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## Genetic variability studies in bread wheat (*Triticum aestivum*) through hybridization cum mutation for agro-morphological traits under rainfed situation

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### Abstract

The present investigation was carried out with the main objective of estimating the extent of genetic variability released through recombination, induced mutation and their combination for yield and its component traits in ten segregating populations of bread wheat. The material consisted of segregating populations ( $F_2$ ,  $M_2$  and  $F_2M_2$ ) developed from two bread wheat varieties *viz.*, GW322 and UASBW11949 after irradiating with gamma-rays. Higher mean and wider range was recorded for grain yield per plant and other traits in  $F_2M_2$  compared to  $F_2$ . Higher genotypic and phenotypic coefficient of variance was observed in  $F_2M_2$  population for plant height, spikelets per spike, grains per spike, productive tillers per plant, spike length and 1000 seed weight indicating greater scope for selection and improvement of the characters in desired direction. The estimates of heritability, GA and GAM were increased from  $F_2$  to  $F_2M_2$  revealing possibility of getting more success by selecting in  $F_2M_2$  compared to  $F_2$  population.

**Keywords:** Wheat, induced mutation, variability

### Introduction

Wheat is known to be temperate crop, however it is being cultivated in tropical ecosystem of India, where prevalence of high temperature during crop growth and peculiar climatic conditions coupled with rainfed cultivation of the crop leads to the lower productivity. Development of superior gene pool needs the genotypes with desired traits for both qualitative and quantitative traits. But owing to their economic importance quantitative characters receive more attention. Hybridization is commonly used for generating variability in all crops. Further, the extent of variation released by hybridization in case of *T. aestivum* may be inadequate in developing target specific cultivars. In such situations, induced mutagenesis, as an alternative or as a supplement to hybridization, offers opportunities to create new variability which can be utilized in developing target specific cultivars. However, the range and frequency of desirable mutants induced may differ with mutagen and the genotype chosen for study (Konzak, 1987)<sup>[5]</sup>. It is also suggested that the application of induced mutagenesis along in segregating population may be one of the means of creating the variability. Experiments on peanut and wheat showed more variation in both irradiated parents and irradiated crosses than in the next generation derived from unirradiated crosses in terms of standard deviation and hypothesized that the variation induced by irradiation might be cumulative with that of hybridization (Ram, *et al*, 1987)<sup>[8]</sup>. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters (Santosh *et al.*, 2013)<sup>[10]</sup>. A very few efforts have been made so far to combine recombination and induced mutation in wheat to generate desirable variability and alter character association. Hence, in the present study, an attempt was made to evaluate and compare the magnitude of variation in few quantitative traits created by different approaches *viz.*, hybridization and induced mutation and their combination.

### Materials and Methods

The experimental material was developed by using two genetically diverse bread wheat genotypes GW322 and UASBW 11949. The  $F_2$  seeds of the cross GW322 x UASBW 11949 and their respective parental seeds were exposed to gamma rays with different doses *viz.*, 150,200 and 250 Grey at Bhabha Atomic Research Centre (BARC), Trombay, Mumbai. Following irradiation of seeds, different  $M_1$  and  $F_2M_1$  generations were advanced to get  $M_2$  and  $F_2M_2$  seeds, respectively. Consequently the part of  $F_2$  seeds were reserved for further

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evaluation. Each segregating population along with their respective parents was grown in a plot size of 2.76 m and 6 m in All India Coordinated Research Project on Wheat at Main Research Station, University of Agricultural Sciences, Dharwad. The spacing of 23 cm between the row and 10 cm within a row was maintained. Observations were recorded on randomly selected plants in parents and individual plants in  $F_2$ 's,  $F_2M_2$ 's and  $M_2$ 's for seven quantitative traits. The data were subjected to statistical analysis and various genetic parameters. The variability parameters *viz.*, mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) was calculated as per the formula suggested by Burton and De Vane (1953) <sup>[14]</sup>, heritability in broad sense (Robinson, *et al.*, 1949) <sup>[15]</sup> and genetic advance as per cent of mean (Johnson *et al.*, 1955) <sup>[3]</sup>. Data was recorded on grain yield per plant and its attributing traits *viz.*, number of productive tillers per plant, plant height, spike length, number of spikelets per spike, number of grains per spike and 1000-grain weight.

### Results and Discussion

The comparison of mean performance of different quantitative traits between the  $F_2$ ,  $F_2M_2$  and  $M_2$  populations indicated an increase in mean values in  $F_2M_2$  compared to  $F_2$  for grain yield per plant and other traits in general (Table 1). The results obtained the occurrence of desirable mutations in the polygenes and effectiveness of irradiation in creating additional variability as evident from the higher mean values for grain yield in the  $F_2M_2$  and  $M_2$  population. Similar trend was reported for number of tillers per plant, number of spikelets per spike, number of grains per spike, 1000-grain weight and grain yield per plant in winter wheat (Singh, *et al.*, 2009) <sup>[12]</sup>. However, mean value was found to be higher in untreated  $F_2$  population for grains per spikes, spike length and 1000 grain weight compared to  $F_2M_2$  population. This negative shifts in mean values after mutagen treatment has been reported as general phenomenon attributed the occurrence of deleterious or harmful mutations which are supposed to occur more frequently in early generations of  $F_2M_2$  and  $M_2$  than the later generations. Such negative shifts in mean values in  $F_2M_2$  populations for majority of traits has been reported by El-rassas (1991) <sup>[2]</sup> in durum wheat, Khader and Shukry (1972) <sup>[4]</sup> and Virk *et al.* (1978) <sup>[13]</sup> in rice and wheat.

Shift in the mean towards positive direction was observed in  $M_2$  populations compared to  $F_2$  and  $F_2M_2$  populations for the characters plant height, productive tillers per plant, grains per spike, 1000 grain weight and grain yield per plant. This is attributed due to the elimination of the undesirable and lethal factors in  $M_2$  generations, while these unfavorable alleles in heterozygous conditions were maintained in  $F_2$  and  $F_2M_2$  thereby exhibiting low mean performance in  $F_2$  and  $F_2M_2$  compared to  $M_2$  population. However, differential level of mean performance for most of the traits in  $F_2M_2$  and  $M_2$  populations is primarily due to differences in genotypic response to mutation involved in the hybridization program.

The irradiated populations ( $F_2M_2$ 's) in general, showed wider range than the unirradiated segregating population ( $F_2$ ) for all the characters. (Table1). Increase in the upper limit of range

for the important yield contributing characters in  $F_2M_2$  populations in comparison to their corresponding  $F_2$  populations offers better scope to isolate rare types (transgressive segregants). The present study indicated an increase in range values in  $F_2M_2$  compared to  $F_2$  is in accordance with the reports of Mahantashivayogayya *et al.*, (2003) <sup>[7]</sup> and Shobha *et al.*, (2013) <sup>[11]</sup>. The increased range of variation in  $M_2$  population for important economic characters was in accordance with the earlier reports (Albokari *et al.*, 2012, Sakin and Yildirim, 2004) <sup>[1, 9]</sup>.

Among the different doses used for irradiating segregating population,  $F_2M_2$  with 250 Grey recorded higher mean values for the traits *viz.*, plant height, productive tillers per plant spike length and spikelets per spike whereas,  $F_2M_2$  with 200 Grey showed increased mean for grains per spike, 1000 grain weight and grain yield per plant. Indicating both 200 and 250 grey are suitable for obtaining favourable mutants for most of the yield related traits.

The phenotypic coefficient of variance and genotype coefficient of variance showed wide variation for most of the characters under study in almost all the populations. As expected PCV was invariably higher than GCV irrespective of  $F_2$  or  $F_2M_2$  or  $M_2$  for all the characters. However, the difference between GCV and PCV values which reflects environmental coefficient of variation was more for productive tillers per plant and grain yield per plant.

The irradiated population revealed the increase in GCV and PCV values from  $F_2$  to  $F_2M_2$  for important yield related traits *viz.*, plant height, spikelets per spike, grains per spike, productive tillers per plant, spike length and 1000 grain weight but the trait grains per plant there did not show increase in PCV and GCV values from  $F_2$  to  $F_2M_2$  populations (Table 2). The increased variations from  $F_2$  to  $F_2M_2$  for one character or set of characters may be due to various radiation effects such as mutation of genes, breaking of tightly linked regions or crossing over within these regions (Mahantashivayogayya *et al.*, 2003 and Shobha *et al.*, 2013 and Laghari, *et al.*, 2018) <sup>[7, 11, 6]</sup>.

Co-efficient of genetic variability together with heritability estimates gave a reliable picture of genetic advance to be expected from selection. High heritability was recorded in  $F_2M_2$  populations compared to their corresponding  $F_2$  populations for all the traits except grain yield per plant. Increase in magnitude of heritability was also observed in mutagen treated  $F_1$ s for different polygenic traits in dicoccum wheat as reported earlier (Mahantashivayogayya *et al.*, 2003 and Shobha *et al.*, 2013) <sup>[7, 11]</sup>. The change in heritability towards higher side is probably due to increased population genetic variance which is likely due to cryptic genetic changes brought out by mutations. Low variability in  $F_2M_2$  for few characters indicated that the irradiation has not added variability and hence mere inter varietal crosses will be enough for improvement of those characters.

In the present study heritability, GA and GAM values were increased in  $F_2M_2$  populations compared to  $F_2$  populations except for the traits spikelets per spike indicating selection in  $F_2M_2$  for these traits gives more success by selecting in  $F_2M_2$  compared to  $F_2$  population.

**Table 1:** Mean and range values for different quantitative characters in F<sub>2</sub>, F<sub>2</sub> M<sub>2</sub> and M<sub>2</sub> populations of bread wheat.

Populations		Mean							Range						
		Plant	Productive tillers	Spike	Spikelets	Grains	1000 Grain	Yield per	Plant	Productive tillers	Spike	Spikelets	Grains	1000 Grain	Yield per
		Height (cm)	per Plant	Length (cm)	per spike	per spike	weight (cm)	Plant (g)	Height (cm)	per Plant	Length (cm)	Per Spike	per spike	weight (g)	Plant (g)
GW322 x UASBW11949	F <sub>2</sub>	70.15	8.75	9.54	17.32	49.19	32.22	11.42	46.00-91.00	3.00-24.00	6.50-17.00	9.00-24.00	12.00-88.00	10.85-48.30	1.25-41.20
GW322 x UASBW11949	F <sub>2</sub> M <sub>2</sub> (150 Gy)	68.79	10.00	9.41	17.68	47.00	22.73	10.09	38.00-95.00	4.00-26.00	5.00-19.50	9.00-28.00	15.00-89.00	5.15-48.74	1.07-38.92
GW322 x UASBW11949	F <sub>2</sub> M <sub>2</sub> (200 Gy)	72.60	11.10	9.49	18.56	48.89	31.01	12.90	38.00-111.00	3.00-31.00	6.00-14.50	12.00-26.00	16.00-94.00	9.00-56.25	2.42-42.39
GW322 x UASBW11949	F <sub>2</sub> M <sub>2</sub> (250 Gy)	74.66	11.69	10.40	18.91	48.46	28.18	12.47	55.50-96.00	5.00-34.00	8.00-14.00	10.00-25.00	19.00-76.00	12.40-47.85	2.59-49.06
GW 322	Control	71.74	11.97	9.97	17.67	52.36	28.81	13.20	58.00-84.00	6.00-23.00	8.00-13.00	14.00-23.00	40.00-71.00	20.35-40.30	5.13-27.33
UASBW 11949	Control	68.52	12.41	8.52	15.18	47.82	41.42	16.49	52.00-78.00	10.00-20.00	7.00-10.00	12.00-21.00	40.00-68.00	21.80-48.85	4.43-32.59
GW 322	M <sub>2</sub> (150 Gy)	67.43	10.44	9.23	16.08	45.24	37.21	13.99	51.00-85.5	4.00-34.00	6.60-13.10	11.00-24.00	25.00-76.00	20.00-51.80	2.91-49.00
GW 322	M <sub>2</sub> (200 Gy)	66.16	9.97	9.28	17.11	44.60	36.43	11.27	45.00-85.00	4.00-33.00	6.00-14.00	10.00-23.00	10.00-85.00	16.90-50.00	1.96-48.25
GW 322	M <sub>2</sub> (250 Gy)	77.04	13.16	10.34	17.45	44.09	36.51	14.59	65.00-89.00	7.00-26.00	8.00-14.00	12.00-22.00	29.00-66.00	18.84-49.60	5.49-33.50
UASBW 11949	M <sub>2</sub> (150 Gy)	70.21	10.50	9.17	17.76	51.84	29.42	13.43	51.00-95.50	4.00-25.00	5.00-15.00	12.00-24.00	24.00-99.00	5.15-52.70	2.09-39.40
UASBW 11949	M <sub>2</sub> (200 Gy)	75.40	11.82	12.18	18.59	54.02	27.64	12.21	61.00-104.00	5.00-24.00	7.50-21.00	11.00-25.00	28.00-78.00	14.88-51.20	2.19-36.78
UASBW 11949	M <sub>2</sub> (250 Gy)	65.00	11.75	9.44	15.13	36.75	33.68	12.11	61.00-76.00	9.00-14.00	8.00-12.00	13.00-18.00	19.00-48.00	21.80-43.30	7.35-17.89

**Table 2:** Estimates of genetic variability parameters for different quantitative characters in F<sub>2</sub>, F<sub>2</sub> M<sub>2</sub> and M<sub>2</sub> population of bread wheat.

Populations		Plant Height (cm)				Productive tillers per plant				Spike length (cm)s				Spikelets per spike			
		PCV	GCV	H %	GAM %	PCV	GCV	H %	GAM %	PCV	GCV	H %	GAM %	PCV	GCV	H %	GAM %
GW322 x UASBW11949	F <sub>2</sub>	10.75	7.13	44.02	9.75	41.53	19.86	22.86	19.56	12.82	1.44	1.27	0.33	12.17	2.65	4.74	1.19
GW322 x UASBW11949	F <sub>2</sub> M <sub>2</sub> (150 Gy)	9.72	6.18	63.58	12.73	39.13	22.02	56.27	45.36	15.30	8.55	55.93	17.62	20.61	10.37	50.34	21.37
GW322 x UASBW11949	F <sub>2</sub> M <sub>2</sub> (200 Gy)	12.16	9.49	60.84	15.24	38.20	22.15	33.62	26.45	14.04	7.53	28.80	8.33	15.02	10.16	45.71	14.15
GW322 x UASBW11949	F <sub>2</sub> M <sub>2</sub> (250 Gy)	10.33	6.34	37.92	8.07	42.02	31.65	57.90	50.12	13.42	6.08	21.16	5.85	13.34	8.15	37.63	10.34
GW 322	M <sub>2</sub> (150 Gy)	11.69	5.87	25.21	6.07	47.12	24.43	26.88	26.09	14.93	1.74	1.35	0.42	13.06	6.46	24.49	6.59
GW 322	M <sub>2</sub> (200 Gy)	11.15	7.70	41.27	9.48	53.26	43.47	66.62	73.09	14.98	9.89	43.58	13.45	13.26	3.71	7.18	2.13
GW 322	M <sub>2</sub> (250 Gy)	7.64	2.14	7.83	95.01	32.48	25.41	61.19	40.95	17.87	14.64	67.11	24.70	17.03	14.05	68.09	23.88
UASBW 11949	M <sub>2</sub> (150 Gy)	10.34	8.27	63.91	13.61	34.14	11.07	10.51	7.39	13.44	9.82	53.38	14.79	14.36	6.51	20.55	6.08
UASBW 11949	M <sub>2</sub> (200 Gy)	9.73	7.58	77.86	15.61	35.16	12.15	34.57	25.03	21.36	19.67	92.06	40.52	17.67	15.23	82.76	33.63
UASBW 11949	M <sub>2</sub> (250 Gy)	7.45	1.18	2.50	0.38	16.87	4.72	7.83	2.72	13.11	9.98	57.94	15.65	12.95	9.68	55.86	14.91
Table 2.contd.....		Grains per spike				1000 grain weight (g)				Grain yield per plant (g)							
		PCV	GCV	H %	GAM %	PCV	GCV	H %	GAM %	PCV	GCV	H %	GAM %				
GW322 x UASBW11949	F <sub>2</sub>	21.93	12.97	35.00	15.81	20.69	10.29	24.74	10.55	64.83	52.55	65.69	87.73				
GW322 x UASBW11949	F <sub>2</sub> M <sub>2</sub> (150 Gy)	24.5	17.65	71.97	36.37	48.27	32.61	67.56	67.18	55.94	16.73	29.91	34.46				
GW322 x UASBW11949	F <sub>2</sub> M <sub>2</sub> (200 Gy)	23.6	17.50	55.25	26.80	31.40	27.17	74.92	48.45	50.00	30.20	36.47	37.57				
GW322 x UASBW11949	F <sub>2</sub> M <sub>2</sub> (250 Gy)	23.70	15.11	39.86	19.46	23.87	10.54	18.72	9.21	58.46	37.17	40.79	49.12				
GW 322	M <sub>2</sub> (150 Gy)	22.33	10.67	22.82	10.50	20.34	9.98	24.09	10.10	62.29	47.78	58.85	75.50				
GW 322	M <sub>2</sub> (200 Gy)	27.27	16.59	37.02	20.80	24.34	20.96	74.11	37.16	64.96	21.70	11.16	14.94				
GW 322	M <sub>2</sub> (250 Gy)	23.50	16.16	47.30	22.89	22.50	21.84	94.26	43.69	46.20	41.44	80.47	76.58				
UASBW 11949	M <sub>2</sub> (150 Gy)	22.52	18.32	66.20	30.71	35.52	32.26	82.47	60.35	47.82	32.78	46.99	46.28				
UASBW 11949	M <sub>2</sub> (200 Gy)	19.72	16.32	82.76	33.63	34.94	27.86	79.74	57.39	53.49	24.02	44.90	49.48				
UASBW 11949	M <sub>2</sub> (250 Gy)	24.63	17.13	48.37	24.54	23.78	15.71	43.63	21.38	27.61	19.10	47.84	27.21				

## Conclusion

The present study revealed that the effect of hybridization and mutagenesis is not always cumulative for all characters. However, mutation of segregating population in the present study helped in improvement of various economic characters of bread wheat and also release of more variability. Hence, mutagenesis in combination with hybridization will be having better scope than hybridization alone for selecting traits for diverse/adverse agro-climatic environments.

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