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# Induction of genetic variability through chemical and antibiotic mutagens in $M_2$ generation of castor (*Ricinus communis* L.)

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**Abstract**

Mutagenesis study in castor (*Ricinus communis* L.) was carried out to induce macro and micro mutational changes in two castor genotypes *i.e*., VP 1 (M) and SKI 215 using sole treatments of chemical and antibiotic *viz*., ethyl methane sulphonate (EMS) and streptomycin sulphate (S.S.). For mutagenesis, the germinating seeds of two genotypes of castor treated with EMS (50 and 60 mM) and streptomycin sulphate (1000 and 1500 ppm) studied by comparing their respective untreated controls. The $LD_{50}$ (Lethal dose) value was determined based upon the seed germination percentage. The analysis of variance between families revealed that mean squares of the ten families differed significantly for all the characters. The analysis of variance in $M_2$ generation between progenies within family indicated that progeny mean squares were significant for all the characters. This indicated that considerable variation was observed between progenies within families due to mutation treatments. The GCV and PCV higher in both the mutagenic treatments for all the characters except number of node up to primary raceme for SKI 215 and number of capsule on primary raceme in VP 1 (M). High estimate of GCV for above said characters indicated that sufficient genetic variability and selection based on genotype would be effective and little influence of environment present. High PCV which indicated that most of the characters were high influenced by the environment and selection should not be efficient. High broad sense heritability with high genetic advance as percent of mean was observed for seed yield per plant which indicates that expression of these traits was governed by additive gene action and as a result there was a scope for improving these traits through adopting selection procedure during advancement of progenies of mutant generations.

**Keywords:** Broad sense heritability, castor, mutation, $M_2$ generation, variability

## Introduction

Castor (*Ricinus communis* L., 2n = 2x = 20) is an industrially important non-edible oilseed crop widely cultivated in the arid and semi-arid regions of the world (Govaerts *et al*., 2000) [9]. Castor is believed to have most probably originated in Ethiopian-East African region. Its monoecious nature favours cross-pollination and it is up to the extent of 50 percent. It is essentially a semi-tropical, intermediate perennial plant, but it has naturalized as annual/seasonal crop plant throughout the world in frost free zones. It has an ability to grow under low-rainfall and low-fertility conditions, and hence it is most suitable for dry land farming.

Castor is a very ancient oil seed crop cultivated because of high oil content of the seeds, which ranges between 42 to 58 percent. The castor oil is unique in the sense that 84-90 percent of it is composed of a single fatty acid, *i.e*., *ricinoleic* acid. The refined oil also has a good domestic market as medicines and storage grains preservatives. The castor oil is different from other vegetable oils in the sense that it does not freeze even under adverse temperatures of -12 °C to -18 °C. It is, therefore, considered as the best lubricating agent particularly for both high speed engines and aeroplanes.

The success of mutation breeding lies in creating appropriate genetic variability without many associated deleterious effects in plant type and its performance in terms of productivity and nutritional alternations. Micro mutation are expected to be more effective in inducing higher proportion of desirable mutations and providing future base for selection through induction of enormous polygenic variability (Solanki and Sharma, 1999) [19].

Mutations are of two types, spontaneous or natural and artificial or induced. Frequency of natural mutation is very low and hence, induced mutations are used to obtain genetic variability for qualitative and quantitative traits. Induced mutagenesis is recognized as a potential tool for genetic improvement in castor.

## Materials and Methods

The experiment entitled "Mutagenesis study in castor (*Ricinus communis* L.)" was carried out at the Center for Oilseeds Research, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat during *Kharif* 2020-21 and *Kharif* 2021-22. Using two genotypes of castor *viz*., Pistillate inbred line: VP 1 (M) and Intersperse staminate inbred line: SKI 215. Both genotypes were obtained from Center for Oilseeds Research, S. D. Agricultural University, Sardarkrushinagar, Gujarat.

One chemical mutagens ethyl methane sulphonate (EMS) with 50 mM and 60 mM and one antibiotic mutagen streptomycin sulphate with 1000 ppm and 1500 ppm were employed for different mutagenic treatments. Application of chemical and antibiotic treatments were performed at Department of Genetics and Plant Breeding, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar in three sets of treatments and each having hundred seeds of respective genotype. For every experimental set the solutions for treatment of EMS and streptomycin sulphate were freshly prepared. Before giving the chemical and antibiotic treatment to the seeds of both genotypes were presoaked in distilled water for 24 hrs than after immersed in mutagen solution for overnight with intermittent shaking. After completion of incubation period, the treated seed samples were surface dried on a blotting paper. Seeds of both the genotypes only presoaked in distilled water were used as control for respective genotypes. The set of treatment were grown in germination paper at laboratory condition and same was also grown in field condition as second set $M_1$ generation and then germination percentage was counted after 15 days at laboratory condition and Center for Oilseeds Research, S. D. Agricultural University, Sardarkrushinagar during *kharif*-2020. Different concentrations were evaluated by counting their germinated healthy seedlings of both genotypes in $M_1$ generation.

$M_2$ generation was raised during *Kharif* 2021 at Center for Oilseeds Research, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat in a Compact Family Block Design with three replications. The experiment consisted of 10 main treatments (families). Ten progenies selected randomly from each treatment of $M_1$ and they were self-fertilized using paper bags enclosed with 'U" pins. Self-seeds of those 10 plant considered as progenies of respective family were utilized for growing $M_2$ generation in a plant to progeny manner from respective treatments which were considered as families. All the treatments including untreated controls of both the genotypes was consisted to families and randomly selected ten plants to progenies which have sufficient seed that were grown to three replication *i.e*., ten dibbled of each progeny grown in compact family block design per replication.

Seeds were dibbled by hand, at a spacing of 120 cm between rows and 60 cm between plants within row. The crop was irrigated as and when required; other cultural and agronomical practices were followed as per recommendation for raising castor crop in this region. Different ten quantitative traits studied, namely days to 50% flowering of primary raceme, days to maturity of primary raceme, plant height up to primary raceme, number of node up to primary raceme, effective length of primary raceme, number of effective branch per plant, number of capsule on primary raceme, seed yield per plant, 100-seed weight and oil content.

## Results and Discussion

Mutations affecting quantitative characters can be inferred by the estimation of mean and genetic parameters *viz*., genotypic coefficient of variation, phenotypic coefficient of variation, broad sense heritability and genetic advance in the mutagen treated population. The analysis of variance (Table 1) between families revealed that mean squares of the ten families differed significantly for all the characters. The chi-square for Barlett's test of homogeneity of error variances being significant for all the characters except days to flowering of primary raceme, 100-seed weight and oil content, it indicated the necessity to perform analysis of variance separately for each of the family. The analysis of variance in $M_2$ generation (Table 1) between progenies within family indicated that progeny mean squares were significant for all the characters. This indicated that considerable variation was observed between progenies within families due to mutation treatments. For control treatment progenies had non-significant mean squares for all the characters except family 5 (untreated VP 1 (M)) for number of capsule on primary raceme and 100-seed weight as well as Family 10 (untreated SKI 215) for 100-seed weight exhibited significant mean square due to progeny. These similar results had also been reported by Khatri *et al*. (2005) [11] and Emrani *et al*. (2012) [6] indicated highly significant effects of mutagenic doses and genotypes indicating the differential response of genotypes to mutagenic treatments in terms of inducing genetic variation.

### Quantitative traits in $M_2$ generations

In the present investigation, EMS and Streptomycin sulphate proved to be very effective to induce variability in quantitative traits of $M_2$ generations of two genotypes of castor (Table 2).

### Days to 50% flowering of primary raceme

**VP 1 (M)**

The highest observed phenotypic range was for 1500 ppm streptomycin sulphate (50.06-55.27 days). Maximum mean for days to 50% flowering (52.59 days) was found in 1500 ppm. Decrease in mean value for days to 50% flowering was observed in treated family when compared with control. With these, early variants were detected in family treated with 50 mM EMS concentration (48.80 days). Similar result was observed by Dhakshanamoorthy *et al*. (2010) [4] in jatropha using gamma rays and EMS treatment in healthy and dry seeds. Highest values for GCV (4.85%) and PCV (5.58%) were recorded in 1500 ppm streptomycin sulphate treatment. High broad sense heritability found in mutagen treatment 60 mM EMS (75.74%) which indicating the treatment effect could inherit in their progenies as well. Maximum Genetic Advance as percent of mean observed in 1500 ppm streptomycin sulphate *i.e*., 8.69 percent. This result was supported by Emrani *et al*. (2012) [6] in canola.

**Table 1:** Analysis of variance (mean square) for different characters in $M_2$ generation of castor

| Sources | d.f. | Days to 50% flowering of primary raceme | Days to maturity of primary raceme | Plant height up to primary raceme (cm) | Number of node up to primary raceme | Effective length of primary raceme (cm) | Number of effective branch per plant | Number of capsule on primary raceme | Seed yield per plant (g) | 100-seed weight (g) | Oil Content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Analysis of variance (mean square) between family** | | | | | | | | | | | |
| Replications | 2 | 3.31 | 4.92 | 4.19 | 0.86 | 25.13 | 11.45 | 105.35 | 5638.00 | 1.87 | 0.90 |
| Families | 9 | 769.54** | 3662.24** | 30663.56** | 195.93* | 142.24** | 510.05** | 687.02** | 17676.22** | 50.60* | 11.46** |
| Error | 18 | 1.25 | 3.00 | 43.35 | 0.98 | 36.55 | 3.34 | 33.64 | 2079.44 | 0.61 | 0.81 |
| Chi-square | | NS | S | S | S | S | S | S | S | NS | NS |
| **Analysis of variance (mean square) between progenies within families for different characters in $M_2$ generation of castor** | | | | | | | | | | | |
| **Family 1 (Genotype: VP 1 (M); Dose: Control)** | | | | | | | | | | | |
| Replications | 2 | 3.82 | 16.56 | 6.65 | 0.32 | 22.56 | 1.22 | 8.91 | 1047.82 | 0.96 | 0.51 |
| Progenies | 9 | 6.24 | 7.06 | 9.77 | 2.68 | 36.57 | 2.12 | 152.33* | 2597.79 | 4.52** | 1.42 |
| Error | 18 | 2.77 | 5.76 | 4.92 | 1.25 | 15.11 | 0.96 | 43.21 | 1126.74 | 0.62 | 0.60 |
| **Family 2 (Genotype: VP 1 (M); Dose: EMS 50 mM)** | | | | | | | | | | | |
| Replications | 2 | 0.36 | 0.26 | 28.74 | 1.04 | 57.17 | 3.53 | 130.61 | 66.83 | 1.14 | 0.77 |
| Progenies | 9 | 3.82* | 6.15* | 26.17* | 4.66* | 84.63** | 3.40* | 155.58* | 3502.67** | 2.73** | 2.68** |
| Error | 18 | 1.55 | 1.94 | 10.58 | 1.31 | 23.36 | 1.05 | 48.17 | 552.64 | 0.66 | 0.55 |
| **Family 3 (Genotype: VP 1 (M); Dose: EMS 60 mM)** | | | | | | | | | | | |
| Replications | 2 | 1.18 | 0.89 | 18.66 | 0.11 | 57.33 | 4.61 | 45.12 | 3237.72 | 0.53 | 1.12 |
| Progenies | 9 | 4.92* | 6.01* | 22.18* | 2.02* | 204.99* | 8.27** | 114.87* | 2308.47* | 4.84** | 4.09** |
| Error | 18 | 1.42 | 2.07 | 8.37 | 0.67 | 16.84 | 1.47 | 36.15 | 935.57 | 1.02 | 0.90 |
| **Family 4 (Genotype: VP 1 (M); Dose: streptomycin sulphate 1000 ppm)** | | | | | | | | | | | |
| Replications | 2 | 1.44 | 2.09 | 7.82 | 3.09 | 93.92 | 1.49 | 16.02 | 150.82 | 0.43 | 1.22 |
| Progenies | 9 | 3.74* | 5.65* | 18.17* | 8.71** | 137.77** | 2.28* | 102.16* | 935.47* | 3.17** | 4.46* |
| Error | 18 | 1.46 | 2.15 | 6.12 | 1.51 | 30.08 | 0.90 | 29.95 | 371.90 | 0.61 | 1.26 |

*,** = Significant at P=0.05 and 0.01%, respectively.

| Sources | d.f. | Days to 50% flowering of primary raceme | Days to maturity of primary raceme | Plant height up to primary raceme (cm) | Number of node up to primary raceme | Effective length of primary raceme (cm) | Number of effective branch per plant | Number of capsule on primary raceme | Seed yield per plant (g) | 100-seed weight (g) | Oil Content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Family 5 (Genotype: VP 1 (M); Dose: streptomycin sulphate1500 ppm)** | | | | | | | | | | | |
| Replications | 2 | 1.16 | 1.16 | 12.25 | 2.44 | 24.03 | 1.30 | 65.13 | 2068.03 | 1.02 | 0.50 |
| Progenies | 9 | 7.22* | 6.96* | 14.78* | 2.76* | 67.70** | 1.76* | 73.51** | 3389.70* | 4.13** | 2.44* |
| Error | 18 | 2.11 | 2.25 | 5.63 | 1.10 | 13.26 | 0.55 | 18.71 | 1329.89 | 0.90 | 0.86 |
| **Family 6 (Genotype : SKI 215; Dose : Control)** | | | | | | | | | | | |
| Replications | 2 | 1.23 | 2.56 | 8.61 | 1.05 | 3.09 | 0.22 | 3.61 | 3527.84 | 0.45 | 0.09 |
| Progenies | 9 | 3.72 | 1.89 | 61.80 | 2.21 | 29.96 | 4.93 | 69.88 | 3151.75 | 5.41** | 1.91 |
| Error | 18 | 1.95 | 2.28 | 41.44 | 0 .94 | 14.31 | 3.80 | 29.66 | 1303.90 | 1.27 | 0.79 |
| **Family 7 (Genotype: SKI 215; Dose: EMS 50 mM)** | | | | | | | | | | | |
| Replications | 2 | 1.76 | 2.23 | 141.96 | 0.46 | 2.80 | 13.08 | 22.80 | 1697.94 | 0.11 | 1.25 |
| Progenies | 9 | 4.00* | 6.09* | 157.23* | 5.14** | 37.73** | 38.52** | 149.12** | 8713.43** | 7.60** | 2.63** |
| Error | 18 | 1.57 | 2.45 | 58.28 | 0.48 | 4.30 | 3.90 | 14.78 | 1331.99 | 0.77 | 0.42 |
| **Family 8 (Genotype: SKI 215; Dose: EMS 60 mM)** | | | | | | | | | | | |
| Replications | 2 | 1.94 | 1.63 | 152.80 | 0.20 | 37.70 | 5.56 | 21.31 | 3199.69 | 1.59 | 1.73 |
| Progenies | 9 | 4.03* | 5.21* | 107.06* | 1.20* | 40.93* | 5.83* | 31.35* | 4757.02* | 3.39* | 1.43* |
| Error | 18 | 1.62 | 2.00 | 43.52 | 0.43 | 11.43 | 2.22 | 11.68 | 1638.87 | 1.09 | 0.56 |
| **Family 9 (Genotype: SKI 215; Dose: streptomycin sulphate 1000 ppm)** | | | | | | | | | | | |
| Replications | 2 | 0.86 | 1.56 | 5.63 | 0.62 | 4.92 | 2.36 | 11.91 | 4704.01 | 0.67 | 0.52 |
| Progenies | 9 | 5.01* | 6.22* | 75.27* | 1.43* | 26.46* | 5.48* | 75.49** | 3904.84* | 2.69* | 1.59* |
| Error | 18 | 1.93 | 2.16 | 29.75 | 0.54 | 10.71 | 2.01 | 18.46 | 1418.63 | 0.99 | 0.56 |
| **Family 10 (Genotype: SKI 215; Dose: streptomycin sulphate 1500 ppm)** | | | | | | | | | | | |
| Replications | 2 | 0.77 | 2.96 | 11.26 | 0.29 | 50.47 | 8.10 | 82.71 | 4648.86 | 0.39 | 0.48 |
| Progenies | 9 | 9.98* | 9.83* | 121.14* | 1.76* | 37.38* | 14.79** | 183.81** | 6450.24** | 2.05* | 2.89** |
| Error | 18 | 3.98 | 3.91 | 48.20 | 0.61 | 15.18 | 2.45 | 24.15 | 1414.82 | 0.75 | 0.68 |

*,** = Significantat P = 0.05 and 0.01%, respectively

**SKI 215**

The highest range was observed in case of 1500 ppm streptomycin sulphate (54.46-61.26 days). Maximum mean value of days to 50% flowering observed in 60 mM EMS (60.85 days). Decrease in mean value for days to flowering was observed in the treated families as compared with control and early variants were observed by 1500 ppm streptomycin sulphate treatment (58.29 days). Similar result was obtained by Ravichandran and Jayakumar (2015) [16] in sesame. Maximum PCV (6.10%) and GCV (5.05%) observed in 1500 ppm streptomycin sulphate. High broad sense heritability found in mutagen treatment 1000 ppm Streptomycin sulphate (69.33%) followed by 1500 ppm streptomycin sulphate (68.50%). The high broad sense heritability estimates obtained may be due to additive gene effects which can be exploited for direct selection for these traits. Maximum Genetic advance as percent of mean observed in mutagen treatment 1500 ppm streptomycin sulphate 8.60 percent. Similar result was supported by Giriraj *et al*. (2004) [7] in sunflower.

**Days to maturity of primary raceme**

**VP 1 (M)**

In VP 1 (M) genotype,all the mutation treatments showed lower phenotypic range as compare to control (121.00-132.67 days). Decrease in mean value for days to maturity was observed in treated family as compared to control (130.13 days) and early variants were observed in 50 mM EMS (114 days) treatment. Similar result was obtained by Gothaliya and Madariya (2019) [8] in castor. Maximum GCV (2.06%) and PCV (2.40%) observed in 50 mM EMS treatment. Maximum broad sense heritability was observed in 50 mM EMS (73.94%). Genetic advance as percent (3.70%) found higher in 1500 ppm streptomycin sulphate. Similar result was obtained by Dwimahyani and Ishak (2004) [5] in Jatropha and Abdullah *et al*. (2005) [1] mustard.

**SKI 215**

In SKI 215 genotype, all the mutation treatments showed lower phenotypic range as compare to control (140.00-142.33 days). Decrease in mean value for days to maturity was observed in treated family as compared to control (141.49 days) and early variant was observed in 1500 ppm streptomycin sulphate (138.30 days) treatment. Similar results was obtained by Emrani *et al*. (2012) [6] in canola. Maximum PCV (2.55%) and GCV (2.11%) was observed in 1500 ppm streptomycin sulphate treatment. Maximum broad sense heritability was observed in 1000 ppm streptomycin sulphate (71.81%). Genetic advance as percent (3.60%) was found higher in 1500 ppm streptomycin sulphate. This result has been supported by finding of Ahmed *et al.* (2012) [2] in castor.

**Plant height up to primary raceme (cm)**

**VP 1 (M)**

Maximum phenotypic range was observed in 50 mM EMS (26.07-34.87 cm). The mean of plant height was higher in 50 mM EMS (30.09 cm) and Similar results has been supported by Ravichandran and Jayakumar (2015) [16] in sesame. Maximum PCV (19.15%) and GCV (15.81%) were observed in 50 mM EMS. Maximum broad sense heritability found in 1000 ppm Streptomycin sulphate mutagen treatment (72.50%). Mutagen treatment 50 mM EMS had high Genetic advance as percent of mean (26.89). This result was supported by Emrani *et al*. (2012) [6] in canola.

**SKI 215**

Maximum phenotypic range was observed in 50 mM EMS (81.27-101.00 cm). The mean values for plant height was shifted in both the direction indicated good variability developed for this character (Table 2). The mean of plant height was observed higher in 1500 ppm streptomycin sulphate treatment (91.77 cm). This result was supported by Gothaliya and Madariya (2019) [8] in castor. Maximum PCV (15.76%) and GCV (13.21%) were observed in 50 mM EMS treatment. Lower difference in GCV and PCV indicated the presence of less environmental effect. Maximum broad sense heritability found in 50 mM EMS mutagen treatment (70.28%). Similar result was obtained by Ahmed *et al*. (2012) [2] in castor. .Mutagen treatment 50 mM EMS had high Genetic advance as percent of mean (22.81%). This result was supported by Pavadai *et al*. (2010) [15] in soybean.

**Number of node up to primary raceme**

**VP 1 (M)**

Higher value of phenotypic range was recorded for 1000 ppm streptomycin sulphate treatment (12.73-17.60). There were minor differences between mean of all treatments as compare to control (Table 2). Maximum mean value for number of nodes up to primary raceme found in 60 mM EMS treatment (15.01). Maximum PCV (22.03%) and GCV (20.25%) were found in 1000 ppm streptomycin sulphate mutagen treatment. Mutagen treatment 1000 ppm streptomycin sulphate had maximum broad sense heritability (84.49%) with high genetic advance as percent of mean (38.34%).

**SKI 215**

In both treatments, phenotypic range was observed high in 50 mM EMS (16.40-19.87) and 1500 ppm streptomycin sulphate (18.47-21.30) treatment as compared to control (17.73-20.40). Maximum mean value for number of nodes up to primary raceme was found in 1000 ppm streptomycin sulphate (19.81). This result is in accordance with Gothaliya and Madariya (2019) [8] in castor. Maximum PCV (13.31%) and GCV (12.71%) were found in 50 mM EMS mutagen treatment. Similar result was obtained by Reddy and Dhaduk (2014) [17] in okra.

**Effective length of primary raceme (cm)**

**VP 1 (M)**

Maximum value of phenotypic range was observed in 60 mM EMS (51.20-74.20 cm). Maximum mean value for number of effective length of primary raceme was found in 1500 ppm streptomycin sulphate (63.89 cm). This result has been supported by Deshmukh *et al*. (2018) [3] in sorghum Parbhani Moti cultivar. Maximum PCV (24.74%) and GCV (23.78%) found in 60 mM EMS mutagen treatment. Mutagen treatment of 60 mM EMS had maximum broad sense heritability (92.21%) with high genetic advance as percent of mean (47.00%). Similar result was obtained by Ahmed *et al*. (2012) [2] in castor.

**Table 2:** The Estimates of genotypic and phenotypic variance and other genetic parameters for quantitative traits in $M_2$ generation of castor

| Treatment | Mean±S.E. | Range | GCV (%) | PCV (%) | $h^2_{(bs)}$ (%) | GA (% of mean) |
|---|---|---|---|---|---|---|
| **Days to 50% flowering of primary raceme** | | | | | | |
| **VP 1 (M)** | | | | | | |
| Control | 60.34±0.30 | 57.86-62.86 | 3.82 | 4.71 | 65.74 | 6.38 |
| 50 mM EMS | 48.80±0.23 | 47.33-50.53 | 3.72 | 4.51 | 68.07 | 6.33 |
| 60 mM EMS | 51.05±0.22 | 49.73-53.60 | 4.12 | 4.74 | 75.74 | 7.40 |
| 1000 ppm S.S | 50.55±0.22 | 49.33-52.26 | 3.57 | 4.30 | 69.04 | 6.11 |
| 1500 ppm S.S | 52.59±0.26 | 50.06-55.27 | 4.85 | 5.58 | 75.52 | 8.69 |
| **SKI 215** | | | | | | |
| | | | | | | |
| Control | 62.07±0.25 | 60.26-63.60 | 2.82 | 3.61 | 61.12 | 4.54 |
| 50 mM EMS | 59.54±0.23 | 57.47-61.40 | 3.13 | 3.77 | 68.95 | 5.36 |
| 60 mM EMS | 60.85±0.23 | 59.8-62.53 | 3.07 | 3.72 | 68.23 | 5.22 |
| 1000 ppm S.S | 60.25±0.25 | 58.13-62.53 | 3.47 | 4.16 | 69.33 | 5.95 |
| 1500 ppm S.S | 58.29±0.36 | 54.46-61.26 | 5.05 | 6.10 | 68.50 | 8.60 |
| **Days to maturity of primary raceme** | | | | | | |
| **VP 1 (M)** | | | | | | |
| Control | 130.13±0.44 | 121.00-132.67 | 1.74 | 2.54 | 47.14 | 2.46 |
| 50 mM EMS | 114.00±0.24 | 112.13-116.87 | 2.06 | 2.40 | 73.94 | 3.65 |
| 60 mM EMS | 116.42±0.26 | 114.80-118.60 | 1.98 | 2.33 | 72.02 | 3.46 |
| 1000 ppm S.S | 120.46±0.27 | 118.60-122.60 | 1.84 | 2.21 | 69.63 | 3.17 |
| 1500 ppm S.S | 122.59±0.27 | 120.07-124.93 | 2.03 | 2.37 | 73.42 | 3.70 |
| **SKI 215** | | | | | | |
| Control | 141.49±0.28 | 140.00-142.33 | 0.75 | 1.30 | 33.07 | 0.89 |
| 50 mM EMS | 139.57±0.29 | 136.60-141.60 | 1.64 | 1.99 | 68.31 | 2.80 |
| 60 mM EMS | 140.73±0.26 | 138.33-142.60 | 1.51 | 1.82 | 69.41 | 2.60 |
| 1000 ppm S.S | 140.17±0.27 | 138.00-142.60 | 1.67 | 1.97 | 71.81 | 2.92 |
| 1500 ppm S.S | 138.30±0.36 | 134.33-141.00 | 2.11 | 2.55 | 68.58 | 3.60 |
| **Plant height up to primary raceme (cm)** | | | | | | |
| **VP 1 (M)** | | | | | | |
| Control | 27.46±0.40 | 23.67-29.53 | 10.38 | 13.15 | 62.32 | 16.89 |
| 50 mM EMS | 30.09±0.59 | 26.07-34.87 | 15.81 | 19.15 | 68.16 | 26.89 |
| 60 mM EMS | 29.23±0.53 | 26.37-33.27 | 15.06 | 18.02 | 69.85 | 25.93 |
| 1000 ppm S.S | 27.91±0.45 | 23.93-31.93 | 14.39 | 16.90 | 72.50 | 25.24 |
| 1500 ppm S.S | 28.05±0.43 | 23.88-30.49 | 12.81 | 15.35 | 69.62 | 22.02 |
| **SKI 215** | | | | | | |
| Control | 89.56±1.17 | 82.87-98.5 | 7.73 | 10.56 | 53.66 | 11.67 |
| 50 mM EMS | 88.87±1.39 | 81.27-101.00 | 13.21 | 15.76 | 70.28 | 22.81 |
| 60 mM EMS | 84.83±1.20 | 75.13-93.87 | 11.34 | 13.75 | 68.02 | 19.27 |
| 1000 ppm S.S | 90.50±1.00 | 82.06-97.67 | 8.93 | 10.77 | 68.72 | 15.25 |
| 1500 ppm S.S | 91.77±1.26 | 85.07-101.00 | 11.17 | 13.49 | 68.55 | 19.05 |
| **Number of node up to primary raceme** | | | | | | |
| **VP 1 (M)** | | | | | | |
| Control | 13.97±0.20 | 12.53-15.33 | 10.77 | 13.42 | 64.39 | 17.80 |
| 50 mM EMS | 14.94±0.21 | 12.60-17.53 | 13.75 | 15.74 | 76.33 | 24.75 |
| 60 mM EMS | 15.10±0.15 | 13.93-16.17 | 8.87 | 10.40 | 72.67 | 15.58 |
| 1000 ppm S.S | 14.15±0.22 | 12.73-17.60 | 20.25 | 22.03 | 84.49 | 38.34 |
| 1500 ppm S.S | 14.07±0.19 | 12.93-15.67 | 10.99 | 13.28 | 68.56 | 18.75 |

PCV-Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, $h^2_{bs}$-Heritability, GA-Genetic advance.as percent of mean

| Treatment | Mean±S.E. | Range | GCV (%) | PCV (%) | $h^2_{(bs)}$ (%) | GA (% of mean) |
|---|---|---|---|---|---|---|
| | | | **SKI 215** | | | |
| Control | 19.09±0.18 | 17.73-20.40 | 7.21 | 8.82 | 66.84 | 12.15 |
| 50 mM EMS | 17.55±0.13 | 16.40-19.87 | 12.71 | 13.31 | 91.16 | 25.00 |
| 60 mM EMS | 19.46±0.12 | 18.60-20.53 | 5.30 | 6.29 | 71.05 | 9.20 |
| 1000 ppm S.S | 19.81±0.13 | 18.87-20.73 | 5.65 | 6.77 | 69.64 | 9.71 |
| 1500 ppm S.S | 19.64±0.14 | 18.47-21.30 | 6.35 | 7.49 | 71.79 | 11.08 |
| **Effective length of primary raceme** | | | | | | |
| **VP 1 (M)** | | | | | | |
| Control | 56.47±0.71 | 51.80-64.80 | 9.94 | 12.09 | 67.60 | 16.84 |
| 50 mM EMS | 61.20±0.88 | 54.20-69.80 | 14.32 | 16.36 | 76.69 | 25.84 |
| 60 mM EMS | 59.43±0.75 | 51.20-74.20 | 23.78 | 24.74 | 92.21 | 47.00 |
| 1000 ppm S.S | 62.80±1.00 | 57.73-80.80 | 18.00 | 20.00 | 80.94 | 33.35 |
| 1500 ppm S.S | 63.89±0.66 | 57.73-73.13 | 12.45 | 13.69 | 82.67 | 23.32 |
| **SKI 215** | | | | | | |
| Control | 60.59±0.69 | 56.33-66.00 | 8.28 | 10.37 | 63.77 | 13.62 |
| 50 mM EMS | 62.28±0.38 | 57.60-67.67 | 9.67 | 10.23 | 89.40 | 18.84 |
| 60 mM EMS | 60.62±0.62 | 55.00-66.07 | 10.05 | 11.49 | 76.46 | 18.10 |
| 1000 ppm S.S | 58.31±0.60 | 53.33-62.07 | 8.20 | 9.94 | 68.12 | 13.95 |
| 1500 ppm S.S | 61.10±0.71 | 56.80-67.30 | 9.30 | 11.28 | 68.04 | 15.81 |
| **Number of effective branch per plant** | | | | | | |
| **VP 1 (M)** | | | | | | |
| Control | 12.44±0.18 | 11.18-14.03 | 10.79 | 13.35 | 65.32 | 17.96 |
| 50 mM EMS | 11.93±0.19 | 10.27-13.32 | 14.64 | 16.97 | 74.49 | 26.03 |
| 60 mM EMS | 14.08±0.22 | 11.40-16.79 | 19.81 | 21.60 | 84.12 | 37.44 |
| 1000 ppm S.S | 12.82±0.17 | 11.46-14.00 | 10.98 | 13.24 | 68.74 | 18.75 |
| 1500 ppm S.S | 12.50±0.14 | 11.30-13.80 | 10.03 | 11.66 | 73.91 | 17.76 |
| **SKI 215** | | | | | | |
| Control | 19.69±0.36 | 17.47-20.87 | 9.72 | 13.87 | 49.11 | 14.03 |
| 50 mM EMS | 23.18±0.36 | 20.27-30.32 | 26.32 | 27.66 | 90.52 | 51.58 |
| 60 mM EMS | 17.57±0.27 | 15.80-20.53 | 12.84 | 15.39 | 69.61 | 22.07 |
| 1000 ppm S.S | 19.73±0.26 | 18.20-22.54 | 11.13 | 13.25 | 70.56 | 19.26 |
| 1500 ppm S.S | 20.23±0.29 | 16.80-23.53 | 18.48 | 20.03 | 85.10 | 35.11 |
| **Number of capsule on primary raceme** | | | | | | |
| **VP 1 (M)** | | | | | | |
| Control | 50.79±1.20 | 43.27-62.58 | 23.12 | 26.50 | 76.14 | 41.56 |
| 50 mM EMS | 54.12±1.27 | 45.00-69.60 | 21.82 | 25.31 | 74.34 | 38.76 |
| 60 mM EMS | 56.09±1.10 | 49.07-66.20 | 18.08 | 21.01 | 73.99 | 32.03 |
| 1000 ppm S.S | 49.21±1.00 | 42.27-58.67 | 19.51 | 22.46 | 75.47 | 34.92 |
| 1500 ppm S.S | 48.98±0.79 | 39.60-53.60 | 16.74 | 18.93 | 78.24 | 30.51 |
| **SKI 215** | | | | | | |
| Control | 55.23±0.99 | 48.07-63.55 | 14.02 | 17.14 | 66.91 | 23.63 |
| 50 mM EMS | 41.16±0.70 | 28.47-50.33 | 29.17 | 30.63 | 90.70 | 57.23 |
| 60 mM EMS | 49.42±0.62 | 43.73-53.07 | 10.60 | 12.66 | 70.15 | 18.29 |
| 1000 ppm S.S | 49.38±0.78 | 42.13-55.47 | 16.86 | 18.97 | 78.97 | 30.87 |
| 1500 ppm S.S | 57.61±0.90 | 39.47-68.20 | 23.01 | 24.54 | 87.92 | 44.45 |

PCV-Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, $h^2{}_{bs}$-Heritability, GA-Genetic advance. as percent of mean

| Treatment | Mean±S.E. | Range | GCV (%) | PCV (%) | $h^2_{(bs)}$ (%) | GA (% of mean) |
|---|---|---|---|---|---|---|
| Seed yield per plant (g) | | | | | | |
| VP 1 (M) | | | | | | |
| Control | 299.67±6.13 | 255.27-340.60 | 15.73 | 19.31 | 66.35 | 26.40 |
| 50 mM EMS | 265.68±4.29 | 232.73-326.13 | 21.68 | 23.42 | 85.72 | 41.35 |
| 60 mM EMS | 324.43±6.66 | 292.67-390.47 | 16.73 | 20.16 | 68.90 | 28.61 |
| 1000 ppm S.S | 291.98±3.52 | 268.00-321.27 | 9.76 | 11.78 | 68.57 | 16.64 |
| 1500 ppm S.S | 319.58±5.58 | 273.73-359.27 | 13.98 | 16.94 | 68.10 | 23.77 |
| SKI 215 | | | | | | |
| | | | | | | |
| Control | 283.98±6.59 | 231.20-323.47 | 18.35 | 22.33 | 67.57 | 31.08 |
| 50 mM EMS | 300.48±6.66 | 242.73-400.33 | 30.26 | 32.61 | 86.13 | 57.86 |
| 60 mM EMS | 325.78±7.39 | 279.90-421.93 | 19.92 | 23.48 | 71.98 | 34.81 |
| 1000 ppm S.S | 297.74±6.87 | 245.07-404.08 | 25.97 | 28.88 | 80.86 | 48.11 |
| 1500 ppm S.S | 350.08±6.88 | 291.27-394.40 | 16.73 | 19.89 | 70.75 | 29.00 |
| 100-seed weight (g) | | | | | | |
| VP 1 (M) | | | | | | |
| Control | 24.91±0.14 | 23.24-26.57 | 8.33 | 8.92 | 87.37 | 16.05 |
| 50 mM EMS | 24.01±0.15 | 22.06-25.16 | 6.60 | 7.42 | 79.16 | 12.10 |
| 60 mM EMS | 23.13±0.18 | 21.77-25.41 | 9.17 | 10.16 | 81.52 | 17.06 |
| 1000 ppm S.S | 24.14±0.14 | 22.73-25.71 | 7.14 | 7.84 | 83.03 | 13.41 |
| 1500 ppm S.S | 25.52±0.17 | 23.89-27.39 | 7.67 | 8.52 | 80.95 | 14.21 |
| SKI 215 | | | | | | |
| Control | 26.34±0.21 | 24.23-28.36 | 8.48 | 9.50 | 79.68 | 15.59 |
| 50 mM EMS | 26.03±0.16 | 24.11-28.61 | 10.41 | 10.94 | 90.50 | 20.40 |
| 60 mM EMS | 24.85±0.19 | 23.58-26.24 | 7.00 | 8.17 | 73.62 | 12.39 |
| 1000 ppm S.S | 25.52±0.18 | 23.97-27.12 | 6.01 | 7.17 | 70.27 | 10.38 |
| 1500 ppm S.S | 27.64±0.16 | 26.45-28.98 | 4.85 | 5.77 | 70.53 | 8.39 |
| Oil content (%) | | | | | | |
| VP 1 (M) | | | | | | |
| Control | 46.00±0.14 | 44.41-46.71 | 2.40 | 2.93 | 67.18 | 4.06 |
| 50 mM EMS | 47.17±0.17 | 45.67-48.85 | 4.13 | 4.59 | 80.87 | 7.64 |
| 60 mM EMS | 47.56±0.14 | 46.21-49.15 | 3.32 | 3.67 | 81.84 | 6.19 |
| 1000 ppm S.S | 46.90±0.20 | 45.15-48.32 | 4.28 | 4.91 | 76.25 | 7.71 |
| 1500 ppm S.S | 47.05±0.17 | 45.84-48.32 | 3.12 | 3.69 | 71.46 | 5.43 |
| SKI 215 | | | | | | |
| Control | 46.76±0.16 | 45.12-48.12 | 2.74 | 3.34 | 67.48 | 4.64 |
| 50 mM EMS | 46.43±0.12 | 44.91-47.8 | 3.40 | 3.68 | 85.42 | 6.47 |
| 60 mM EMS | 47.30±0.14 | 46.29-48.25 | 2.35 | 2.84 | 68.78 | 4.02 |
| 1000 ppm S.S | 47.39±0.14 | 46.32-48.39 | 2.50 | 2.95 | 71.51 | 4.35 |
| 1500 ppm S.S | 48.22±0.15 | 47.29-50.42 | 3.39 | 3.79 | 79.69 | 6.23 |

PCV-Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, $h^2_{bs}$-Heritability, GA-Genetic advance as percent of mean

**SKI 215**

In this genotype phenotypic range was observed high in 60 mM EMS treatment (55.00-66.07 cm). Maximum mean value for effective length of primary raceme was found in 50 mM EMS treatment (62.28 cm). This result was supported by Gothaliya and Madariya (2019) [8] in castor using gamma radiation. Maximum PCV (11.49%) and GCV (10.05%) were found in 60 mM EMS mutagen treatment. Mutagen treatment of 50 mM EMS had maximum broad sense heritability (89.40%) with high genetic advance as percent of mean (18.84%). The result was in confirmation with Sarwar and Chaudhry (2008) [18] in castor and Srivastava *et al*. (2011) [20] in wheat.

**Number of effective branch per plant**

**VP 1 (M)**

Maximum value of phenotypic range was observed in 60 mM EMS treatment (11.40-16.79). Maximum mean value for number of effective branch per plant was found in 60 mM EMS (14.08). This result supported by Ravichandran and Jayakumar (2015) [16] in sesame. Difference between PCV and GCV indicates less effect of environment on number of effective branches per plant. Maximum PCV (21.60%) and GCV (19.81%) were found in 60 mM EMS mutagen treatment. Mutagent reatment of 60 mM EMS had maximum broad sense heritability (84.12%) with high genetic advance as percent of mean (37.44%). This result was supported by Mensah and Obadoni (2007) [13] in groundnut.

**SKI 215**

Phenotypic range was observed high with respect to control for all the treatments. Maximum value of phenotypic range was observed in 50 mM EMS treatment (20.27-30.32). Maximum mean value for number of effective branch per plant was found in 50 mM EMS treatment (23.18). Maximum PCV (27.66%) and GCV (26.32%) were found in 50 mM EMS mutagen treatment. Mutagen treatment of 50 mM EMS had maximum broad sense heritability (90.52%) with high genetic advance as percent of mean (51.58%). Similar result was obtained by Pavadai *et al*. (2010) [15] in soybean and Reddy and Dhaduk (2014) [17] in okra.

**Number of capsule on primary raceme**

**VP 1 (M)**

In both the treatments, phenotypic range was higher than control (43.27-62.58) in 50 mM EMS treatment (45.00-69.60). Maximum mean value for number of capsule on primary raceme was found in 60 mM EMS treatment (56.09). Similar result was obtained by Gothaliya and Madariya (2019) [8] in castor. Maximum PCV (25.31%) and GCV (21.82%) were found in 50 mM EMS mutagen treatment. Mutagen treatment of 1500 ppm streptomycin sulphate had maximum broad sense heritability (78.24%) with genetic advance as percent of mean (30.51%). This result was supported by Sarwar and Chaudhary (2008) [18] in castor.

**SKI 215**

Phenotypic range was higher than control (48.07-63.55) in 50 mM EMS treatment (28.47-50.33). Maximum mean value for number of capsule on primary raceme was found in 1500 ppm streptomycin sulphate treatment (57.61). Similar result was obtained by Ravichandran and Jayakumar (2015) [16] in sesame. Maximum PCV (30.63%) and GCV (29.17%) were found in 50 mM EMS mutagen treatment. Mutagen treatment of 50 mM EMS had maximum broad sense heritability (90.70%) with genetic advance as percent of mean (57.23%). Thus, 50 mM EMS treatment seems to be good for improving this character. Similar result was obtained by Maibam *et al*. (2018) [12] in sesame.

**Seed yield per plant (g)**

**VP 1 (M)**

For seed yield per plant, phenotypic range was higher than control (255.27-340.60 g) in 50 mM EMS treatment (232.73-326.13 g). Maximum mean value for seed yield per plant was found in 60 mM EMS treatment (324.43). This result was supported by Gunasekaran and Pavadai (2015) [15] in groundut. Maximum PCV (23.42%) and GCV (21.68%) were found in 50 mM EMS mutagen treatment. Mutagen treatment of 50 mM EMS had maximum broad sense heritability (85.72%) with genetic advance as percent of mean (41.35%). Similar result was obtained by Ahmed *et al*. (2012) [2] in castor and Reddy and Dhaduk (2014) [17] in okra.

**SKI 215**

For seed yield per plant, phenotypic range was higher than control (231.20-323.47 g) in 1000 ppm streptomycin sulphate treatment (245.07-404.08 g). Maximum mean value for seed yield per plant was found in 1500 ppm streptomycin sulphate treatment (350.08 g) as compared to control (283.98 g). Maximum PCV (32.61%) and GCV (30.26%) were found in 50 mM EMS mutagen treatment. Mutagen treatment of 50 mM EMS had maximum broad sense heritability (86.12%) with genetic advance as percent of mean (57.86%). Similar result was also observed by Emrani *et al*. (2012) [6] in canola and Maibam *et al*. (2018) [12] in sesame.

**100- seed weight**

**VP 1**

Phenotypic range for 100-seed weight was found higher than control (23.24-26.57 g) in 60 mM EMS treatment (21.77-25.41 g). Mean values were low for all mutagenic treatments as compared to control (24.91 g) except 1500 ppm streptomycin sulphate treatment (25.52 g). The similar result was reported by Gothaliya and Madariya (2019) [8] in castor. Maximum PCV (10.16%) and GCV (9.17%) were found in 60 mM EMS mutagen treatment. Low broad sense heritability was observed in all treatments as compared to control (87.37%). In all mutagen treatments low genetic advance as percent of mean was found as compared to control (16.05%) except 60 mM EMS (17.06%) mutagenic treatment. This result was supported by Ahmed *et al*. (2012) [2] in castor.

**SKI 215**

Phenotypic range for 100-seed weight was found lower than control (24.23-28.36 g) in all the mutagenic treatments except 50 mM EMS treatment (24.11-28.61 g). Mean values were low for 100-seed weight for all mutagenic treatments as compared to control (26.34 g) except 1500 ppm streptomycin sulphate treatment (27.64 g). Similar result was obtained by Mensah *et al*. (2003) [14] in rice and Gunasekaran and Pavadai (2015) [15] in groundnut. Maximum PCV (10.94%) and GCV (10.41%) were found in 50 mM EMS mutagen treatment. Low broad sense heritability was observed in all treatments as compared to control (79.68%) except 50 mM EMS treatment (90.50%). In all mutagen treatments, low genetic advance as percent of mean was found as compared to control (15.59%), except 50 mM EMS treatment (20.40%). Similar result was obtained by Dwimahyani and Ishak (2004) [5] in jatropha and Emrani *et al*. (2012) [6] in canola.

**Oil content (%)**

**VP 1 (M)**

Maximum phenotypic range was observed in 1000 ppm streptomycin sulphate treatment (45.15-48.32%). Maximum mean value for oil content was found in 60 mM EMS treatment (47.56%) as compared to control (46.00%). Similar result was obtained by Gothaliya and Madariya (2019) [8] in castor. Maximum PCV (4.91%) and GCV (4.28%) were found in 1000 ppm streptomycin sulphate. Mutagen treatment of 60 mM EMS had maximum broad sense heritability (81.84%) with genetic advance as percent of mean (6.19%).

**SKI 215**

In SKI 215, phenotypic range was lower than control (45.12-48.12%) in all the mutagenic treatments except 1500 ppm streptomycin sulphate treatment (47.29-50.42%). Maximum mean value for oil content was found in 1500 ppm streptomycin sulphate treatment (48.22%) as compared to control (46.76%). The similar result was found by Gunasekaran and Pavadai (2015) [15] in groundnut. Maximum PCV (3.79%) was found in 1500 ppm streptomycin sulphate and GCV (3.40%) in 50 mM EMS treatment. Mutagen treatment of 50 mM EMS had maximum broad sense heritability (85.42%) with genetic advance as percent of mean (6.47%).

**Conclusion**

Doses near to $LD_{50}$ value of the mutagens were more effective for inducing beneficial mutants as compared to higher concentration. Early mutants were observed in both genotypes VP 1 (M) and SKI 215 of days to 50% flowering of primary raceme and days to maturity of primary raceme with the mutagenic treatment of 50 mM EMS and 1500 ppm streptomycin sulphate, respectively. The genotypic and phenotypic coefficient of variation higher in both the mutagenic treatments for all the characters except number of node up to primary raceme for SKI 215 and number of capsule on primary raceme in VP 1 (M). High estimate of GCV for above said characters indicated that sufficient genetic variability and selection based on genotype would be effective and little influence of environment present. High PCV which indicated that most of the characters were high influenced by the environment and selection should not be efficient. High broad sense heritability with high genetic advance as percent of mean was observed for plant height up to primary raceme, number of node up to primary raceme, effective length of primary raceme, number of effective branch per plant, number of capsule on primary raceme and seed yield per plant, which indicated that expression of these traits was governed by additive gene action and as a result there was a scope for improving these traits through adopting selection procedure during advancement of mutant generations. Treatments of chemical and antibiotic mutagen showed higher mutagenic effect in most of the characters when compared to control. Mutagenic treatments increase the genetic variability, which can be utilized in future breeding programme of castor.

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