

EVALUATION OF GENETIC VARIABILITY FOR AGRONOMIC TRAITS IN M2 GENERATION OF SORGHUM THROUGH INDUCED MUTATION

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Abstract— Different doses of Gamma ray (0 Gy to 700 Gy), with increment of 100 Gy, were used to create variation of sorghum variety (yezine-7). Mean values, genetic variability and heritability induced by Gamma ray were investigated for twelve agronomic traits viz., plant height, stem width, leaves per plant, stalk weight, juice volume, Brix %, panicle length, panicle width, primary branches per panicle, 100 seed weight, seeds per plant and grain yield per plant. Mean values in traits showed both positive and negative increases. The highest positive mean values were noticed at 300 Gy-treatment for most agronomic traits (stem width, leaves per plant, stalk weight, panicle width, 100 seed weight, seeds per plant and grain yield per plant). High Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for stem width, seeds per plant and grain yield per plant. High heritability (h^2) accompanied with high genetic advance as percentage of mean (GAM) were recorded for plant height, stem width, seeds per plant and grain yield per plant. As considering high genetic parameters, treatments with 400 Gy and 300 Gy induced the highest variability for most of the studied traits such as plant height, leaves per plant, stalk weight, primary branches per panicle and stem width, panicle length, respectively. For seeds per plant and grain yield per plant, 400 Gy-treatment showed the highest GCV and PCV while the highest h^2 with high GAM were recorded at 300 Gy-treatment

Index Terms : sorghum, Gamma ray, agronomic traits, mean values, genetic variability, heritability.

I. INTRODUCTION

Sorghum (*Sorghum bicolor* L.) is the fifth most important cereal grain crop in the world and reportedly feeds over 500 million people on a daily basis in the developing world providing dietary starch, dietary protein and some vitamins and minerals [1]. As feedstock for fuel ethanol, sweet sorghum is a high biomass and sugar yielding crop with high photosynthetic efficiency [2] and has the potential of becoming a useful energy crop [3] [4]. Sorghum is well adapted to the Semi-Arid Tropics (SAT) and more water use efficient (310 kg water/kg dry matter) compared to maize (370 kg water/kg dry matter) to convert atmospheric CO₂ into sugars which makes it the most promising bioenergy crop[5].

Induced mutations have played a great role in increasing world food security, since new food crop varieties embedded with various induced mutations have contributed to the significant increase of crop production at locations people could directly access [6]. Gamma and X rays have been extensively used to induce mutations in crop plants. Dose of irradiation of plant materials and the management of induced variations are critical factors in successful adoption of the technology [7].

Increase in variance may be result of irradiation bringing about sssmutation in the minor genes governing polygenically inherited characters thereby increasing the frequency of crossing over between the genes governing closely related traits [8]. Estimate of genotypic coefficient of variation, heritability and genetic advance expected by selection for yield and its component traits are useful in designing an effective breeding programme [9]. The objective of present study is to access the optimum dose rate of Gamma ray to induce variation in some agronomic traits of sorghum.

II. MATERIALS AND METHODS

The experiment is carried out in the field of Biotechnological Research Department, Kyaukse during 2013 to 2014. The seeds of sorghum variety (yezine-7) were used for the induced mutation. They were irradiated with different doses (100, 200, 300, 400, 500, 600 and 700 Gy) of Gamma ray at the Department of Atomic Energy, Yangon. The LD-50 % of sorghum variety (Yezine-7) was observed as 780 Gy. According to IAEA [10], the effective dose for inducing mutations should be lower than that of the LD-50 value.

The seeds subjected to Gamma irradiation were sown along with the control following randomized block design (RBD) with 3 replications, at the spacing of 15 cm within plants and 45 cm between plants in M1 generation. Harvesting was done by using bulk harvesting method. For each treatment, more than 250 seeds from M1 generation were taken randomly to grow in M2 generation. Cultivation was carried out according to the method in M1 generation. Data were collected and analysed statistically to assess the extent of induced genetic variability for twelve agronomic traits viz., plant height, stem

width, leaves per plant, stalk weight, juice volume, Brix %, panicle length, panicle width, primary branches per panicle, 100 seed weight, seeds per plant and grain yield per plant.

Data were subjected to analysis of variance (ANOVA) using SPSS 16.0 software. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2) and genetic advance as percentage of mean (GAM) were calculated using the following equations.

$$GCV (\%) = [(\sigma^2_g)/X^-] \times 100$$

$$PCV (\%) = [(\sigma^2_p)/X^-] \times 100$$

$$h^2 (\%) = (\sigma^2_g/\sigma^2_p) \times 100$$

$$GAM = (k \times \sigma_p \times h^2) / X^-$$

Where; X^- = mean value

σ^2_g = genotypic variance

σ^2_p = phenotypic variance

σ_p = phenotypic standard deviation

$k = 2.64$, constant for 1% selection intensity.

III. RESULTS AND DISCUSSION

The means and genetic parameters can help to deduce variation induced by mutation on agronomic traits of the crop plants. The mean values of twelve agronomic traits in M2 generation were showed in Table I and II.

In the present investigation, different doses of Gamma ray shifted mean values in both positive and negative directions from parent progeny for all studied agronomic traits. The mean values of almost all mutagenic treatments for plant height reduced as compared to control except two treatments (100 Gy and 200 Gy). For stem width, four mutagenic treatments (100 Gy, 200 Gy, 300 Gy and 500 Gy) induced higher mean values than control. The positive mean values for leaves per plant

were observed at three mutagenic treatments (100 Gy, 300 Gy and 400 Gy). Only three mutagenic treatments (100 Gy, 300 Gy and 500 Gy) exhibited higher mean values for stalk weight than the control. Gamma irradiation induced positive increases in not only juice volume except 700 Gy-treatment but also Brix % except 100 Gy and 200 Gy- treatments.

Positive mean values of primary branches per panicle were noticed with three high mutagenic treatments (from 400 Gy to 600 Gy). Mutagenic treatments negatively influenced panicle length while the positive mean values of panicle width were found at four low mutagenic treatments (from 100 Gy to 400 Gy). The larger seed sizes as compared to control were recorded at four treatments (from 200 Gy to 500 Gy). For seeds per plant and grain yield per plant, almost all mutagenic treatments expect two highest doses (600 Gy and 700 Gy) induced higher positive mean values as compared to parent progeny.

Treatment with 300 Gy possessed the largest mean values for stem width, leaves pre plant, stalk weight, panicle width, 100 seeds weight, seeds per plant and grain yield per plant. 400 Gy-treatment showed the highest mean values of Brix % and primary branches per panicle. The highest mean values for plant height and juice volume were noticed at 100 Gy-treatment. Mutation induction with high dose (600 Gy) reduced mean values for almost all studied traits except juice volume, Brix % and primary branches per panicle. The highest dose of Gamma ray (700 Gy) also showed negative mean values for all agronomic traits except Brix %. Especially, 300 Gy-treatment showed considerably higher mean values for panicle width, seeds per plant and grain yield per plant followed by 400 Gy-treatment.

Table I. Estimates of Mean Values for Plant Height, Stem Width, Leaves per Plant, Stalk Weight, Juice Volume and Brix %

Treatments	Plant Height (cm)		Stem Width (cm)		Leaves per plant		Stalk Weight (g)		Juice Volume (l)		Brix %	
	Mean	Shift in Mean	Mean	Shift in Mean	Mean	Shift in Mean	Mean	Shift in Mean	Mean	Shift in Mean	Mean	Shift in Mean
Control	276.02		7.50		14.23		376.90		90		16.30	
100 Gy	280.67	+ 4.65	7.67	+ 0.17	14.60	+ 0.37	403.23	+ 26.33	110	+ 20	15.80	- 0.50
200 Gy	277.52	+ 1.50	7.52	+ 0.02	13.70	- 0.53	371.03	- 5.87	105	+ 15	14.87	- 1.43
300 Gy	270.08	- 5.94	8.47	+ 0.97	14.73	+ 0.50	441.47	+ 64.57	95	+ 5	16.67	+ 0.37
400 Gy	275.38	- 0.64	6.83	- 0.67	14.27	+ 0.04	351.77	- 25.13	100	+ 10	17.47	+ 1.17
500 Gy	269.86	- 6.16	8.07	+ 0.57	14.13	- 0.10	420.97	+ 44.07	91	+ 1	16.33	+ 0.03
600 Gy	250.62	- 25.4	6.83	- 0.67	13.27	- 0.96	321.43	- 55.47	109	+ 19	16.67	+ 0.37
700 Gy	228.14	- 47.88	6.67	- 0.83	12.83	- 1.40	251.53	- 125.37	74	- 16	16.43	+ 0.13

Table II. Estimates of Mean Values for Primary Branches per Panicle, Panicle Length, Panicle Width, 100 seed Weight, Seeds per Plant and Grain yield per Plant

Treatments	Primary branches/panicle		Panicle length (cm)		Panicle width (cm)		100 seed weight (g)		Seeds/plant		Grain yield/plant (g)	
	Mean	Shift in Mean	Mean	Shift in Mean	Mean	Shift in Mean	Mean	Shift in Mean	Mean	Shift in Mean	Mean	Shift in Mean
Control	58.93		28.81		19.58		1.99		624.13		12.39	
100 Gy	56.20	- 2.73	27.47	- 1.34	19.81	+ 0.23	1.98	- 0.01	669.07	+ 44.94	13.15	+ 0.76
200 Gy	58.50	- 0.43	26.94	- 1.87	19.94	+ 0.36	2.00	+ 0.01	645.20	+ 21.07	12.88	+ 0.49
300 Gy	58.57	- 0.36	26.43	- 2.38	22.13	+ 2.55	2.08	+ 0.09	716.83	+ 92.70	14.84	+ 2.45
400 Gy	62.60	+ 3.67	27.91	- 0.90	21.57	+ 1.99	2.05	+ 0.06	702.63	+ 78.50	14.41	+ 2.02
500 Gy	62.30	+ 3.37	28.76	- 0.05	18.56	- 1.02	2.03	+ 0.04	636.23	+ 12.10	12.93	+ 0.54
600 Gy	61.17	+ 2.24	26.15	- 2.66	18.47	- 1.11	1.97	- 0.02	585.53	- 38.60	11.49	- 0.90
700 Gy	58.70	- 0.23	25.89	- 2.92	17.19	- 2.39	1.95	- 0.04	576.60	- 47.53	11.23	- 1.16

Genetic variability plays an important role in selection and isolation of superior genotypes for improvement of crop plants. Estimation of genotypic and phenotypic coefficient of variation, heritability and genetic advance as percentage of mean for twelve agronomic traits of eight mutagenic treatments were presented in Table III, IV, V and VI.

In the present study, GCV and PCV showed a wide range of variation for most of the studied traits in M2 generation. A consistently greater PCV was observed than GCV in all agronomic traits among eight mutagenic treatments. It indicated that there was the influence of environment on the expression of these traits as the observed phenotypic variability includes both genotypic and environmental variation.

In general, the high GCV and PCV were observed for stem width, seeds per plant and grain yield per plant. These results are concurrent with the report of Unche *et al.* (2008) [11] and Y.Anand & S.T.Kajjidoni (2014) [12] who reported that high GCV and PCV were exhibited for grain yield per plant in sorghum. The moderate GCV and PCV were recorded for plant height, stalk weight and juice volume. Leaves per plant, Brix %, primary branches per panicle, panicle length, panicle width and 100 seed weight exhibited the low GCV and PCV.

Heritability in broad sense is a measure of the extent of phenotypic variation caused by the action of genes. Heritability plays an imported role in deciding the suitability and strategy for selection of a character [13]. In present investigation, the estimate of heritability also showed wide variation for studied traits in M2 generation. The high heritability values of more than 90 percent were observed for plant height in five treatments (from 100 Gy to 500 Gy) and grain yield per plant in three treatments (300 Gy, 400 Gy and 500 Gy). These results for plant height are in accordance with the reports of Biradar *et al.* (1996) [14], Deepalaxmi *et al.* (2007) [15] and Y.Anand & S.T.Kajjidoni (2014) [12]. The low heritability values were found for panicle length and 100 seeds weight that was contradictory with the report of Y.Anand & S.T.Kajjidoni (2014) [12] who reported that panicle length and 100 seed had high heritability.

If the heritability of that particular trait is high, it favors effective selection on single plant basis but if the trait concerned has lower heritability estimate, breeder has to rely on progeny mean rather than on single plant [16]. Heritability

alone provides no indication of amount of genetic improvement that would result from selection of individual genotype; hence knowledge about genetic advance coupled with heritability is most useful [17].

In the present study, the high heritability values noticed for plant height, stem width, seeds per plant and grain yield per plant. All of these traits also have high genetic advances as percentage of mean (GAM). These results agree with Veerabathiran & Kennedy (2001) [18], Unche *et al.* (2008) [11] and Y.Anand & S.T.Kajjidoni, (2014) [12] who reported that high heritability coupled with high genetic advance as percent of mean was observed for grain yield per plant. High heritability accompany with high genetic advance indicates that preponderance of additive gene effect [19]. Therefore, these results indicate that most likely the heritability is due to additive gene effect and as a result there is scope of improving these traits selection procedure.

The moderate heritability accompany with moderate GAM were noticed for stalk weight and juice volume while moderate heritability accompany with low GAM was found for leaves per plant, Brix %, primary branches per panicle and panicle width. It shows that these traits are most probably governed by non additive genes. The low heritability values were recorded for panicle length and 100 seeds weight and both of that also had low GAM.

As considering high GCV, PCV, heritability and GAM, treatment with 400 Gy induced the highest amount of variation for many traits in M2 generation of sorghum. It exhibited higher genetic parameters than all other treatments for plant height, leaves per plant, stalk weight and primary branches per panicle. Moreover, the highest heritability was found for Brix % and 100 seeds weight at 400 Gy-treatment. Treatment with 300Gy showed the highest genetic parameters for stem width and panicle length while it possessed the highest heritability for juice volume, seeds per plant and grain yield per plant. For panicle width, the highest heritability and GAM were found at 500 Gy-treatment. On the other hand, the treatments with 700 Gy exhibited the lowest genetic parameters among all other treatments for all traits except juice volume and 100 seeds weight whereas the lowest genetic parameters were observed at control.

Table III. Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Heritability in broad sense (h^2) and Genetic Advance as Percentage to Mean (GAM) for Plant Height, Stem Width and Leaves per Plant

Treatments	Plant height (cm)				Stem width (cm)				Leaves/plant			
	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)
Control	23.05	24.87	85.91	56.41	25.91	31.46	67.84	56.35	6.16	11.05	31.11	9.07
100 Gy	26.40	27.18	94.32	67.69	33.62	37.27	81.39	80.08	9.12	15.07	36.59	14.56
200 Gy	22.57	28.73	91.75	69.60	33.42	37.78	78.26	78.06	7.77	11.84	43.03	13.45
300 Gy	26.25	26.88	95.35	67.66	39.35	43.10	83.37	94.87	9.37	13.73	46.58	16.88
400 Gy	31.29	31.90	96.21	81.04	38.24	43.58	76.99	88.58	14.48	19.82	53.34	27.92
500 Gy	26.81	27.62	94.19	68.68	28.35	34.08	69.20	62.26	7.05	10.37	46.18	12.64
600 Gy	24.80	28.96	73.32	56.05	35.91	44.15	66.15	77.10	10.92	19.70	30.73	15.98
700 Gy	23.54	28.16	69.90	51.96	25.64	31.55	66.06	55.02	10.45	21.24	24.22	13.58

Table IV. Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Heritability in broad sense (h^2) and Genetic Advance as Percentage to Mean (GAM) for Stalk Weight, Juice Volume and Brix %

Treatments	Stalk weight (g)				Juice volume (l)				Brix %			
	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)
Control	21.73	42.53	26.13	29.33	13.94	20.94	44.36	24.52	7.82	14.84	27.75	10.87
100 Gy	24.35	39.17	38.62	39.94	23.98	29.85	64.53	50.86	8.03	13.70	34.33	12.41
200 Gy	24.76	39.60	39.11	40.89	19.87	25.01	63.10	41.66	9.06	16.29	30.97	13.32
300 Gy	23.22	33.59	47.81	42.39	24.10	29.05	68.84	52.79	8.52	12.15	49.12	15.76
400 Gy	23.08	32.71	49.80	43.00	20.53	25.03	67.28	44.46	6.49	8.80	54.38	12.63
500 Gy	23.21	35.10	43.73	40.52	22.42	28.61	61.40	46.37	5.80	8.72	44.26	10.19
600 Gy	20.26	40.50	25.03	26.76	25.13	33.44	56.44	49.84	6.22	11.67	28.42	8.76
700 Gy	18.88	43.45	18.87	21.65	17.39	24.87	48.94	32.13	5.11	10.23	24.93	6.73

Table V. Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Heritability in broad sense (h^2) and Genetic Advance as Percentage to Mean (GAM) for Primary Branches per Panicle, Panicle Length and Panicle Width

Treatments	Primary branches/panicle				Panicle length (cm)				Panicle width (cm)			
	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)
Control	7.20	11.76	37.48	11.64	3.13	14.14	4.89	1.82	6.58	11.81	31.06	9.68
100 Gy	4.05	5.83	48.13	7.41	2.33	7.02	11.05	2.05	9.36	15.55	36.19	14.86
200 Gy	10.09	14.67	47.35	18.34	6.13	16.55	13.71	5.99	9.40	16.42	32.73	14.19
300 Gy	10.72	16.02	44.76	18.94	7.55	17.99	17.63	8.37	9.10	14.59	38.88	14.98
400 Gy	14.24	20.47	48.42	26.16	5.03	13.03	14.92	5.13	10.07	14.59	47.67	18.36
500 Gy	11.29	16.69	45.70	20.14	6.96	21.26	10.72	6.02	10.04	14.35	48.90	18.52
600 Gy	5.12	7.64	44.88	9.05	3.70	14.90	6.16	2.42	6.91	15.02	21.18	8.40
700 Gy	6.13	12.37	24.57	8.02	1.53	7.67	3.69	0.78	6.38	14.49	19.39	7.42

Table VI. Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Heritability in broad sense (h^2) and Genetic Advance as Percentage to Mean (GAM) for 100 seed Weight, Seeds per Plant and Grain yield per Plant

Treatments	100 seed weight (g)				Seeds/plant				Grain yield/plant (g)			
	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)	GCV (%)	PCV (%)	h^2 (%)	GAM (% of mean)
Control	3.79	10.12	14.00	3.74	30.25	35.05	74.50	68.93	35.88	38.99	84.69	87.17
100 Gy	5.05	10.95	21.28	6.15	30.24	33.45	78.54	73.26	34.46	36.27	87.65	88.03
200 Gy	6.71	15.00	20.00	7.70	33.18	36.30	83.10	75.20	41.47	42.79	86.40	95.04
300 Gy	5.49	10.33	28.26	7.88	36.51	38.98	89.20	80.11	39.52	40.06	95.21	96.81
400 Gy	5.98	11.03	29.41	8.57	39.40	42.56	88.68	77.92	46.11	47.47	90.42	98.17
500 Gy	3.59	8.29	18.73	4.10	35.35	38.35	83.76	76.89	41.31	43.04	90.70	94.63
600 Gy	4.82	11.82	16.67	5.20	27.24	31.02	77.15	63.17	34.97	37.70	86.01	85.58
700 Gy	4.86	12.75	14.52	4.89	22.64	26.43	73.38	51.20	29.69	32.60	82.94	71.37

IV. CONCLUSION

In the present study, treatment with 300 Gy exhibited the highest mean values for seven agronomic traits (stem width, leaves pre plant, stalk weight, panicle width, 100 seeds weight, seeds per plant and grain yield per plant). 400 Gy-treatment showed the largest mean values for two traits (Brix % and primary branches per panicle). 100 Gy-treatment possessed the highest mean value for plant height and juice volume. All mutagenic treatments induced negative effect for panicle length while they gave positive effect for juice volume except 700 Gy-treatment. The high GCV, PCV, heritability and GAM were observed for four traits (plant height, stem width, seeds

per plant and grain yield per plant). The heritability of these traits was governed by additive gene action and selection may be affected. The moderate genetic parameters were noticed for two traits (stalk weight and juice volume). But the moderate heritability accompany with low GCV, PCV and GAM was recorded for four traits (leaves per plant, Brix %, primary branches per panicle and panicles width). The heritability of these traits may be due to favorable influence of environment rather than genotypic and selection may not be rewarding. Among all treatments, 400 Gy-treatment induced the highest variation for six traits (plant height, leaves per plant, stalk weight, Brix %, primary branches per panicle and 100 seeds weight), as considering high genetic parameters. Treatment

with 300 Gy showed higher genetic parameters than all other treatments for three traits (stem width, juice volume and panicle length). For seeds per plant and grain yield per plant, although the highest GCV and PCV were observed at 400 Gy-treatments, the highest heritability accompany with high GAM were exhibited at 300 Gy-treatment. Mutation induction with higher doses (600 Gy and 700 Gy) reduced mean values and showed low genetic parameters for most of the studied traits

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