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STUDIES ON INDUCED MICRO-MUTATIONS IN SESAME (*SESAMUM INDICUM* L.)

C. Praveen Sampath Kumar, C. K. Shivaganeshindirajith and S. Thirugnanakumar

Dept. of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar-608 002 (T.N.)

Abstract

Studies on induced micro mutants in sesame (*Sesamum indicum* L.) genotype TMV4 was conducted with gamma rays at 2.5kR, 5.0kR, 10.0kR, 12.5kR, 15.0kR, 17.5kR, 20.0kR, 22.5kR, 25.0kR, 27.5kR, 30.0kR and 32.5kR. Studies on induced genetic variations owing to micromutations in nine different quantitatively inherited characters *viz.,* days to first flowering, plant height at maturity, number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight, seed yield per plant, pollen fertility and seed fertility. It revealed that the mean was shifted to both positive and negative directions. Thus, the extent of genetic variations and genetic variance were widened.

As evident from the genotypic coefficient of variations plant height at maturity was highly responding character. 1000 seed weight, pollen fertility and seed yield per plant were the least responding character. Gamma rays at 2.5kR, 5.0kR, 7.5kR, 15.0kR, 20.0kR, 22.5kR and 25.0kR for the trait plant height at maturity induced and released additive genetic variability. These mutagenic treatments could well be recommended for the induction of useful micromutation in sesame genotype TMV 4.

Key words : Gamma rays, M_3 generation, Sesame.

Introduction

The extent of genetic variability available in the breeding population and the selection techniques determine the efficiency in any breeding programme. In conventional plant breeding programme, variation is generated by hybridization and selections are made from the resulting segregating generations. Induced mutagenesis can either supplement hybridization or replace as a source of variability. Thus, mutation provides the raw material for evolution (Mahadeva and Randerson, 1982) and it provides the fundamental variability required for plant improvement by breeding (Konzak, 1984). Mutation breeding technique may have a greater role in self pollinated crops like, sesame (*Sesamum indicum* L.), where a large part of natural variation may have been eliminated in the process of adaptation. Sesame in India has received relatively little attention from the view of their genetic improvement due to various reasons. Experimental mutagenesis is an effective method to enlarge genetically conditioned variation considerably, within a short time. Much attention is now directed towards inducing micromutations involving quantitative traits, so as to bring in directional selection by appropriate selection of ideal and proper combinations of quantitative traits to maximise the yielding ability. The study demonstrated that sesame is an excellent material for studying the experimental mutagenesis and gene action. The present investigation "studies on induced micromutations in sesame (*Sesame indicum* L.)" genotype TMV 4 was carried out with physical (Gamma rays) mutagens.

Materials and methods

The seed material of sesame (*Sesamum indicum* L.) genotype TMV 4 was chosen for the present study. Handpicked uniform capsules from main stem were chosen. The capsules were hand threshed and cleaned. Plumpy, uniform and sound seeds were used for the mutagenic treatments. The moisture content of seeds was 8.5 per cent. Gamma rays (ionizing radiations) represented the physical mutagen of the present study. Gamma rays irradiation was performed in Gamma rays chamber installed at the Centre for Plant Breeding and Genetics, TNAU, Coimbatore exposing the seeds to Gamma rays from ^{60}CO source.

A sample of 300 seeds per treatment was packed in butter-paper covers and placed in the 1000 curie ^{60}CO Gamma cell. The treatments were given for various

duration depending on the doses required. The doses adopted were 2.5 to 32.5 kR. Non-irradiated dry seeds were used as the control.

Sixty seeds from each of the treatment along with the control were sown in Randomized Block Design replicated thrice. The seeds gathered from the seven randomly selected normal looking M_1 plants were forwarded for the study of M_2 generation. Five M_2 plants were selected at random from each M_2 family in all the treatments replication-wise, including the control were forwarded for the study of M_3 generation. A single M_2 plant formed a single family in M_3 generation. The lay out was a randomized block design replicated thrice. Each family was raised in a three row plots of 4.5 m length. The seeds were sown with a spacing of 30 cm × 15 cm. Five M_3 plants were selected at random from each M_3 family in all the treatments replication-wise, including the control. Observations were recorded on the following characters *viz.*, days to first flowering, plant height at maturity, number of branches per plant, number of capsules per plants, number of seeds per capsule, 1000 Seed weight, seed yield per plant, pollen fertility and seed fertility. Standard statistical methods were adopted.

Results and discussion

The induction of micro-mutations in M_3 generation was measured in terms of mean and variance. Broad sense heritability and the expected genetic gain through selection in the mutated population were also computed. The means of the different treatments were observed on either sides of the control representing a bi-directional distribution of the mutated loci. Perhaps each treatment might have acted on a different gene or block of genes which are involved in the genetic pathway determining the morphogenetic potentiality of the exophenotypes.

Table 1: Components of variance for days to first flowering in M_3 generation

T. No.	Treatments (kR)	Mean ± SE	$\sigma^2 g$	h^2 (%)	GA as % over mean (%)
T_1	2.5	35.90 ± 0.49	0.76	1.11	0.15
T_2	5.0	37.19 ± 0.61	2.09	25.10	4.01
T_3	7.5	36.38 ± 0.70	8.62	74.55	14.36
T_4	10.0	37.66 ± 0.50	0.25	16.03	1.09
T_5	12.5	37.57 ± 0.58	4.24	55.15	8.39
T_6	15.0	37.76 ± 0.66	6.16	59.86	10.48
T_7	17.5	37.85 ± 0.55	3.65	52.27	7.52
T_8	20.0	37.95 ± 0.53	5.29	84.86	11.50
T_9	22.5	38.19 ± 0.46	3.63	82.97	9.36
T_{10}	25.0	38.14 ± 0.48	4.81	93.08	11.41
T_{11}	27.5	36.85 ± 0.64	3.56	40.58	6.91
T_{12}	30.0	37.14 ± 0.48	3.48	71.04	9.97
T_{13}	32.5	38.42 ± 0.49	0.84	17.38	2.04
T_{14}	Control	37.14 ± 0.55			

Table 2: Components of variance for plant height at maturity in M_3 generation

T. No.	Treatments (kR)	Mean ± SE	$\sigma^2 g$	h^2 (%)	GA as % over mean (%)
T_1	2.5	54.80 ± 3.05	177.7	84.26	46.44
T_2	5.0	60.88 ± 3.01	137.7	71.24	33.52
T_3	7.5	62.91 ± 2.85	165.4	87.27	39.34
T_4	10.0	81.64 ± 1.70	1.94	14.01	1.24
T_5	12.5	79.15 ± 1.99	32.86	36.66	9.03
T_6	15.0	74.45 ± 2.84	133.54	71.27	26.99
T_7	17.5	86.14 ± 0.83	3.65	52.27	7.52
T_8	20.0	76.68 ± 3.01	127.19	62.68	23.98
T_9	22.5	65.16 ± 2.52	126.08	85.90	32.89
T_{10}	25.0	64.71 ± 2.81	167.12	93.47	39.78
T_{11}	27.5	64.21 ± 2.19	1.19	32.33	1.63
T_{12}	30.0	78.27 ± 1.84	24.13	31.10	7.20
T_{13}	32.5	81.50 ± 1.48	39.58	78.99	14.13
T_{14}	Control	74.37 ± 1.79			

Table 3: Components of variance for number of branches per plant in M_3 generation

T. No.	Treatments (kR)	Mean ± SE	$\sigma^2 g$	h^2 (%)	GA as % over mean (%)
T_1	2.5	4.95 ± 0.28	0.40	24.06	12.97
T_2	5.0	5.00 ± 0.32	0.07	41.73	3.08
T_3	7.5	4.66 ± 0.26	0.38	35.00	16.28
T_4	10.0	5.00 ± 0.29	0.23	13.16	7.29
T_5	12.5	5.38 ± 0.20	0.15	19.00	6.48
T_6	15.0	5.47 ± 0.21	0.18	16.91	6.72
T_7	17.5	4.61 ± 0.22	0.13	16.67	6.42
T_8	20.0	5.42 ± 0.20	0.23	26.32	9.41
T_9	22.5	5.38 ± 0.20	0.21	25.47	8.94
T_{10}	25.0	5.04 ± 0.24	0.14	10.84	5.07
T_{11}	27.5	5.23 ± 0.19	0.19	19.23	7.75
T_{12}	30.0	5.33 ± 0.22	0.11	10.00	4.07
T_{13}	32.5	4.95 ± 0.21	0.07	6.08	2.47
T_{14}	Control	4.95 ± 0.22			

Yield is the end product. It does not possess gene *per se* as such. The *per se* performance was less compared to the control. It may be due to the negative complementation among the unfavourably mutated alleles of the component characters. A similar trend was also observed by Suresh (1975) in green gram; Nadarajan *et al.* (1983) in redgram and Arun Kumar (2011) in sesame.

The genetic changes in quantitative characters induced were realized by the increased genetic variance among progenies in M_3 generation. The extent of induced

Table 4: Components of variance for number of capsules per plants in M_3 generation

T. No.	Treatments (kR)	Mean ± SE	σ^2g	h^2 (%)	GA as % over mean (%)
T_1	2.5	34.66±0.53	1.25	21.12	3.05
T_2	5.0	34.76 ± 0.66	1.66	9.41	6.96
T_3	7.5	33.80±0.65	0.60	8.28	3.70
T_4	10.0	34.09± 0.46	0.13	2.52	0.23
T_5	12.5	33.90 ± 0.52	1.24	10.36	5.93
T_6	15.0	35.04 ± 0.54	2.18	16.61	8.63
T_7	17.5	35.09 ± 0.65	1.08	13.95	2.28
T_8	20.0	35.90± 0.64	2.82	29.87	12.39
T_9	22.5	35.23 ± 0.64	3.63	37.91	6.86
T_{10}	25.0	35.33± 0.60	1.78	21.47	3.60
T_{11}	27.5	34.76 ± 0.71	1.92	11.20	7.09
T_{12}	30.0	35.66± 0.63	4.81	56.10	9.49
T_{13}	32.5	36.04± 0.80	6.73	44.22	9.86
T_{14}	Control	35.00 ± 0.75			

Table 5: Components of variance for number of seeds per capsule in M_3 generation

T. No.	Treatments (kR)	Mean ± SE	σ^2g	h^2 (%)	GA as % over mean (%)
T_1	2.5	38.66 ± 0.50	4.05	68.87	8.90
T_2	5.0	37.09 ± 0.41	0.34	9.13	0.99
T_3	7.5	37.57 ± 0.29	0.05	3.40	0.23
T_4	10.0	38.28 ± 0.49	1.45	31.40	3.56
T_5	12.5	37.85 ± 0.41	2.39	62.14	6.64
T_6	15.0	37.23 ± 0.46	2.70	55.36	6.77
T_7	17.5	37.57 ± 0.47	3.01	57.23	7.20
T_8	20.0	37.95± 0.48	4.23	80.91	10.05
T_9	22.5	36.85 ± 0.43	2.47	61.42	6.89
T_{10}	25.0	36.23± 0.54	3.90	57.21	8.49
T_{11}	27.5	35.52 ± 0.50	1.04	15.90	1.78
T_{12}	30.0	35.16 ± 0.43	0.90	25	3.05
T_{13}	32.5	36.00 ± 0.34	1.18	30.66	3.45
T_{14}	Control	39.14 ± 0.34			

Table 6: Components of variance for 1000 Seed weight in M_3 generation

T. No.	Treatments (kR)	Mean ± SE	σ^2g	h^2 (%)	GA as % over mean (%)
T_1	2.5	2.90 ± 0.009	0.0003	20.70	0.55
T_2	5.0	3.02 ± 0.03	0.0002	10.01	0.28
T_3	7.5	2.84 ± 0.02	0.003	28.97	0.71
T_4	10.0	2.82 ± 0.02	0.0003	24.40	0.66
T_5	12.5	2.94 ± 0.007	0.00	9.2	0.22
T_6	15.0	2.86 ± 0.01	0.009	38.17	1.35
T_7	17.5	2.91 ± 0.01	0.002	44.33	2.18
T_8	20.0	2.89 ± 0.18	0.004	54.68	3.31
T_9	22.5	2.86 ± 0.01	0.0038	58.85	3.42
T_{10}	25.0	2.92 ± 0.02	0.016	88.56	8.42
T_{11}	27.5	2.86 ± 0.02	0.0002	5.51	0.23
T_{12}	30.0	2.88 ± 0.02	0.002	28.25	1.96
T_{13}	32.5	2.88 ± 0.019	0.0039	52.44	3.23
T_{14}	Control	2.90 ± 0.014			

Table 7: Components of variance for seed yield per plant in M_3 generation

T. No.	Treatments (kR)	Mean ± SE	σ^2g	h^2 (%)	GA as % over mean (%)
T_1	2.5	3.92 ± 0.07	0.25	6.61	1.53
T_2	5.0	3.92 ± 0.12	0.17	33.17	2.62
T_3	7.5	3.66 ± 0.08	0.08	11.16	1.06
T_4	10.0	3.75 ± 0.07	0.36	47.50	4.38
T_5	12.5	4.73 ± 0.92	0.07	9.60	0.87
T_6	15.0	3.76 ± 0.07	0.26	31.73	3.09
T_7	17.5	3.82 ± 0.07	0.65	46.36	5.82
T_8	20.0	3.91 ± 0.11	0.53	48.86	5.44
T_9	22.5	3.69±0.12	0.09	5.85	0.77
T_{10}	25.0	3.82 ± 0.11	0.27	33.23	3.20
T_{11}	27.5	19.10 ± 0.25	0.51	68.77	6.44
T_{12}	30.0	3.8 ± 0.11	0.21	35.53	2.95
T_{13}	32.5	20.81 ± 0.28	0.42	59.27	4.44
T_{14}	Control	3.96 ± 0.09			

genotypic variation was as high as 177.7 (at 2.5 kR) for plant height at maturity. 1000 seed weight showed the least genotypic variation (0.0002 at 5.0kR). Rawlings *et al.* (1958) had stated that the changes induced by the mutagens in chromosomes or the treated population and this could be the cause for the extended genetic variation observed in M_3 generation. The least genotypic variance observed for 1000 seed weight also confirmed the dispersion of the mutated alleles in and around the central mean.

The broad sense heritability estimates showed maximum for plant height at maturity (93.47 per cent at 25 kR), days to first flowering (93.08 per cent at 25 kR), 1000 seed weight (88.56 per cent at 25kR) and plant height at maturity (87.27 per cent at 7.5kR). Estimated genetic gain was as high as 46.44 per cent for plant height at maturity at 2.5kR.

In the present study, no consistent relationship could be evidenced between the dose of the mutagens and the observed genetic variability, heritability and genetic advance. The higher values of predicted heritability and genetic advance suggested that the mutations might have mostly involved the loci having additive effects. Brock (1965) has hypothesized that mutation will occur in the direction that it opposite to the previous selection history. In the present study, the test object TMV 4 was selected

Table 8: Components of variance for pollen fertility in M_3 generation

T. No.	Treatments (kR)	Mean ± SE	$\sigma^2 g$	h^2 (%)	GA as % over mean (%)
T_1	2.5	59.45 ± 0.87	4.40	26.54	3.74
T_2	5.0	67.11 ± 0.39	3.48	63.81	2.20
T_3	7.5	74.91 ± 0.57	0.10	1.62	0.11
T_4	10.0	75.80 ± 0.61	3.27	23.81	2.46
T_5	12.5	77.29 ± 0.69	6.62	61.61	5.38
T_6	15.0	77.64 ± 0.25	0.96	72.78	2.22
T_7	17.5	77.39 ± 0.50	0.29	8.35	0.41
T_8	20.0	75.75 ± 0.40	0.06	2.38	0.10
T_9	22.5	76.02±0.79	0.19	8.73	0.27
T_{10}	25.0	75.53 ± 0.64	0.34	10.48	0.40
T_{11}	27.5	75.49 ± 0.76	1.80	31.74	1.63
T_{12}	30.0	74.80 ± 0.79	4.79	39.20	3.77
T_{13}	32.5	75.86 ± 0.67	3.43	33.16	2.89
T_{14}	Control	71.64 0.72			

Table 9: Components of variance for seed fertility in M_3 generation

T. No.	Treatments (kR)	Mean ± SE	$\sigma^2 g$	h^2 (%)	GA as % over mean (%)
T_1	2.5	65.02 ± 0.66	0.54	35.8	1.51
T_2	5.0	72.31 ± 0.53	1.66	25.37	1.08
T_3	7.5	77.59± 0.42	0.35	13.88	0.58
T_4	10.0	74.52± 0.61	17.05	37.97	7.24
T_5	12.5	75.10 ± 0.77	2.40	15.78	1.44
T_6	15.0	75.86 ± 0.76	4.78	26.33	2.70
T_7	17.5	74.41 ± 0.73	16.8	60.80	7.54
T_8	20.0	74.53 ± 0.64	3.68	39.05	3.31
T_9	22.5	75.74 ± 1.04	2.56	10.50	1.41
T_{10}	25.0	74.05 ± 0.51	3.80	29.09	2.54
T_{11}	27.5	73.45 ± 0.58	3.39	34.34	2.81
T_{12}	30.0	73.96± 0.65	1.53	20.70	1.57
T_{13}	32.5	73.17± 0.47	1.13	24.72	1.49
T_{14}	Control	76.44 ± 0.43			

and released for higher see yield. And hence, it was in negative direction, in general. However, the observed higher mean seed yield with the treatments *viz.*, 12.5 kR, 27.5 kR and 23.5 kR added further scope for selection for seed yield. However, the enlarged genetic variability, heritability and genetic gain offer a wider scope for further selection. Among the nine quantitative traits studied, plant height at maturity was the highly responding character. 1000 seed weight was the least responding character. It may be concluded that the variety TMV 4 of sesame can be improved upon by selecting for the plant height at maturity.

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