



Research Article

# Gamma ray induced early generation polygenic variability in medium grain aromatic non-basmati rice

<sup>1\*</sup>Nihar Ranjan Chakraborty and <sup>2</sup>Paresh Chandra Kole

<sup>1\*,2</sup> Department of Crop Improvement, Horticulture & Agril. Botany, Institute of Agriculture, Visva-Bharati, Sriniketan-731 236, West Bengal, India

Two advanced breeding lines of aromatic non-basmati rice, IET 14142 and IET 14143, irradiated with 250Gy, 350Gy and 450Gy of gamma ray induced wide variation for polygenic characters in M<sub>2</sub> and M<sub>3</sub> generations. Wide range of genotypic and phenotypic coefficients of variation (GCV and PCV) for different characters indicated differential radio-sensitivity of the characters. Increase in values of GCV and PCV in M<sub>3</sub> over M<sub>2</sub> generation for flag leaf length and spikelet number was due to “release of additional variability”. Heritability in M<sub>3</sub> generation increased over M<sub>2</sub> in IET 14142 for days to flower and flag leaf angle at all three doses, and for other characters only at certain doses. The genetic advance increased from M<sub>2</sub> to M<sub>3</sub> in IET 14142 for some characters due to increase in variance, while it decreased in M<sub>3</sub> generation in IET 14143 for certain characters due to increase in mean values. The overall results indicated the scope for isolating promising segregants in micro mutational population even in early generations.

**Key words:** Aromatic rice, gamma irradiation, micromutation, M<sub>2</sub> and M<sub>3</sub> generations, selection, variability

## INTRODUCTION

Aromatic rice occupies a special place in World rice markets, being the highest priced rice due to fine appealing flavour it produces during cooking and in the cooked rice. The leading aromatic rice in world trade is ‘Basmati’ produced in Punjab area along both sides of the Indus River in India and Pakistan. But, in West Bengal, an important rice growing state in India, performance of ‘Basmati’ varieties is not satisfactory due to high humid conditions along with heavy infestation of insect-pests. Moreover, ‘Basmati’ varieties, when grown in West Bengal, produce grains with reduced aroma than they do in traditional Basmati growing zones of northwestern India. Hence, some non-basmati aromatic rice cultivars such as Tulaipanja, Gobindabhog, Seetabhog, Kaminibhog, Gopalbhog, Radhunipagol etc., are very popular in West Bengal. Although these varieties have excellent grain quality and appealing aroma, they are not recognized as ‘Basmati’ rice due to their small to medium grain size. In addition, these cultivars are handicapped by low yield potential (2.5 to 3.0 t/ha),

susceptibility to lodging due to very tall and less sturdy stem and droopy leaves. Farmers are reluctant to replace these varieties because of their excellent grain quality, aroma, high premium market price, and export to Middle East countries. Besides, the demand for high grain-quality rice in India is on increase due to rising standard of living and to promote export. Therefore, there is an urgent need to improve the yield potential of such aromatic non-Basmati rice cultivars.

**Corresponding author:** Dr. Nihar Ranjan Chakraborty, Department of Crop Improvement, Horticulture & Agril. Botany, Institute of Agriculture, Visva-Bharati, Sriniketan-731 236, West Bengal, India, Email: nrchakraborty@gmail.com, +91-9434559884

The complex nature of the quality characters and the complicated inheritance of the quality components make it very difficult to retain the quality characteristics of aromatic rice through hybridization with non-aromatic high yielding genotypes. Alternatively, induced mutations provide for an important source of genetic variability. Sigurbjornsson and Micke (1974) have shown the increasing role of induced mutation in crop improvement. It has been demonstrated that induced mutation, being able to induce even polygenic mutation, can be useful in improving yield as well as other agronomic characters such as stiffness of straw, time of maturity, adaptability, disease resistance, protein content, baking quality, malting quality and numerous other characters (Borojevic, 1990 and Brunner, 1991) in addition to quick rectification of defects in varieties and advanced breeding lines, and development of ideotypes for various agro-climatic conditions.

Even though the frequency of desirable mutation is very low; the occurrence of even a few desirable mutations could be exploited to isolate superior genotypes in a couple of generations. Mutation breeding has been very successful worldwide in different crops including rice. A great majority of directly developed mutant varieties were obtained with the use of radiations, particularly gamma rays as mutagen (Kharkwal *et al.*, 2004).

Keeping these points in view, gamma ray mutagenesis in two non-basmati aromatic rice genotypes was carried out to study magnitude and nature of variability, heritability and genetic advance for different characters besides determining the generation in which high degree of genetic variation is expected.

## MATERIAL AND METHODS

The seeds of two semi-dwarf medium grain non-basmati lines *viz.*, IET 14142 (designated as T<sub>1</sub>) and IET 14143 (designated as T<sub>2</sub>) derived from aromatic rice cultivar Tulaipanja were irradiated with three different doses of gamma rays *viz.*, 250Gy, 350Gy and 450Gy (1 Gray = 1 joule per kg of matter undergoing irradiation = 0.1 kR) from <sup>60</sup>Co source at Central Research Institute for Jute and Allied Fibre (CRIJAF), Barrackpore, West Bengal. The seeds unexposed to radiation from each genotype were used as control. Seeds from bagged panicles of suspected mutant plants in M<sub>1</sub> generation were sown in nursery bed to raise M<sub>2</sub> generation. Thirty-day-old seedlings from each of those nursery beds, where at least one type of chlorophyll mutation occurred, were transplanted in puddled field as progeny-row with one seedling per hill. Total number of M<sub>2</sub> families planted was 142 for T<sub>1</sub> and 112 for T<sub>2</sub>. Each family consisted of two rows of fifteen plants each with a spacing of 15 × 20 cm. The M<sub>2</sub> populations were thoroughly screened for segregation of chlorophyll and other mutations based on

visual observation. M<sub>3</sub> generation was raised from the seeds of ten randomly selected M<sub>2</sub> mutant plants showing segregation in the progeny-row. Therefore, in all, 60 plants (2 genotypes × 3 doses × 10 plants) were selected in M<sub>2</sub> generation, which were advanced to M<sub>3</sub> generation. The above selected 60 M<sub>2</sub> plants were tested for aroma (Singh *et al.*, 1986). Thirty-day-old M<sub>3</sub> seedlings from nursery @ one seedling per hill were transplanted in compact family block design along with control with three replications. A mutant family plot consisted of three rows of fifteen plants each with a spacing of 15 × 20 cm.

Standard cultural practices were followed to raise a good healthy crop in both the generations. Data on following quantitative characters *viz.*, days to flower, flag leaf angle, flag leaf length(cm), plant height(cm), panicle number, panicle length, spikelet number, grain number, grain yield per plant(gm) were recorded from the five plants selected at random. Data were analysed following standard statistical and biometrical methods (Burton, 1952; Johnson *et al.*, 1955; Snedecor and Cochran, 1967)

## RESULTS AND DISCUSSION

### Polygenic variation in M<sub>2</sub> and M<sub>3</sub> generations

Analyses of variance for between families and within families of induced mutants derived from each genotype for different polygenic characters indicated that the mean sum of squares due to between families for all the characters were highly significant in both M<sub>2</sub> and M<sub>3</sub> indicating the induction of genetic variability through irradiation (Table 1 and 2). Wide variability for different characters observed within different mutant families in comparison to control might be accounted for by the accumulation of micromutations through segregation of mutant genes.

The mutagenic treatments induced wider range of values (Table 3) compared with control (positive or negative direction) for all the economic characters in M<sub>2</sub> generation. In this regard, high doses of gamma ray (350Gy and 450Gy) deserve a special mention for inducing wide variability particularly for flag leaf angle, plant height, spikelet number, grain number and grain yield. However, in general, the mean values of M<sub>2</sub> families for days to flower, flag leaf length, plant height, panicle number, panicle length, spikelet number per panicle, grain number per panicle and grain yield per plant did not deviate substantially from that of respective control population. But, there was an increase in mean values of grain number per panicle and grain yield per plant at 450Gy in T<sub>1</sub>; spikelet number and grain number per panicle at 250Gy and 350Gy and grain yield per plant at 250Gy in T<sub>2</sub>. The negative shift in the mean values was

**Table 1. ANOVA for between and within families in M<sub>2</sub> generation for nine characters in four aromatic rice genotypes in three treatments**

<b>T<sub>1</sub> genotype</b>										
Source	df	Days to flower	Flag leaf angle	Flag leaf length	Plant height	Panicle number	Panicle length	Spikelet number	Grain number	Grain yield
<b>250Gy</b>										
Between families	28	18.44*	124.74**	65.13**	726.86*	68.28*	41.33**	1574.30*	1165.20**	92.14**
Within families	116	10.43	60.14	24.9	375.1	44.14	17.94	620.49	443.28	21.48
<b>350Gy</b>										
Between families	20	25.29**	67.09**	18.27**	541.93*	28.16*	22.99*	2212.80**	1282.70**	53.38**
Within families	84	11.42	28.73	4.02	225.6	14.36	11.48	772.48	450.8	22.33
<b>450Gy</b>										
Between families	28	43.80*	94.93**	14.19**	854.62**	48.26**	33.78**	1989.20**	1154.30**	69.94*
Within families	116	11.99	51.1	4.57	334.29	18.54	8.44	843.47	564.27	31.20
<b>T<sub>2</sub> genotype</b>										
<b>250Gy</b>										
Between families	15	29.77*	39.65*	32.34*	1488.40*	14.38*	19.99*	1414.80*	1382.60**	92.28*
Within families	64	14.89	21.84	11.67	444.05	5.42	9.79	630.8	429.26	42.45
<b>350Gy</b>										
Between families	10	77.46**	90.93*	46.88**	1387.40*	21.81*	25.98**	1328.80*	1189.70*	127.03*
Within families	44	19.72	44.36	11.26	621.81	9.26	8.55	648.39	584.13	46.85
<b>450Gy</b>										
Between families	7	51.54**	31.76*	37.31*	1679.60*	15.43*	14.48*	1354.40*	995.26*	48.67**
Within families	32	16.33	12.59	12.49	580.08	6.69	6.2	547.06	413.57	20.84

**Table 2. ANOVA for between and within families in M<sub>3</sub> generation for nine characters in four aromatic rice genotypes in three treatments**

<b>T<sub>1</sub> genotype</b>										
Source	df	Days to flower	Flag leaf angle	Flag leaf length	Plant height	Panicle number	Panicle length	Spikelet number	Grain number	Grain yield
<b>250Gy</b>										
Between families	9	98.56**	123.96**	45.04*	625.83**	82.85*	14.32*	1886.60**	1366.20*	96.96**
Within families	140	7.82	7.19	18.66	224.53	38.34	6.21	581.7	656.45	21.28
<b>350Gy</b>										
Between families	9	74.05**	71.78**	51.11*	529.77**	50.78**	23.90**	2087.30**	742.26**	39.46**
Within families	140	1.99	9.38	22.28	131.69	22.25	5.98	645.72	225.25	13.67
<b>450Gy</b>										
Between families	9	58.80**	82.67**	86.62**	461.59**	60.78*	30.55**	2317.30*	1266.10*	51.09*
Within families	140	1.46	13.38	31.75	151.17	28.03	8.49	1091.34	515.86	19.85
<b>T<sub>2</sub> genotype</b>										
<b>250Gy</b>										
Between families	9	30.45**	38.24**	56.92**	645.59**	12.88*	13.49*	1222.60**	789.22*	88.26**
Within families	140	1.52	12.69	17.12	211.02	5.21	5.64	470.82	342.99	34.48
<b>350Gy</b>										
Between families	9	28.37**	35.26**	36.36**	575.94**	14.02*	17.77*	1897.90**	1185.00**	59.37*
Within families	140	2.09	11.05	11.37	189.1	6.16	7.53	444.25	469.09	26.86
<b>450Gy</b>										
Between families	9	40.29**	42.09*	40.36**	592.03**	12.32*	16.18*	1676.10**	972.76**	78.59**
Within families	140	1.6	18.36	12.87	197.94	5.39	6.34	487.99	428.92	19.33

\*, \*\* Significant at P = 0.05 , 0.01 respectively

observed for flag leaf angle at all three doses in both genotypes.

Gopinathan Nair (1972) reported that the mean values for various quantitative characters in rice were not altered significantly following treatments with radiations. The

mean of the treated population tended to shift away from that of control either in the negative or in the positive direction. Similar results have been recorded by Madhusudana Rao and Siddiq (1976). The positive shifts in mean of different characters over control values may

be attributed to the induction of a higher proportion of positive mutations than the negative ones.

All the selected 60 M<sub>2</sub> plants were aromatic and testing of 25 M<sub>3</sub> seeds from each of the 60 M<sub>2</sub> plants indicated true-breeding nature of aroma. This is expected as aroma in this group of rice is controlled by a single recessive gene pair (Kole, 2005). Moreover, chances of obtaining non-aromatic plants in mutated population are less, because frequency of dominant mutation, in general, is less.

In M<sub>3</sub> generation, wide range of variation (Table 3) among different mutant families derived from a radiation dose was observed for all the polygenic characters in both the genotypes. However, variation within some mutant families decreased over M<sub>2</sub> generation due to increase in homozygosity.

Flag leaf angle at all three doses in both genotypes showed lower mean than control in M<sub>3</sub>. The mean values of spikelet number, grain number and grain yield per plant at all doses of gamma radiation in both genotypes were higher than their respective control. The shift in mean of characters in M<sub>3</sub> could be due to the elimination of detrimental effects through selfing in M<sub>2</sub>.

#### Phenotypic and Genotypic Coefficients of Variation (PCV and GCV)

The highest estimates of PCV (39.58 to 61.81%) and GCV (33.16 to 54.13%) were observed in grain yield in both T<sub>1</sub> and T<sub>2</sub> genotypes in M<sub>2</sub> generation as well as M<sub>3</sub> generation across the three doses (Table 4) followed by flag leaf angle while, lowest estimates were observed for days to flower (2.18% to 7.36%). These estimates, in general, were high in M<sub>2</sub> generation as expected, which was particularly so in T<sub>2</sub> mutants. However, PCV and GCV increased in M<sub>3</sub> generation in mutant families of T<sub>1</sub> for days to flower, flag leaf angle and panicle number in all doses indicating the presence of hidden variability in M<sub>2</sub> generation. Thus it might be better to wait till M<sub>3</sub> generation to start practicing selection for these characters. Besides, five out of remaining six characters showed increase in these estimates at 450Gy.

In addition, the values of GCV and PCV were high (>20%) for flag leaf angle, spikelet number, panicle number and grain number per panicle in both T<sub>1</sub> and T<sub>2</sub> mutant families in both M<sub>2</sub> and M<sub>3</sub> generations at all three doses. For flag leaf length, GCV and PCV were high at all the three doses in M<sub>3</sub> generation in both T<sub>1</sub> and T<sub>2</sub> (except at 350Gy). High estimates of GCV and PCV at 450Gy in both generations were observed in T<sub>1</sub> for panicle length, which showed moderate values at the remaining doses and in T<sub>2</sub>. For plant height, high PCV were observed in mutants of both genotypes in both generations while high GCV were observed in M<sub>2</sub> generation among T<sub>2</sub> mutants only. Remaining character and dose combinations showed moderate GCV and PCV.

Similar results with high GCV and PCV values for flag leaf angle (Basak and Ganguli, 1996), panicle number

(Hasib and Kole, 2004), spikelet number (Hasib, 2005), grain number (Kole and Hasib, 2003; Hasib and Kole, 2004) and grain yield (Kole and Hasib, 2003; Hasib and Kole, 2004; Hasib, 2005) were reported earlier.

Moderate GCV and PCV for plant height (Hasib *et al.*, 2000; Kole and Hasib, 2003), low GCV and PCV for days to flower (Hasib and Kole, 2004) and panicle length (Hasib and Kole 2008) have also been reported.

From M<sub>2</sub> generation to M<sub>3</sub> generation, variability increased for flag leaf length at 350Gy and 450Gy in T<sub>1</sub> and at 250Gy in T<sub>2</sub>, and spikelet number per panicle at 350Gy in T<sub>2</sub>, which could be attributed to increase in genetic variation due to release of potential variability existed in M<sub>2</sub> generation. However, it decreased for flag leaf length at 350Gy in T<sub>2</sub> and plant height at all three doses in T<sub>2</sub>.

#### Heritability

The heritability estimates (Table 4) were moderate (<75%) for most of the characters in both the generations at different doses of gamma ray. However, estimates were high in M<sub>3</sub> generation among mutant families of both the genotypes for days to flower, and for flag leaf angle in T<sub>1</sub> mutants only. In addition, heritability estimates were high in few trait-dose-genotype-generation combinations. For instance, heritability was high in M<sub>2</sub> generation for flag leaf length at 350Gy in the mutant families of both T<sub>1</sub> and T<sub>2</sub>; and in M<sub>3</sub> generation for grain yield per plant at 250Gy only in T<sub>1</sub> and at 450Gy in T<sub>2</sub>, plant height at 350Gy in T<sub>1</sub>, panicle length at 450Gy in T<sub>1</sub> and spikelet number at 350Gy in T<sub>2</sub>. Further, mutants of T<sub>1</sub> showed low heritability for days to flower and plant height at 250Gy, flag leaf angle at 450Gy, and panicle number at 250 and 350Gy in M<sub>2</sub> generation. In T<sub>2</sub> mutants, all treatment-trait combinations showed either moderate (in most cases) or high heritability in both M<sub>2</sub> and M<sub>3</sub> generations except days to flower and flag leaf angle at 250Gy, which recorded low estimates in M<sub>2</sub>.

High estimates of heritability in above economic characters in both generations indicated a close correspondence between the genotype and the phenotype and hence, single plant selection could be effective for these characters. The results are in agreement with Hasib and Kole (2004) for days to flowering, plant height and grain yield. Kole and Hasib (2003) and Hasib (2005) also obtained high heritability for grain yield and panicle length. High heritability has also been reported by Hasib *et al.* (2000) for days to flower and grain number, and Basak and Ganguli (1996) for spikelet number and flag leaf angle. However, moderate to low heritability for panicle number (Hasib *et al.*, 2000; Kole and Hasib, 2003), grain number (Kole and Hasib, 2003) and plant height (Hasib *et al.*, 2000) have also been reported.

Heritability increased from M<sub>2</sub> to M<sub>3</sub> generations for days to flower at all three doses T<sub>1</sub> and at 250 and

**Table 3. Phenotypic variation in gamma ray induced mutant families of T<sub>1</sub> and T<sub>2</sub> genotypes in M<sub>2</sub> and M<sub>3</sub> for nine polygenic traits**

Characters	Treatment	Grand mean				Range							
		T <sub>1</sub>		T <sub>2</sub>		Minimum				Maximum			
		M <sub>2</sub> M <sub>3</sub>		M <sub>2</sub> M <sub>3</sub>		T <sub>1</sub>		T <sub>2</sub>		T <sub>1</sub>		T <sub>2</sub>	
		M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>
Days to flower	Control	129.00	129.00	128.00	128.00	127.00	128.00	125.00	125.00	132.00	132.00	132.00	133.00
	250Gy	129.73	129.42	128.59	128.17	125.67	122.60	125.67	125.00	134.20	134.13	133.00	136.00
	350Gy	129.22	128.58	128.87	126.93	125.00	123.47	125.50	125.00	133.50	136.07	132.50	133.00
	450Gy	130.55	129.78	131.44	129.99	125.00	126.20	125.67	125.40	137.67	134.07	135.67	140.27
Flag leaf angle (°)	Control	30.00	25.50	20.00	19.00	25.00	20.50	15.00	12.50	40.00	35.00	25.00	25.00
	250Gy	24.33	20.87	13.04	16.83	11.25	11.00	10.00	10.00	38.33	38.33	18.33	24.33
	350Gy	15.03	16.93	14.81	16.80	11.25	11.67	10.00	10.67	26.67	24.00	21.67	21.67
	450Gy	15.91	16.53	13.91	14.83	11.25	12.33	10.00	10.67	22.50	22.67	19.00	24.00
Flag leaf length (cm)	Control	26.50	25.50	30.00	28.50	21.00	22.50	25.00	25.00	35.00	32.50	35.00	35.00
	250Gy	25.77	25.65	25.66	27.81	19.00	23.31	20.00	22.44	35.67	28.67	32.30	33.49
	350Gy	25.35	24.02	25.48	26.55	20.00	18.87	19.00	20.47	35.30	28.23	34.30	33.20
	450Gy	26.98	25.20	24.11	24.63	22.67	21.00	17.67	21.47	29.25	28.93	31.24	28.70
Plant height (cm)	Control	110.00	110.00	110.00	110.50	95.00	95.50	90.50	90.50	132.00	130.00	130.00	134.00
	250Gy	111.16	105.60	111.53	110.19	80.00	75.45	78.30	80.43	138.00	135.60	145.00	140.20
	350Gy	114.56	110.61	116.17	115.28	90.00	82.57	87.50	88.10	133.75	138.60	140.30	142.57
	450Gy	116.40	111.31	106.87	110.35	90.00	86.67	75.00	78.07	135.00	136.80	130.00	142.93
Panicle number	Control	15.00	15.00	14.00	14.00	10.00	10.00	12.00	12.00	25.00	25.00	18.00	18.00
	250Gy	17.39	16.33	11.76	13.77	7.67	11.60	8.67	10.20	27.50	25.67	14.30	16.80
	350Gy	12.58	16.52	12.05	12.15	7.50	11.13	7.67	9.87	17.20	24.93	17.50	16.33
	450Gy	15.67	16.08	10.75	14.19	9.30	11.13	7.33	11.67	24.50	24.07	13.00	18.33
Panicle length (cm)	Control	25.00	24.50	25.50	24.50	20.50	20.00	20.50	19.00	28.00	28.50	30.00	28.00
	250Gy	24.41	20.48	23.88	24.49	18.67	17.64	21.67	22.57	29.75	23.91	27.30	17.49
	350Gy	24.60	22.40	22.99	23.73	19.00	19.07	18.38	21.57	27.67	28.20	28.80	26.13
	450Gy	24.59	22.41	23.34	22.82	15.30	16.20	20.67	21.03	29.00	29.27	27.50	25.91
Spikelet number	Control	80.00	80.00	105.00	105.50	50.50	50.50	80.00	80.50	105.00	105.50	130.00	130.00
	250Gy	76.91	91.07	125.71	124.88	49.33	72.13	99.16	98.67	113.30	115.40	151.00	150.80
	350Gy	87.12	87.27	132.49	135.46	51.67	62.67	112.00	115.65	122.00	120.80	158.00	163.13
	450Gy	95.32	92.18	117.43	115.85	61.25	66.40	95.67	89.35	132.50	129.73	142.60	140.00
Grain number	Control	64.00	65.00	85.00	85.00	40.00	42.50	60.00	60.50	95.00	95.00	115.00	115.50
	250Gy	74.29	73.40	105.02	105.43	50.67	54.87	75.30	77.25	96.20	95.80	135.50	133.80
	350Gy	75.19	77.17	114.70	116.24	52.50	55.67	88.00	90.15	98.00	97.33	140.67	142.33
	450Gy	83.56	82.10	96.62	94.75	57.50	60.00	70.67	68.24	109.50	105.40	122.80	120.25
Grain yield (g)	Control	12.15	12.57	12.50	13.75	5.75	6.00	8.00	9.35	19.50	18.95	18.50	19.54
	250Gy	15.53	16.15	16.95	20.45	6.17	7.58	8.73	13.55	22.53	22.65	25.18	25.91
	350Gy	12.74	15.14	18.65	17.25	5.78	10.32	7.42	11.22	19.06	20.76	31.62	23.65
	450Gy	16.22	12.60	13.66	22.40	12.22	9.33	6.36	16.62	20.46	14.38	19.35	25.35

**Table 4. Estimates of genetic parameters in gamma ray induced mutant families of T<sub>1</sub> and T<sub>2</sub> in M<sub>2</sub> and M<sub>3</sub> for nine polygenic traits**

Characters	Treatment	Coefficient of variation(%)								Heritability(%)				GA as % of mean			
		GCV				PCV				T <sub>1</sub>		T <sub>2</sub>		T <sub>1</sub>		T <sub>2</sub>	
		T <sub>1</sub>		T <sub>2</sub>		T <sub>1</sub>		T <sub>2</sub>		T <sub>1</sub>	T <sub>2</sub>	T <sub>1</sub>	T <sub>2</sub>	T <sub>1</sub>	T <sub>2</sub>		
		M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>	M <sub>2</sub>	M <sub>3</sub>		
Days to flower	Control																
	250Gy	2.18	7.36	3.00	4.20	3.31	4.24	4.24	4.31	43.44	92.07	49.98	95.01	2.96	14.55	4.37	8.43
	350Gy	2.88	6.65	5.90	4.04	3.89	6.83	6.83	4.20	54.84	98.66	74.54	92.63	4.40	13.60	10.49	8.01
	450Gy	4.32	5.83	4.51	4.79	5.07	5.46	5.46	4.88	72.63	97.52	68.32	96.03	7.58	11.87	7.69	9.66
Flag leaf angle (°)	Control																
	250Gy	33.03	51.78	32.36	30.03	45.91	48.29	48.29	36.74	51.79	94.20	44.92	66.81	48.97	103.52	44.68	50.57
	350Gy	41.21	46.66	46.08	29.29	54.50	64.39	64.39	35.35	57.18	86.93	51.22	68.66	64.19	89.62	67.93	49.99
	450Gy	41.61	50.36	31.48	32.85	61.24	40.51	40.51	43.75	46.17	83.82	60.36	56.38	58.25	94.97	50.38	50.81
Flag leaf length (cm)	Control																
	250Gy	24.61	20.02	17.72	22.69	31.32	22.16	22.16	27.13	61.77	58.57	63.91	69.92	39.85	31.57	29.18	39.08
	350Gy	14.89	22.74	23.42	18.83	16.86	26.87	26.87	22.71	78.00	57.24	75.98	68.73	27.09	35.44	42.06	32.16
	450Gy	11.50	29.39	20.66	21.29	13.96	25.33	25.33	25.79	67.79	63.35	66.52	68.11	19.50	48.19	34.72	36.19
Plant height (cm)	Control																
	250Gy	16.87	18.97	28.98	18.92	24.25	34.59	34.59	23.06	48.39	64.12	70.17	67.31	24.18	31.29	50.00	31.97
	350Gy	15.53	18.26	23.82	17.06	20.32	32.06	32.06	20.82	58.37	75.60	55.18	67.17	24.43	32.71	36.45	28.80
	450Gy	19.60	15.83	31.03	17.99	25.12	38.35	38.35	22.05	60.88	67.25	65.46	66.57	31.50	26.74	51.71	30.24
Panicle number	Control																
	250Gy	28.25	40.85	25.45	20.11	47.52	32.25	32.25	26.06	35.35	53.72	62.31	59.55	34.61	61.69	41.39	31.97
	350Gy	29.53	32.33	29.40	23.07	42.18	38.76	38.76	30.82	49.01	56.18	57.54	56.06	42.58	49.92	45.94	35.59
	450Gy	34.79	35.59	27.50	18.55	44.33	36.54	36.54	24.74	61.58	53.88	56.64	56.25	56.24	53.82	42.64	28.66
Panicle length (cm)	Control																
	250Gy	19.81	13.91	13.37	11.44	26.34	18.72	18.72	15.00	56.59	56.63	51.03	58.19	30.70	21.56	19.68	17.98
	350Gy	13.79	18.90	18.16	13.49	19.49	22.17	22.17	17.76	50.07	74.98	67.09	57.63	20.10	33.71	30.64	21.09
	450Gy	20.47	20.96	12.33	13.75	23.64	16.30	16.30	17.63	75.01	72.21	57.18	60.82	36.52	36.69	19.20	22.08
Spikelet number	Control																
	250Gy	40.16	39.67	22.27	21.96	51.59	29.92	29.92	28.00	60.59	69.17	55.42	61.49	64.39	67.96	34.16	35.47
	350Gy	43.56	43.51	19.69	28.15	54.00	27.51	27.51	32.16	65.09	69.06	51.20	76.59	72.40	74.48	29.02	50.74
	450Gy	35.51	37.98	24.20	29.75	46.79	31.34	31.34	35.34	57.60	52.90	59.61	70.88	55.52	56.91	38.48	51.60
Grain number	Control																
	250Gy	36.17	36.30	29.40	20.04	45.95	35.41	35.41	26.65	61.96	51.95	68.95	56.54	58.64	53.89	50.29	31.04
	350Gy	38.36	29.46	21.45	23.02	47.63	30.07	30.07	29.61	64.86	69.65	50.90	60.42	63.64	50.66	31.53	36.86
	450Gy	29.07	33.36	24.96	24.61	40.66	32.65	32.65	32.92	51.12	59.26	58.45	55.91	42.81	52.90	39.31	37.91
Grain yield (g)	Control																
	250Gy	54.13	53.87	41.65	35.86	61.81	56.67	56.67	45.94	76.69	78.05	54.00	60.93	97.64	98.03	63.04	57.67
	350Gy	43.74	33.54	48.01	33.16	57.35	60.43	60.43	44.67	58.17	65.36	63.12	55.10	68.71	55.86	78.58	50.70
	450Gy	38.37	44.36	38.62	34.37	51.56	51.07	51.07	39.58	55.39	61.15	57.18	75.40	58.83	71.46	60.16	61.47

450Gy in T<sub>2</sub>; flag leaf angle at all three doses in T<sub>1</sub>; plant height and panicle length at 350Gy in T<sub>1</sub>; spikelet number per panicle at 350Gy in T<sub>2</sub> and grain yield per plant at 450Gy in T<sub>2</sub>. Increase in the estimates of heritability of such characters is due to higher contribution of genetic factors, which might have resulted due to release of potential variability present in M<sub>2</sub> generation. In M<sub>3</sub> generation, heritability decreased for flag leaf length at 350Gy in T<sub>1</sub> and T<sub>2</sub>. Decrease in the estimates of heritability of this character is due to reduction in genetic variability as a result of increase in homozygosity in the mutant populations.

### Genetic Advance

The estimates of genetic advance (Table 4) were high for grain yield (50.70% in T<sub>2</sub> at 350Gy in M<sub>3</sub> generation to 97.64% in T<sub>1</sub> at 450Gy in M<sub>2</sub> generation) while it was low for days to flower (2.96% to 14.55% in T<sub>1</sub> at 250Gy in M<sub>2</sub> generation) at all the combinations of dose-genotype-generation. Besides, in the mutant families of T<sub>1</sub> high genetic advance were recorded for grain number and spikelet number at all dose-generation combinations. Some combinations of trait-dose-genotype-generation showed more than or close to 50% genetic advance e.g., flag leaf angle at all combinations and grain number as well as spikelet number in T<sub>1</sub>. Most of the remaining combinations recorded moderate genetic advance and it was more so for the mutant families of T<sub>2</sub>.

However, the values of genetic advance were low in the mutant families of T<sub>1</sub> for flag leaf length at 450Gy in M<sub>2</sub>, plant height at 250 and 350Gy in M<sub>2</sub>, panicle length at 350Gy in M<sub>2</sub> and at 250Gy in M<sub>3</sub> generation. The same was true for panicle length at 250 and 450Gy in M<sub>2</sub> generation and at all three doses in M<sub>3</sub> generation in the mutants of T<sub>2</sub> genotype.

The high estimates of genetic advance as per cent of mean obtained in the present study are in agreement with the results of Basak and Ganguli (1996) for flag leaf angle, panicle number, spikelet number per panicle, grain number per panicle; Hasib *et al.* (2000), Kole and Hasib (2003) and Hasib and Kole (2004) for grain number per panicle and grain yield per plant and Hasib (2005) for spikelet number per panicle and grain yield per plant.

As in the present study, estimates of genetic advance in both M<sub>2</sub> and M<sub>3</sub> were low in the earlier studies for days to flower (Hasib *et al.*, 2000; Kole and Hasib, 2003) and panicle length (Hasib and Kole, 2004; Kole and Hasib, 2003; Hasib, 2005). Moderate genetic advance for plant height was recorded by Hasib *et al.* (2000) and Kole and Hasib (2003).

Some of the characters showed increase in genetic advance in M<sub>3</sub> over M<sub>2</sub> generation, the frequency of which was more in the mutants of T<sub>1</sub> (days to flower, flag leaf angle and spikelet number across the doses; Flag leaf length and panicle length at 350 and 450Gy;

flag leaf angle at 250Gy; panicle number at 250Gy and grain number at 450Gy). Similar results were obtained in very few trait-dose combinations in T<sub>2</sub>, such as spikelet number across doses; days to flower, flag leaf length and flag leaf angle at 250 and 450Gy; grain number at 350Gy and panicle length at 450Gy. Such increase could be attributed to increase in variation and heritability in M<sub>3</sub> generation due to release of hidden variability (Solanki and Sharma, 2001).

Genetic advance as percentage of mean decreased in T<sub>2</sub> genotypes from M<sub>2</sub> to M<sub>3</sub> generation for flag leaf angle at 350Gy, plant height at 450Gy and grain number at 250Gy. In the M<sub>3</sub> generation, the genetic advance as percent of mean for different characters decreased owing to increase in means (Solanki and Sharma, 2001).

According to Johnson *et al.* (1955) and Lerner (1958) heritability when used in conjunction with genetic advance provides better information for selecting the best individuals than the heritability alone. High to moderate estimates of heritability accompanied with high to moderate genetic advance indicated the predominance of additive gene action for the expression of the characters in respective generation, which further indicated that selection would be effective for improving such characters.

In M<sub>2</sub> generation, high to moderate heritability accompanied with high to moderate genetic advance were observed for flag leaf angle at 450 Gy in T<sub>2</sub>; plant height at 450 Gy in T<sub>1</sub> and at 250Gy and 450Gy in T<sub>2</sub>; panicle length at 450Gy in T<sub>1</sub>; flag leaf length, spikelet number, grain number and grain yield per plant at all three doses in both the genotypes.

In M<sub>3</sub> generation, high to moderate heritability along with high to moderate genetic advance were observed for panicle number, flag leaf angle, spikelet number per panicle, grain number per panicle and grain yield per plant at all three doses in both the genotypes

The results of PCV, GCV,  $h^2$  and GA revealed differential response of polygenic characters to different doses of mutagen. It would be worth noting that flag leaf angle recorded high genetic variation, high to moderate heritability and genetic advance coupled with decreased mean value over control in both M<sub>2</sub> and M<sub>3</sub>. Thus it would be possible to select plants to improve the droopy nature of leaves, one of the weaknesses in the studied aromatic rice. The variability induced for different attributes would appear to be independent of genotypes as well as doses of mutagen as no common trend could be observed between the genotypes. The increased variation might have been brought about by the formation of new alleles or by the increased recombination by breaking linkages (Amirthadevarathinam *et al.*, 1990). According to Brock (1970) the theoretical expectation of inducing mutations in a quantitatively inherited character will depend upon the total number of genes involved, the relative proportion of genes with positive and negative effects and the

degree to which the parental genome operates as a balanced set. Ganeshan and Subramanian (1990) stated that change in the direction from one segregating generation to next segregating generation might be due to differential segregation and recombination, whereas change in a particular direction between generations may result from change in gene frequency due to selection.

The M<sub>2</sub> being the first segregating generation, it would be reasonable to expect the manifestation of mutagen-induced variability in the M<sub>2</sub> itself. Selection in M<sub>2</sub> can certainly help identify progenies that are likely to show more variability and better response to selection and simultaneously reduce the volume of unwanted material by rejecting the unmutated "roughage" (Sharma, 1986).

The increase in variability of different characters in M<sub>3</sub> generation over M<sub>2</sub> generation was due to the "release of additional variability" in M<sub>3</sub> (Solanki and Sharma, 2001). The "release of additional variability" might be due to segregation and recombination of mutant genes induced through radiation treatment.

Decrease in variability of different characters in both genotypes in M<sub>3</sub> over M<sub>2</sub> was due to increase in homozygosity in M<sub>3</sub>. Increase in homozygosity is sometimes quickly attained due to inheritance of mutant genes as a block. The change in the values of different genetic parameters over generations may be due to changes in the genetic components of the populations. From one segregating generation to the next the dominance components decreased due to increase in homozygosity. Shebeski (1967) advocated that the most desirable gene combinations could be identified even in the heterozygous population and proportion of plants with the most desirable combination of genes decreases rapidly with the advancing generations and these may be lost if not selected in the early generations.

The outcomes of the present study have given strong cues for higher chances of success in the macro-mutational population for isolation of promising progeny even for polygenic variants (Solanki and Sharma, 1999 and Tikoo and Chandra, 1999). In fact, selection for polygenic characters can also be applied to the normal looking M<sub>2</sub> plants, for concentration on such progenies can lead to a great economy of effort with simultaneous improvement in selection efficiency (Sarkar and Sharama, 1988). The heterozygotes for macromutations among such promising selections can be discarded on the basis of segregation in M<sub>3</sub> generation.

## CONCLUSION

The present studies conclude that breeders point of view, working with a reduced volume of mutagenized material which was obtained in M<sub>2</sub> and M<sub>3</sub>, by rejecting unwanted material and selecting desirable ones in M<sub>2</sub>, consequently, resulting in higher frequency of promising progenies. Higher estimates of heritability and genetic

advance for different characters were observed in both the generations. Thus there is ample scope for improving the grain yield and its component characters in aromatic rice, especially where aroma is controlled by single recessive gene pair(s), by exercising selection in M<sub>2</sub> and M<sub>3</sub> generations.

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