



Research Note

Induction of genetic variability in okra [*Abelmoschus esculentus* (L.) Moench] by gamma and ems.

Peddi Sudharshan Reddy^{1*}, L. K. Dhaduk²

¹ Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh- 362001, Gujarat.

² Vegetable Research Station, Junagadh, Junagadh Agricultural University, Junagadh- 362001, Gujarat.

*E-mail: peddisudharshanreddy85@gmail.com

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Abstract

An investigation was carried out to study the extent of genetic variability induced through physical and chemical mutagens in okra. Seeds of two popular okra varieties viz. GO-2 and GJO-3 were treated with 20 kR, 30 kR and 40 kR of gamma rays and 0.15% and 0.25% EMS to raise M₁ generation in summer 2011 and the seed obtained from all of the M₁ competitive plants were used to raise M₂ in progeny rows of each of the treatments including control (the untreated one) in kharif 2011. In M₂ generation, increase in GCV, heritability and genetic advance was considerable under different mutagenic treatments for most of the traits studied in both varieties. In GO-2, high heritability and genetic advance was observed for some important yield contributing characters like fruit length at 40 kR and 0.25% EMS; fruit weight at 20 kR and 40 kR; and fruit yield per plant at 20, 30, 40 kR and 0.15% EMS. Similarly in GJO-3, high heritability coupled with high genetic advance was observed for fruit length at 30 kR and fruit yield per plant at 20 kR. YVMV percentage exhibited high PCV and GCV with high heritability and genetic advance in 0.25% EMS treatment in GO-2 and 40kR treatment in GJO-3. Thus selection for these characters at specific mutagenic treatments will be effective for improvement in okra.

Keywords:

Okra, Variability, Induced Mutations, Gamma rays, EMS

Okra [*Abelmoschus esculentus*(L.)Moench] is an annual vegetable crop grown in tropical and subtropical regions of the world. In India, it is grown on an area of 4.98 lakh hectares with a production of 57.84 lakh tones and productivity of 11.6 metric tonnes/ hectare (Annon, 2012). Okra has tremendous export potential as fresh vegetable. It accounts for 70 per cent of the 30 per cent exchange earnings other than onion, from export of vegetables (Annon, 2000). Okra fruit is good source of vitamins. Tender green fruits are cooked in curry and are also used in soups. Mature fruits and stems are used in the paper industry. Apart from its commercial uses, it is said to be very useful against genitor-urinary disorders, spermatorrhoea and chronic dysentery. It is an excellent source of iodine and useful for the control of goitre disease (Krishnamurthy, 1994)

Most of the crop improvement programmes attempted through conventional breeding methods have exploited only the natural variability available in the germplasm. Selection within local types exercised for a long time, exhausted the natural genetic variability of the crop. Under such circumstances, induced mutagenesis can be efficiently employed as an alternative to induce the variability in different quantitative characters. Hence, the present study was undertaken with the objective of assessing the induced phenotypic and genotypic variability, heritability and genetic advance for yield and yield component traits.

Two genotypes of okra, GO-2 and GJO-3 were selected and 1000 seeds of each genotype were sent for gamma rays treatment at Nuclear Agriculture and Biotechnological Division, Bhabha Atomic Research Center, Trombay, Mumbai where the seeds were subjected to acute doses of 20, 30 and 40 kR. For ethyl methane sulphonate (EMS) treatments, 1000 seeds of each genotype were soaked in distilled water for 6h followed by soaking of seeds in freshly prepared EMS solution (0.15% and 0.25%) for 6h. The EMS treated seeds were washed thoroughly for an hour under running tap water to remove the traces of EMS from seed surface. A set of unirradiated and untreated seeds of same lot of varieties were used as control. The treated seeds of both the genotypes along with their respective controls were sown during summer 2011 at Vegetable Research Station, Junagadh in 60 x 30 split plot design with three replications for raising M₁ generation. M₂ generation was raised in a layout of compact family block design with three replications. The seeds from 30 different plants selected at random from each treatment in M₁ generation were sown for raising M₂ generation in a plant to progeny method. The experiment consisted of 10 treatments each having 10 families and 10 seeds per family in each replication.

Observations were recorded on five randomly tagged plants in each replication on days to flowering, plant height at maturity, number of branches per plant, number of nodes on main stem, internodal length, fruit length, fruit diameter, fruit

weight, number of seeds per fruit, number of fruits per plant, fruit yield per plant and YVMV percentage. The data recorded on five randomly chosen competitive plants from experimental plot were used to calculate the mean values for each genotype/ replication. The mean values obtained were used for analysis of variance and to estimate genotypic coefficient of variation, heritability (broad sense) and genetic advance as percent of mean. The analysis of variance for each trait was estimated as per the method suggested by Panse and Sukhatme (1985). The phenotypic and genotypic coefficients of variation were estimated as per formula suggested by Burton & De Vane (1953). Heritability in broad sense and genetic advance were calculated by using formula given by Hanson *et al.* (1956) and Johnson *et al.* (1955).

The analysis of variance for compact family block design was carried out for twelve characters and is presented in Table 1 and 2. The analysis of variance between families in M₂ generation in okra (Table 1), revealed that the twelve treatments differed significantly for all the characters. The analysis of variance (mean square) between progenies within family for different characters in M₂ generation of okra (Table 2), indicated that all treatments differed significantly from each other for all the characters except days to flowering in family GJO-3(40 kR) and GJO-3 (0.25% EMS), plant height in family GJO-3 (0.15% EMS), YVMV percentage in family GO-2 (0.15% EMS) and GJO-3 (20 kR).

In GO-2, the highest genotypic coefficient of variability (GCV) was noted for YVMV percentage and internodal length at 0.25% EMS dose; for number of branches per plant, number of nodes on main stem, fruit length and fruit yield per plant at dose 40 kR; for days to flowering, fruit weight and number of fruits per plant at dose 20 kR; for plant height, fruit diameter and number of seeds per fruit at 0.15% EMS dose (Table 3). The values of genotypic variability also showed an increase over the control group for all of the traits. Similar findings for various crops were also reported by Jehangir and Chandrasekharan (1978), Malani *et al.* (1992), Gonge and Kale (1996) and Senthil Kumar *et al.*(1998). InGJO-3, YVMV percentage, number of fruits per plant, fruit weight, fruit diameter and number of branches per plant showed the highest GCV at dose 40 kR; days to flowering, internodal length and fruit yield per plant at dose 20 kR; plant height, fruit length and number of seeds per fruit at 30 kR; and number of nodes on main stem at 0.15% EMS dose (Table 3). However, GCV alone is not enough to determine the amount of heritable variability as heritability and GA with GCV are required to assess the heritable portion of the total variation.

Heritability in the broad sense (h^2) was estimated for 10 treatments and their respective controls for all of the traits. The heritability value of GO-2 was highest within the population for number of fruits per plant and number of nodes on main stem at 0.25% EMS dose; for fruit yield per plant, fruit weight, fruit length, number of branches per plant at 40 kR; for fruit diameter and plant height at 30 kR; for internodal length and number of seeds per fruit at 0.15% EMS; and for days to flowering and YVMV percentage at control (Table 4). The maximum heritability value in GJO - 3 was determined for fruit length, number of nodes on main stem and number of branches per plant at 30 kR; for YVMV percentage, fruit diameter and internodal length at 40 kR; for number of fruits per plant and days to flowering at 0.15% EMS dose, for fruit yield per plant at 20 kR; for number of seeds per fruit and fruit weight at 0.25% EMS dose; and for plant height at control (Table 4). High estimates of heritability are a reliable guide for any selection program based on the phenotypic performance of induced mutants. Sheeba *et al.* (2003) reported that broad-sense heritability estimates would be reliable only when accompanied with high GA.

The genetic advance (GA) in GO-2 was highest for YVMV percentage and number of fruits per plant at 0.25% EMS dose; for fruit yield per plant, fruit length, number of nodes on main stem and number of branches per plant at 40 kR; for fruit weight and days to flowering at 20 kR; for number of seeds per fruit, fruit diameter and plant height at 0.15% EMS; and internodal length at 30 kR (Table 5). Similarly GA for GJO-3 was highest for YVMV percentage and fruit diameter at 40 kR; for plant height, number of branches per plant, fruit length and number of seeds per fruit at 30 kR; for days to flowering, intermodal length, fruit weight and fruit yield per plant at 20 kR; for number of fruits per plant at 0.15% EMS dose and number of nodes on main stem at 0.25% EMS dose (Table 5).

The knowledge of the heritability along with genetic advance aids in drawing valuable conclusions for selection of breeding methods to be employed for further improvement of the traits. Detection of significant genetic variability indicates that existence of genetic variance in the genotypes alone while broad sense heritability estimate provides information on relative magnitude of genetic and environmental variation in germplasm pool. Heritability, along with high GA, has additive and epistatic gene effects, which are fixable and can provide the desirable gain (Sheeba *et al.* 2003). Thus, it becomes necessary to consider all three estimates to ensure effective selection for a particular trait. In GO -2, high heritability and genetic advance was observed for some important yield contributing characters like fruit length at 40 kR and 0.25% EMS; fruit weight



at 20 kR and 40 kR; fruit yield per plant at 20, 30, 40 kR and 0.15% EMS; and YVMV percentage at 0.25% EMS. Whereas in GJO-3, high estimate of heritability coupled with high genetic advance was observed for number of branches per plant at 20 kR and 30 kR; fruit length at 30 kR; fruit yield per plant at 20 kR and YVMV percentage at 40 kR indicating additive gene effects which shows the effectiveness of selection for these traits. Sathiyamurthy *et al.* (1998) also observed high heritability coupled with high genetic advance for fruit length, fruit diameter, fruit weight, number of seeds per fruit, number of fruits per plant and fruit yield per plant and Suryakumari (2002) also recorded the same in fruit length, number of fruits per plant and fruit yield per plant.

In GO-2, high heritability and moderate genetic advance was observed for the characters like plant height at 30 kR and 40 kR; number of branches per plant at 0.25% EMS; number of nodes per plant at 30 kR, 40 kR and 0.25% EMS; internodal length at 0.15%; fruit length at 30 kR; fruit diameter at 30 kR and 0.15% EMS; fruit weight at 30 kR and 0.15% EMS; and number of fruits per plant at 20 kR and 0.25% EMS. Whereas in GJO-3, high heritability and moderate genetic advance was observed for the characters like number of nodes per plant at 0.25% EMS; internodal length at 40 kR and 0.15% EMS; fruit diameter at 40 kR; fruit weight at 20 kR, 0.15% EMS and 0.25% EMS; number of fruits per plant at 20 kR and 0.15% EMS; and fruit yield per plant at 0.15% EMS indicating non-additive gene effects including dominance and epistasis. This indicates the role of environment in the expression of the traits. Selection in later generations after these traits are stabilized in the population would be effective in recovering desired genotype(s).

On the basis of the above findings, it may be concluded that there is a considerable increase in the GCV, heritability and genetic advance under different mutagenic treatments for most of the traits studied in both the varieties. In general, according to the results of the present work, the best treatment was the 20 kR gamma irradiation which showed the higher GCV, h^2 and GA for fruit yield per plant in both the varieties.

References

- Anonymous.2000.Agro-export statistics. Agriculture and Processed Food Export Development Agency, New Delhi.
- Anonymous.2012.Indian Horticulture Database 2012, NHB, Department of agriculture and cooperation, Government of India.
- Burton, G. W. and Devane, E. M., 1953. Estimating heritability in tall fescue (*Festuca*

- arundinacea*) from replicated clonal material. *Agron. J.*, **45** : 478-481.
- Gonge, V. S. and Kale, P. B. 1996.Effect of gamma rays in M_2 generation of okra.*PKV Res. J.*, **20**(1): 40-42.
- Hanson, G. H., Robinson, H. F. and Comstock, R. E., 1956. Biometrical studies of yield in segregating population of Korean lespedeza. *Agron. J.*, **48** : 267-282.
- Johnson, H.W., Robinson, H.F. and Comstock, R.F., 1955.Estimates of genetic and environmental variability in soybean. *Agron. J.*, **47**: 314-318.
- Jehangir, K.S. and Chandrasekharan, P. 1978.Comparative mutagenic effects of gamma rays and diethyl sulphate in Bhendi [*Abelmoschus esculentus* (L.)Moench].*Madras agril. J.*,**65** (4): 211-217.
- Krishnamurty, K. H. 1994. Okra In: “Vegetable Health Series, Traditional Family Medicine”. Publ. by Books for all, Ashok Vihar, Delhi, p.12-15.
- Malani, S.S., Kale, P.B. and Gonge, V.S. 1992. Gamma rays induced mutations in okra [*Abelmoschus esculentus* (L.) Moench].*PKV Res. J.*,**16** (2): 189-192.
- Panse, V.G. and Sukhatme, P.V. 1985.Statistical methods for agricultural workers. (3rd Revised eds.) I.C.A.R., New Delhi.
- Sathiyamurthy, V. A., Natarajan, S., Thamburaj, S. and Vaidyanathan, P. 1998. Genetic studies in bhendi [*Abelmoschus esculentus* (L.) Moench].*South Indian Horti.*,**46**: 316-318.
- Sheeba, A., Ibrahim, S. M., Yogameenakshi, P. and Babu, S.2003.Effect of mutagens on quantitative traits in M_2 generation in sesame (*Sesamum indicum* L.).*Indian J Genet.*,**63**: 173-174.
- Senthil Kumar, M., Natarajan, S. and Thamburaj.1998. Effect of gamma rays on fruit and seed characters in bhendi. *South Indian Horti.*,**46**(5&6): 312-315.
- Suryakumari, S. 2002. Induced polygenic mutations in okra [*Abelmoschus esculentus* (L.)Moench]. *South Indian Horti.*,**50**: 533-537.



Table 1. Analysis of variance (mean square) between families for different characters in M₂ generation of okra

Source	d.f	DTF	PH	NBP	NNMS	IL	FL	FD	FW	NSF	NFP	FYP	YVMV %
Replication	2	9.21	252.40*	2.99*	38.14*	7.08*	11.12*	0.10*	22.09*	56.02	11.01*	2654.91*	188.55
Family	11	22.01*	17825.43*	0.69*	10.13*	122.78*	128.66*	0.18*	19.86*	562.36*	18.48*	11851.70*	2159.31*
Error	22	7.06	56.45	0.30	3.28	1.07	2.97	0.02	1.52	63.40	1.28	453.14	183.02

REP = Replication, ER = Error, DTF = Days to Flowering, PH = Plant Height, NBP = Number of branches per plant, NNMS = Number of nodes on main stem, IL = Internodal Length, FL = Fruit Length, FD = Fruit Diameter, FW = Fruit Weight, NSF = Number of seeds per fruit, NFP = Number of fruits per plant, FYP = Fruit yield per plant, YVMV % = YVMV percentage

Table 2. Analysis of variance (mean square) between progenies within family for different characters in M₂ generation of okra

Source	GO-2 (20kR)			GO-2 (30kR)			GO-2 (40kR)			GO-2 (0.15% EMS)			GO-2 (0.25% EMS)			GO-2 (CONTROL)		
	REP	PRO	ER	REP	PRO	ER	REP	PRO	ER	REP	PRO	ER	REP	PRO	ER	REP	PRO	ER
d.f	2	9	18	2	9	18	2	9	18	2	9	18	2	9	18	2	9	18
DTF	2.8	5.07*	1.06	26.53*	2.58*	0.76	3.23	3.89*	1.2	0.63	6.06*	2.23	1.9	4.31*	1.57	2.63*	2.37*	0.37
PH	84.93	354.16*	113.9	5.63	434.15*	101.37	213.43	443.26*	108.06	27.03	723.26*	240	168.13	568.87*	229.32	115.73	93.11*	32.99
NBP	0.93	1.35*	0.41	0.23	0.95*	0.27	1.23*	1.54*	0.31	0.7	0.60*	0.22	0.53	0.69*	0.16	0.23	0.24*	0.09
NNMS	8.13	7.27*	2.76	7.63	8.69*	2.15	3.7	9.49*	2	2.53	7.64*	2.87	9.10*	8.09*	1.54	7.23	5.84*	2.05
IL	6.47*	3.95*	1	3.57	4.18*	1.23	1.12	2.28*	0.92	0.89	3.73*	0.81	3.84	6.55*	2.29	0.24	1.74*	0.51
FL	9.41	11.33*	3.52	1.37	8.21*	1.23	1.55	15.71*	1.78	3.29	20.52*	6.34	1.53	11.09*	1.28	0.5	5.34*	1.15
FD	0.017	0.032*	0.011	0.076*	0.031*	0.003	0.005	0.018*	0.007	0.003	0.041*	0.007	0.015	0.026*	0.007	0.005	0.024*	0.007
FW	3.79	11.62*	1.49	2.11	4.52*	0.72	5.22*	9.85*	0.58	1.88	3.96*	0.89	3.14	3.64*	0.95	0.06	2.73*	0.81
NSF	10	229.54*	81.96	11.2	104.76*	35.76	7.3	148.92*	60.08	327.03*	322.28*	79.51	68.43	99.34*	25.14	34.53	44.80*	18.09
NFP	2.23	8.23*	0.83	5.03*	3.27*	1.33	1.73	4.52*	1.47	2.53	4.87*	1.83	3.73	7.13*	0.21	1.6	4.09*	1.38
FYP	364.47	3339.36*	409.63	536.55	2490.76*	305.45	294.65	5373.44*	379.29	29.2	1695.75*	645.74	172.72	3760.70*	282.96	366.06	1749.69*	352.68
YVMV %	62.96	428.82*	123.99	328.13	380.73*	125.37	264.8	333.91*	127.69	30.49	143.8	129.46	96.88	406.43*	95.21	158.96	645.14*	72.53

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

REP = Replication, PRO = Progeny, ER = Error, DTF = Days to Flowering, PH = Plant Height, NBP = Number of branches per plant, NNMS = Number of nodes on main stem, IL = Internodal Length, FL = Fruit Length, FD = Fruit Diameter, FW = Fruit Weight, NSF = Number of seeds per fruit, NFP = Number of fruits per plant, FYP = Fruit yield per plant, YVMV % = YVMV percentage



Table 2. Contd.

Source	GJO-3 (20kR)			GJO-3 (30kR)			GJO-3 (40kR)			GJO-3 (0.15% EMS)			GJO-3 (0.25% EMS)			GJO-3 (CONTROL)		
	REP	PRO	ER	REP	PRO	ER	REP	PRO	ER	REP	PRO	ER	REP	PRO	ER	REP	PRO	ER
d.f	2	9	18	2	9	18	2	9	18	2	9	18	2	9	18	2	9	18
DTF	4.3	7.35*	2.26	6.53*	4.52*	1.64	10.00*	0.59	0.48	23.33*	0.59*	0.15	2.8	1.87	0.8	2.13	1.51*	0.61
PH	186.03	168.61*	67.33	13.33	331.79*	129.26	25.43	152.37*	58.4	5.73	98.22	49.96	10.43	114.55*	32.06	17.43	112.74*	23.84
NBP	0.63*	0.87*	0.15	0.13	1.04*	0.17	0.53	1.39*	0.46	0.4	0.90*	0.21	0.53	0.69*	0.27	0.13	0.36*	0.13
NNMS	0.93	2.83*	0.82	0.93	3.39*	0.53	8.40*	5.84*	2.1	8.93	7.24*	2.6	12.43*	5.28*	0.88	4.23	3.57*	1.38
IL	0.33	3.99*	1.03	1.44	2.81*	0.86	0.36	1.55*	0.27	0.23	1.48*	0.26	0.26	0.71*	0.19	0.13	0.77*	0.21
FL	3.22	2.96*	1.19	2.57*	4.97*	0.2	0.25	1.73*	0.57	3.65	3.03*	1.11	2.16	2.10*	0.82	14.27*	3.53*	1.07
FD	0.014	0.020*	0.005	0.006	0.015*	0.004	0.049*	0.037*	0.004	0.037	0.029*	0.011	0.013*	0.008*	0.003	0.016	0.027*	0.006
FW	0.32	3.78*	0.61	13.35*	4.22*	1.47	0.94	5.47*	2.16	0.52	2.51*	0.47	1.43	3.71*	0.6	6.2	5.44*	1.88
NSF	27.7	52.24*	17.85	18.63	165.57*	50.6	16.13	69.72*	21.65	46.8	40.53*	13.58	49.73*	43.63*	8.92	96.13*	47.17*	18.5
NFP	0.43	4.30*	0.77	0.4	3.39*	0.88	2.53	5.57*	1.57	3.03*	5.07*	0.29	0.93	4.76*	1.38	0.93	3.76*	0.9
FYP	72.83	2770.02*	298.75	2867.27*	1161.54*	353.78	43.85	1914.50*	583.82	932.19*	1437.43*	206.07	756.23	1466.54*	438.76	1202.54	2502.24*	653.05
YVMV %	195.24	223.56	209.04	258.48	306.34*	123.61	423.76*	498.41*	29.12	160.17	539.10*	168.39	42.63	265.75*	107.01	179.23	416.31*	154.27

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

Table 3. Genotypic coefficient of variability (GCV) for different characters in M₂ families in varieties GO - 2 and GJO - 3

Treatment	DTF	PH	NBP	NNMS	IL	FL	FD	FW	NSF	NFP	FYP	YVMV %
GO - 2												
20kR	2.3	6.03	19.46	6.99	8.44	9.91	4.99	15.41	10.72	10.31	17.23	37.71
30kR	1.53	7.1	16.2	8.28	9.29	9.58	5.98	10.13	7.07	5.21	15.66	25.5
40kR	1.86	7.12	21.86	8.83	6.19	14.74	3.73	13.02	8.46	6.57	19.57	21.66
0.15% EMS	2.29	8.17	11.45	6.83	7.97	13.29	6.63	7.8	14.57	6.6	9.44	6.86
0.25% EMS	1.91	7.01	13.18	8.12	9.5	11.54	4.72	7.91	7.8	10.03	18.65	52.25
Control	1.65	2.99	8.04	6.22	5.41	7.57	4.6	6.59	4.9	6.25	11.69	35.06
GJO - 3												
20kR	2.63	5.31	17.95	4.86	11.49	6	3.98	8.59	6.61	7.45	16.37	5.68
30kR	1.95	7.62	20.16	5.73	9.78	11.36	3.6	8.88	10.01	6.73	11.2	18.77
40kR	0.39	5.37	20.41	6.41	8.47	5.16	5.78	9.06	6.73	8.17	12.86	35.63
0.15% EMS	0.79	4.16	17.11	7.44	8.39	6.63	4.32	6.4	4.46	7.87	9.8	26.76
0.25% EMS	1.21	5.14	13.07	6.79	5.52	5.78	2.32	7.84	5.26	6.44	8.66	27.42
Control	1.13	5.17	9.96	5.06	5.38	7.28	4.76	8.73	5.05	6.21	12.62	18.13

DTF = Days to Flowering, PH = Plant Height, NBP = Number of branches per plant, NNMS = Number of nodes on main stem, IL = Internodal Length, FL = Fruit Length, FD = Fruit Diameter, FW = Fruit Weight, NSF = Number of seeds per fruit, NFP = Number of fruits per plant, FYP = Fruit yield per plant, YVMV % = YVMV percentage



Table 4. Heritability (broad sense) for different characters in M₂ families in varieties GO - 2 and GJO - 3

Treatment	DTF	PH	NBP	NNMS	IL	FL	FD	FW	NSF	NFP	FYP	YVMV %
GO - 2												
20kR	55.8	41.29	42.86	35.24	49.44	42.56	38.46	69.45	37.51	74.92	70.45	45.04
30kR	44.57	52.25	45.52	50.3	44.57	65.4	75.01	63.67	39.15	32.77	70.46	40.44
40kR	42.83	50.83	57.22	55.56	33.14	72.27	33.06	84.21	33.02	40.77	81.44	34.99
0.15% EMS	36.47	40.16	36.56	35.71	54.42	42.73	62.91	53.61	50.44	35.68	35.15	3.56
0.25% EMS	36.87	33.05	51.65	58.55	38.22	71.95	46.17	48.55	49.6	91.47	80.38	52.14
Control	64.06	37.79	37.84	38.14	44.37	54.77	43	44.03	32.99	39.61	56.9	72.46
GJO - 3												
20kR	42.84	33.4	61.32	44.91	49.02	33.23	52.76	63.22	39.11	60.57	73.39	2.26
30kR	36.84	34.31	62.9	64.5	42.94	88.74	47.93	38.29	43.1	48.71	43.22	33.01
40kR	7.14	34.91	40.38	37.17	61.72	40.07	71.49	33.87	42.53	45.92	43.17	84.31
0.15% EMS	50	24.36	51.67	37.32	61.33	36.48	35.41	59.09	39.82	84.48	66.58	42.32
0.25% EMS	30.77	46.17	33.33	62.56	47.35	34.29	34.76	63.37	56.47	44.97	43.85	33.09
Control	32.79	55.42	35.71	34.56	47.66	43.31	53.13	38.7	34.05	51.6	48.56	36.15

DTF = Days to Flowering, PH = Plant Height, NBP = Number of branches per plant, NNMS = Number of nodes on main stem, IL = Internodal Length, FL = Fruit Length, FD = Fruit Diameter, FW = Fruit Weight, NSF = Number of seeds per fruit, NFP = Number of fruits per plant, FYP = Fruit yield per plant, YVMV % = YVMV percentage

Table 5. Genetic advance (%) for different characters in M₂ families in varieties GO - 2 and GJO - 3

Treatment	DTF	PH	NBP	NNMS	IL	FL	FD	FW	NSF	NFP	FYP	YVMV %
GO - 2												
20kR	3.54	7.98	26.24	8.55	12.22	13.32	6.37	26.45	13.53	18.38	29.79	52.13
30kR	2.1	10.57	22.52	12.09	12.78	15.96	10.66	16.65	9.12	6.14	27.07	33.4
40kR	2.5	10.46	34.06	13.55	7.34	25.81	4.42	24.61	10.02	8.64	36.38	26.39
0.15% EMS	2.85	10.66	14.26	8.41	12.11	17.9	10.83	11.76	21.32	8.12	11.52	2.67
0.25% EMS	2.38	8.3	19.51	12.79	12.1	20.17	6.6	11.35	11.31	19.76	34.44	77.72
Control	2.72	3.79	10.18	7.91	7.42	11.54	6.21	9.01	5.79	8.11	18.16	61.48
GJO - 3												
20kR	3.55	6.32	28.96	6.71	16.57	7.13	5.95	14.08	8.52	11.94	28.88	1.76
30kR	2.44	9.19	32.93	9.48	13.2	22.04	5.13	11.32	13.54	9.67	15.16	22.21
40kR	0.22	6.54	26.71	8.05	13.7	6.73	10.07	10.86	9.04	11.4	17.4	67.4
0.15% EMS	1.15	4.23	25.34	9.36	13.54	8.25	5.3	10.14	5.8	14.9	16.48	35.86
0.25% EMS	1.38	7.19	15.54	11.06	7.83	6.97	2.82	12.86	8.14	8.9	11.82	32.49
Control	1.34	7.93	12.26	6.13	7.65	9.87	7.15	11.19	6.07	9.19	18.12	22.45

DTF = Days to Flowering, PH = Plant Height, NBP = Number of branches per plant, NNMS = Number of nodes on main stem, IL = Internodal Length, FL = Fruit Length, FD = Fruit Diameter, FW = Fruit Weight, NSF = Number of seeds per fruit, NFP = Number of fruits per plant, FYP = Fruit yield per plant, YVMV % = YVMV percentage