective control for all the traits. These results are in broad conformity with those of earlier researchers (Khan, 1984; Khan and Khan, 1984 and Solanki and Sharma, 2005).

The genotypic and phenotypic coefficient of variation gave an idea about the relative magnitude of variability. Gap between genotypic coefficient of variation and phenotypic coefficient of variation was narrow which reflected lesser degree of environmental influence on the genotypic variability. Similar trend were also observed by Ahmed and Yaqoob (1993) in mungbean and Hipziba and Subramanium (1994) in black gram.

EMS 0.4 per cent with IAA induced high genotypic and phenotypic coefficient of variations for most of the yield traits. The efficiency with which genotypic variability can be exploited for improvement through selection depends on its heritability (Burton 1952). A character possessing higher GCV with high heritability can be easily improved by selection. In present investigation high heritability was recorded for seed protein content, biological yield and harvest index in almost all the families. These results were in accordance with the findings of Vandna and Dubey (1992) in black gram.

In present study, high value of genetic gain was observed in all most all the families for biological yield per plant and harvest index. Variability coupled with high heritability and greater expected genetic gain is an induction of greater role of additive gene effects in genetic control of the given character. Character with greater contribution and additive gene effect can be easily improved through selection (Panse, 1978). Higher genotypic variability along with high heritability and greater genetic gain was recorded in family EMS 0.4 + 3 x 10^{-3} M IAA ,EMS 0.4 +3 x 10^{-4} M IAA and DMS 0.04 + 3 x 10^{-3} M GA for grains yield and most of the traits. These results are in agreement with those reported by Hipziba and Subramaniam (1994).

Table 3: Estimates of variability parameters in Barkha variety of black gram in M2 generation

Characters/ families	GV (%)	PV (%)	GCV (%)	PCV (%)	H (in broad sense) (%)	GG (%)
Days to 75 per cent maturity						
Control	0.11	0.32	0.42	0.71	34.60	0.50
EMS 0.4 per cent	1.52	3.12	1.55	2.22	48.66	2.22
EMS 0.6 per cent	0.55	1.17	0.92	1.34	47.04	1.30
DMS 0.04 per cent	1.77	2.19	1.66	1.84	80.90	3.07
DMS 0.06 per cent	2.57	2.82	1.99	2.08	91.20	3.91
EMS 0. 4 + 3 x 10^{-3} M IAA	**4.51**	**4.67**	**2.69**	**2.74**	**96.59**	**5.45**
EMS 0. 4 + 3 x 10^{-4} M IAA	3.45	3.83	2.36	2.48	90.23	4.61
EMS 0.6 + 3 x 10^{-3} M IAA	2.76	3.17	2.09	2.23	87.15	4.01
EMS 0.6 + 3 x 10^{-4} M IAA	2.84	3.48	2.12	2.35	81.57	3.94
DMS 0.04 + 3 x 10^{-3} M GA	2.29	2.74	1.91	2.09	83.40	3.59
Seed yield per plant						
Control	0.00	0.01	0.00	0.00	0.00	0.00
EMS 0.4 per cent	0.06	0.08	6.47	7.55	73.47	11.43
EMS 0.6 per cent	0.00	0.01	1.63	3.57	20.98	1.54
DMS 0.04 per cent	0.02	0.03	4.28	4.77	80.66	7.92
DMS 0.06 per cent	0.01	0.03	0.00	0.00	0.00	0.00
EMS 0. 4 + 3 x 10^{-3} M IAA	0.03	0.04	4.41	5.11	74.48	7.84
EMS 0. 4 + 3 x 10^{-4} M IAA	**0.06**	**0.06**	**6.86**	**7.06**	**94.46**	**13.73**
EMS 0.6 + 3 x 10^{-3} M IAA	0.03	0.04	4.87	5.76	71.45	8.47
EMS 0.6 + 3 x 10^{-4} M IAA	0.00	0.03	0.00	0.00	0.00	0.00
DMS 0.04 + 3 x 10^{-3} M GA	**0.03**	**0.04**	**5.44**	**5.63**	**93.39**	**10.83**
DMS 0.04 + 3 x 10^{-4} M GA	0.03	0.04	5.46	5.90	85.78	10.42

Conclusion

Based on the results summarized above it is concluded that family EMS 0.4 + 3 x 10^{-3} M IAA ,EMS 0.4 +3 x 10^{-4} M IAA and DMS 0.04 + 3 x 10^{-3} M GA exhibited higher values for variability parameters for most of the traits studied. EMS 0.4 treatment along with modifier was found to be the most efficient treatment, which induced early maturity along with high mean for yield and yield contributing traits. Range and variance was also increased for most of traits. It also exhibited high values of variability parameters indicating polygenic mutants. In all, there were eight progenies identified, which were higher in yield and yield contributing traits. Eighteen progenies were early in maturity than control. Therefore, these treatments and progenies should be carried further in M_3 generation to isolate early maturing, high yielding lines.

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