Inducing mutations by using chemical, electric shock and physical mutagens in bread wheat (*Triticum aestivum* L.)

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Abstract

The present investigation was carried out at the Experimental Farm, Faculty of Agriculture, Al-Azhar University, Assiut, Egypt during three successive winter seasons of 2019/2020, 2020/2021 and 2021/2022. Two bread wheat (*Triticum aestivum* L.) cultivars named Gemmiza 11and Shandweel 1 are treated with different concentrations of Sodium azide, Hydrazine hydrate, Electric shock and Gamma rays. According to the final results in M3 generation for Gemmiza 11, the best mutagens were electric shock for number of grains/ spikelet and 1000 grain weight and gamma rays for grain yield per plant. While Shandwel1was treated by Hydrazine hydrate for number of grains/spikelet, Electric shock for 1000 grain weight and Gamma rays for grain yield per plant. Heritability estimates were high for all characters studied except 1000 grain weight for Gemmiza11, no. spikes /plant and grain yield /plant for Shandweel 1 which was moderate. The phenotypic coefficients of variation (PCV) values were high for no. spikes /plant for Shandweel 1. The moderate PCV and genotypic coefficients of variation (GCV) were estimated for grain yield /plant and no. of spikes /plant for Gemmiza 11, GCV for no. of spikes /plant for Shandweel 1. Low estimates of the PCV and GCV were recorded for no. of grains /spikelet and1000 grain weight for Gemmiza 11, no. of grains /spikelet, 1000 grain weight and grain yield /plant for Shandweel 1. Estimates of genetic advance as percent of mean were high for grain yield /plant and no. of spikes /plant for Gemmiza 11, no. of spikes /plant for Shandweel 1. Moderate estimates were no. of grains/spikelet for Gemmiza 11, no. of grains /spikelet and 1000 grain weight for Shandweel. Low estimates for 1000 grain weight for Gemmiza 11and grain yield /plant for Shandweel. These results indicated that the effective mutagen to induce mutations can be used directly or through breeding programs to obtain superior mutants in parent genotypes for yield and its components.

Keywords: mutations, bread wheat, chemical mutagens, electric shock, gamma rays, genetic parameters.

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1. Introduction

Wheat (*Triticum aestivum* L.) belongs to family *poaceae* and one of the most important cereal crops of the world, including Egypt. About 21.48 million tons of consumption of wheat grains in Egypt, while the production is about 9.10 million tons (Bulletin of food balance sheet Arab republic of Egypt, 2020). Therefore, the gap between annual local production and consumption of wheat grains is about 12.380 million tons. This gap could be narrowed by increasing local production of wheat in two ways. The first way is through horizontal expansion, *i.e.*, by increasing the area cultivated with wheat. The second way is through vertical expansion, i.e., increasing wheat production per unit area through the development of new cultivars of high yielding ability. Plant breeding is an important aspect of agriculture. The major aim of plant breeding is to ensure future global food security. Plant breeding scientists are able to develop new plant varieties with many improved characteristics, such as climate resilience, yield, maturation time, and pest and disease resistance. There are many techniques in plant breeding; mutation breeding is one of the techniques applied for improving high yielding ability. Mutation breeding is more effective and less time-consuming. Manjaya and Nandanwar (2007) reported that induced mutations have been successfully for improvement of some economic and quality traits during short time. In nature,

mutations happen at a much slower rate, which hinders scientists' efforts at crop improvement. On the contrary, mutagens have provided the solution to the slow mutation rate by inducing mutations at much faster rates (Udage, 2021). Mutations are important in evolution in several ways. All current genetic variations originally arose because of mutations. Mutations are therefore the ultimate source of differences among species. In addition, mutations span the entire range of fitness effects from lethal to mildly deleterious to neutral to beneficial. A mutation is a heritable change in the genetic material that is not due to genetic recombination. Mutation alters the structure or number of genes or entire chromosomes (Johnston, 2003). According to FAO/IAEA (2009), 77 mutant varieties were released in 1969, which grew dramatically to 1330 by 1989, By 2009, about 3100 mutant cultivated varieties of about 190 plant species were listed in the (FAO /IAEA 2009). Chemical mutagenesis is regarded as an effective and important tool in improving the yield and quality character of crop plants. In alkylating, agents are very effective mutagens in higher plants (Ahmed, 2019). Gamma rays were effective in increasing genetic variability as reflected by high heritability estimates accompanied with high values of expected genetic advance from selection in the resulting heterogeneous populations for grain yield and its components in wheat (Al-Naggar *et al.*, 2015). In the near future, the author

expect that the new technique will become the third essential source for artificial mutation induction beside radiation and chemical mutagens and this system will be developed by identification expecting the electric mutagen dose, exact chemical kind and concentration and mutation period. This new unique technique is an amazing mutation tool, very effective; many different mutations, available, very simple and very safe with no residual effects (Ahmad, 2011). The aims of this study were to induce genetic variability in bread wheat using chemical, electric shock and physical mutagens and evaluate the impact of using different doses on major agronomic traits in two commercial bread wheat genotypes. Additionally, to identify the most potential mutants in terms of improving agronomic traits compared to parents.

2. Materials and methods

2.1 Experimental site and plant material

The present investigation was carried out at the Experimental Farm, Faculty of Agriculture, Al-Azhar University, Assiut, Egypt during three successive winter seasons of 2019/2020, 2020/2021 and 2021/2022. Two bread wheat (*Triticum aestivum* L.) genotypes were used. The names, pedigree and origin of these genotypes are shown in Table (1).

Table (1): Name, pedigree and origin of the studied wheat genotypes.

Name	Pedigree	Origin
Gemmiza-11	GM7892-2GM-1GM-2GM-1GM-0GM	Egypt
Shandaweel-1	SITE/MO/4/NAC/TH.AC//3*PVN/3MIRLO/BUC CMSS93B00567S-010M010Y-010M-3Y-0M-0HTY-0SH	Egypt

2.2 Treatments

The present study was carried out to induce genetic variability in bread wheat by using sodium azide, hydrazine hydrate, electric shock and gamma rays to obtain superior mutants in both genotypes for yield and its components.

2.2.1 Chemical mutagenic

2.2.1.1 Sodium Azide (SA) (NaN$_3$)

Forty gm seeds from each variety were soaked in a prepared aqueous solution of sodium azide at three different concentrations (SA$_1$ (100), SA$_2$ (400) and SA$_3$ (900) ppm) for 16 hours. As well as 40gm of germinated seeds from each genotype were soaked in prepared aqueous solution of sodium azide SA$_4$ (400 ppm) for three hours.

2.2.1.2 Hydrazine hydrate (HZ) (N$_2$H$_4$.H$_2$O)

Forty gm seeds from each variety were soaked in a prepared aqueous solution of hydrazine hydrate at three different concentrations (HZ$_1$ (100), HZ$_2$ (400) and HZ$_3$ (900) ppm) for 16 hours. As

well as 40 gm germinated seeds from each genotype were soaked in prepared aqueous solution of hydrazine hydrate HZ_4 (400 ppm) for three hours.

2.2.2 Electric shock

Forty gm seeds from each genotype were germinated to exploit the DNA activity through the cell division during germination of the seeds and put germinated seeds between two parallel poles of iron submerged in a chemical solution (Table 2) for 20 seconds using

electricity conductions (220 v) inside special electric analysis set for mutations induction (Ahmad, 2011).

2.2.3 Gamma ray irradiation

Forty gm fresh air-dried seeds from each of the two wheat genotypes used in the present study were subjected to treatment with two different doses of gamma rays, 10 and 15 krad (R_{10} and R_{15} respectively). All these treatments were carried out at the Nuclear Research Center, the Egyptian Atomic Energy Authority.

Table (2): Chemical solutions used for electric shock.

Treatment no.	Chemical components	Concentration	Brief
1	Monosodium phosphate NaH_2PO_4	30000ppm	E_1
2	Monosodium phosphate NaH_2PO_4	40000ppm	E_2
3	Monosodium phosphate NaH_2PO_4	50000ppm	E_3
4	Calcium nitrate $Ca(NO_3)_2$	30000ppm	E_4
5	Calcium nitrate $Ca(NO_3)_2$	40000ppm	E_5
6	Calcium nitrate $Ca(NO_3)_2$	50000ppm	E_6

2.3 Field Experiments

In the first season (2019-2020), seeds were immediately sown after treatment (M1). In addition, untreated seeds of each genotype were used as control treatment by the broadcasting method in experimental plots with area of 2 m × 2 m. The recommended agricultural practices for wheat production were followed. At the beginning of the flowering, the mutant plants appeared, and the important characters were measured (spikes number/plant, grain number/spikelet, 1000 grain weight (gm) and grain yield /plant (gm)). Seeds of mutant plants and studied genotype were

collected and kept for sowing in the next season (2020/2021) in a randomized complete block design (RCBD) with three replications on lines 3 m along 70 cm apart and the plants spaced 10cm within line on the two sides. When the plants grew (M2), observations were recorded on randomly selected plants from each mutation and genotype as a sample for evaluation of economic traits with the studied genotypes. The best five plants from each treatment were selected and planted in the next season (2021/2022) in a randomized complete block design with three replications on lines 3 m along 70 cm apart and the plants spaced 20cm within line on the

two sides.

2.4 Field Experiments

Data for the 2020/2021 and 2021/2022 growing seasons were subjected to statistical analysis as outlined by Snedecor and Cochran (1967) for the randomized complete blocks design (RCBD). Estimates of phenotypic and genotypic variances were calculated from EMS of the variance and covariance components in Table (3). Where: r and g: number of replications and genotypes, respectively. The phenotypic (σ^2_{ph}) and genotypic (σ^2_g) variances were calculated according to the following formula:

The genotypic variance $\sigma^2_g = (M2-M1)/r$

The phenotypic variance $\sigma^2_{ph} = \sigma^2_g + (\sigma^2_e/r)$

Table (3): The analysis of variance and expected mean squares (EMS).

Source of variance	D.F	M.S	Expected mean square	
			Variance	Covariance
Replications	r-1	M3	$\sigma^2e + g\,\sigma^2r$	
Treatments	t-1	M2	$\sigma^2e + r\,\sigma^2g$	Cov.e + r Cov.g
Error	(r-1)(t-1)	M1	σ^2e	Cov.e

Heritability in the broad sense (H_{bs}) was estimated as the ratio of genotypic (σ^2_g) to the phenotypic (σ^2_{ph}) variance according to Walker (1960). The phenotypic (PCV) and genotypic (GCV) coefficients of variability were estimated using the formula developed by Burton (1952):

$PCV = (\sigma_p / \overline{x}) \times 100$
$GCV = (\sigma_g / \overline{x}) \times 100$

Where: σ_p and σ_g are the phenotypic and genotypic standard deviations, respectively, and $\overline{x}$ means a given trait.

The coefficient of variation (C.V) was calculated according to Gomez and Gomez (1984), according to the following formula:

$C.V = (\sqrt{MSe}/ \overline{x}) \times 100$

Mean comparisons were calculated using LSD, where LSD = least significant differences (LSD) was at a 5% and 1% level of probability, according to Gomez and Gomez (1984), and was calculated as:

$LSD = (t) \sqrt{(2MSe/r)}$

Where t' is the t value from t-Table "in experimental error D.F.

The expected genetic advance (GA) from selection was computed by the formula given by Allard in (1960) and outlined by Singh and Chaudhary (1985), according to the following formula:

$GA = k \times H_{bs} \times \sqrt{\sigma2_p}$

Where: k = 1.76 constant for 10 % selection intensity.

GA % was estimated according to Miller *et al*. (1958):

$$GA\% = (GA / \bar{x}) \times 100$$

3. Results and discussion

3.1 Gemmiza 11

3.1.1 Analysis of variance in the M2 and M3 generations

The analysis of variance (mean squares) for different quantitative traits of bread wheat genotype Gemmiza 11 under different concentrations of sodium azide, hydrazine hydrate, electric shock under different concentration of monosodium phosphate and calcium nitrate and gamma rays in the M2 and M3 generation is shown Table (4). ANOVA results revealed highly significant differences among mutagens treatments for all studied characters in the M2 and M3 generation.

Table (4): Analysis of variance for the studied characters in both M2 and M3 generations for genotype Gemmiza 11 of bread wheat (*Triticum aestivum* L.).

S.O.V	D.F	Generation	M.S			
			Number of spikes/plant	Number of grains/spikelet	1000 grain weight	Grain yield/plant
Blocks	2	M_2	01.57	0.03	00.61	030.05
		M3	10.10	0.11	02.56	308.89
Treatments	16	M2	46.25**	2.49**	17.22**	787.88**
		M3	23.87**	0.57**	07.19**	307.08**
Error	32	M2	01.91	0.05	01.25	029.10
		M3	03.43	0.05	01.83	057.36

[*], [**] Significant at 0.05 and 0.01 levels probability, respectively.

3.1.2 Mean performance

The presented results in Table (5) show the means of studied traits in M_2 at all mutagenic treatments. The height numbers of spikes per plant were 20.06, 19.82, 18.06, 17.41, 17.00 and 16.40 were obtained from E_4, E_3, E_5, E_6, E_1 and HZ_3 respectively. For the number of grains per plant in M_2, the height values were 7.02, 6.55 and 5.36 obtained from E_2, SA_4 and HZ_4 respectively. The highest 1000 grain weight was 50.78 obtained from E_1 treatment. For grain yield per plant, the best treatments in M_2 were E_4 and E_3 with values of 69.32 and 67.98. The results of current study are in line with those obtained by Ahmad (2011), Al-Shamma (2013), Okaz *et al.* (2016), Al-Shamma, Hawash (2018) and Sakr *et al.* (2020). Mean performance values in M_3 generation for all studied traits at all mutagenic treatments are presented in Table (5). The highest number of spikes per plant obtained from R_{15} treatment with value 23.51. This result is in agreement with those obtained with Khah and Verma (2015) and Ahmed *et al*. (2017). For the number of grains per plant, the best treatments were E_2, HZ_4 and SA_2 with values of 6.53, 5.49 and 5.04 respectively. The highest 1000

grain weight was 55.02 obtained from E_6 treatment. For grain yield per plant, the best treatments were 85.07, 79.20 and 78.73 obtained from R_{15}, E_6 and SA_4 respectively. These results are in agreement with the results obtained by Mansour *et al.* (2012), and Laghari *et al.* (2018).

Table (5): Mean performance for investigated characters of M2 and M3 for genotype Gemmiza 11 of bread wheat (*Triticum aestivum* L.).

Character / Treatment	Number of spikes/plant		Number of grains/spikelet		1000 grains weight (g)		Grains yield/plant (g)	
Generation	M2	M3	M2	M3	M2	M3	M2	M3
Control	10.11	22.56	3.96	4.70	44.61	51.16	22.70	71.18
SA_1	08.56	18.27	3.52	4.89	42.38	51.12	18.99	63.69
SA_2	12.83	20.53	4.06	5.04	44.29	53.24	33.17	78.40
SA_3	10.17	18.11	4.18	4.96	42.76	53.24	23.05	72.57
SA_4	07.69	19.62	6.55	4.91	46.58	54.94	28.41	79.20
Mean	09.81	19.13	4.58	4.95	44.00	53.14	25.90	73.46
HZ_1	12.83	18.62	4.15	4.93	44.42	52.75	31.12	75.60
HZ_2	13.28	18.22	4.68	4.71	46.98	53.77	42.16	71.49
HZ_3	16.40	17.18	4.44	4.89	49.30	52.77	52.55	64.77
HZ_4	10.44	17.49	5.36	5.49	49.02	51.18	30.16	70.43
Mean	13.24	17.88	4.65	5.01	47.43	52.62	39.00	70.57
E_1	17.00	15.98	4.51	4.79	50.78	53.83	58.19	58.92
E_2	10.22	10.58	7.02	6.53	49.13	49.31	52.69	40.96
E_3	19.82	17.76	4.64	4.84	48.45	53.64	67.98	73.04
E_4	20.06	18.33	4.57	4.84	48.08	53.58	69.32	71.80
E_5	18.06	19.07	4.44	4.77	48.13	54.34	53.79	77.91
E_6	17.41	18.80	4.29	4.91	46.76	55.02	50.14	78.73
Mean	17.09	16.75	4.91	5.11	48.55	53.29	58.69	66.89
R_{10}	11.32	21.20	4.08	4.66	47.59	51.27	27.97	77.48
R_{15}	12.78	23.51	3.96	5.00	46.76	52.55	30.41	85.07
Mean	12.05	22.36	4.02	4.83	47.18	51.91	29.19	81.28
$LSD_{0.01}$	3.09	4.14	0.49	0.48	2.50	3.03	12.06	16.93
$LSD_{0.05}$	2.30	3.08	0.37	0.36	1.86	2.25	8.97	12.60
C.V	10.27	9.97	4.79	4.30	2.38	2.56	13.24	10.63

3.1.3 Genotypic response to mutagens

Table (6) shows the means of all studied characters. For the number of spikes per plant, the mean value in M2 was 13.47, and then increased in M3 to 18.58. The mean number of grains per spikelet increased from 4.61 in M2 to 4.99 in M3 generation. The mean weighing of the 1000 grains was 46.82 in M2 generation, and then increased to 52.81 in M3 generation. The mean of grain yield per plant increased from 40.75 in M2 generation to 71.25 in M3 generation.

The results are in agreement with those obtained by Abdel-hamed *et al.* (2021).

3.1.4 Phenotypic (PCV) and genotypic (GCV) coefficients of variability

Genetic variability in the population is very important because it plays a very important role in any crop breeding program. Statistically, the total variability was expressed in terms of the PCV and the genotypic variability is expressed in terms of the GCV. The GCV and PCV values were categorized

as low (<10%), moderate (10 to 20%) and high (>20%) as indicated by Subramaniam and Menon (1973). The GCV and PCV values obtained in current study were moderate and low for all investigated traits except grain yield /plant and no. spikes/plant in M2 generation were high. The moderate PCV and GCV were estimated for grain yield /plant and number of spikes/plant in M3 and number of grains/spikelet in M2 generation (Table 6). This indicated that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic

performance for these characters in early mutated generations. Low estimates of the PCV and GCV were recorded for number of grains/spikelet in M3 and 1000 grain weight in M2 and M3 generations. The result indicated that the environmental factors had more influence on the expression of this character than the genetic factors, suggesting the limited scope for improvement of these characters by direct selection of high-performing genotypes. Balkan (2018) recorded moderate PCV and GCV estimates of the grain yield in three mutant generations.

Table (6): Means, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2_{bs} %) and expected gain (GA) from selection for the studied traits in both M2 and M3 generations for genotype Gemmiza 11 of bread wheat (*Triticum aestivum* L.).

Characters	Generation	Grand mean	PCV	GCV	h^2_{bs} (%)	GA	GA (%)
Number of spikes/plant	M2	13.47 ± 0.80	29.15	28.54	95.86	6.62	49.18
	M3	18.58 ± 1.07	15.18	14.05	85.62	4.25	22.88
Number of grains/spikelet	M2	4.61 ± 0.13	19.77	19.58	98.04	1.57	34.11
	M3	4.99 ± 0.12	8.77	8.41	91.99	0.71	14.19
1000 grain weight (g)	M2	46.82 ± 0.64	5.12	4.93	92.77	3.91	8.36
	M3	52.81 ± 0.78	2.93	2.53	74.48	2.03	3.84
Grain yield/plant (g)	M2	40.75 ± 3.11	39.77	39.02	96.31	27.47	67.40
	M3	71.25 ± 4.37	14.20	12.81	81.32	14.48	20.32

3.1.5 Heritability in a broad sense

Heritability of a trait was considered as high when the value is 80% or moderate, when it ranged from 40-80% and when it was less than 40% it was low, according to Singh (2001). As shown in Table (6), the heritability estimates were high for all characters studied in both generations except for the 1000 grain weight in M3 which was moderate. This indicated that selection might be effective for these

characters. The results in agreement with Abaza *et al*. (2017).

3.1.6 Genetic advance

Genetic advance, as the percent of mean is low (<10%), moderate (10-20%) and high (>20%), according to Deshmukh *et al*. (1986), As presented in Table (6) genetic advance was high for grain yield/plant and number of spikes/plant in both generations as well as number of

grains/spikelet for M2 generation. Moderate estimates were obtained for number grains/spikelets in the M3 generation. While low estimates were found for 1000 grain weight in both generations.

3.2 Shandweel 1

3.2.1 Analysis of variance in the M2 and M3 generations

Table (7) exhibits the ANOVA for studied traits of Shandaweel 1 under different concentrations of sodium azide, hydrazine hydrate, electric shock (using different concentration of monosodium phosphate and calcium nitrate), and one of treatment of gamma rays in the M2 and M3 generation. The results revealed highly significant differences for all studied traits in the M2 and M3 generations.

Table (7): Analysis of variance for the studied characters in both M2 and M3 generations for genotype Shandweel 1 of bread wheat (*Triticum aestivum* L.).

S.O.V	D.F	Generation	M.S			
			Number of spikes/plant	Number of grains/spikelet	1000 grain weight	Grain yield/plant
Blocks	2	M_2	6.14	0.01	1.79	85.59
		M3	9.92	0.15	1.41	25.68
Treatments	15	M2	28.99**	0.40**	35.38**	308.56**
		M3	52.80**	0.41**	63.57**	60.50**
Error	30	M2	5.16	0.06	1.58	46.48
		M3	11.03	0.04	2.69	17.26

*, ** Significant at 0.05 and 0.01 levels probability, respectively.

3.2.2 Mean performance

Results in Table (8) showed means of studied traits in M2 at all mutagenic treatments. The height numbers of spikes per plant were 30.00, 23.33 and 22.93, obtained from R_{10}, E_2 and HZ_4 respectively. For the number of grains per plant in M2, the height values were 5.31 and 5.28 obtained from HZ_3 and HZ_4 respectively. The highest 1000 grain weight was 47.97 obtained from HZ_1 treatment. The results are in agreement with Khursheed *et al*. (2015). For grain yield per plant, the best treatments in M2 were E_1 of followed by HZ_4 with values of 68.34 and 66.02. Mean performance values in M3 generation for all studied

traits at all mutagenic treatments are shown in Table (8). The highest number of spikes per plant obtained from control with value 30.40, followed by R_{10} treatment with value 30.28. For the number of grains per plant, the best treatments were HZ_4, HZ_3 and HZ_2 with values of 5.91, 5.57 and 5.32 respectively. The highest 1000 grain weight was 52.78 and 52.41 obtained from E_4 and E_3 respectively, while the lowest obtained from R_{10}. The current results are confirmed by the findings of Irfaq and Nawab (2001) and Salari *et al.* (2020). For grain yield per plant, the best treatments were 82.69 and 80. 11 obtained from R_{10} and HZ_2 respectively, the results agree with those obtained by

Sakin and Sencar (2002), El- Degwy and Hathout (2014), Aly *et al.* (2018), Nazarenko *et al.* (2018), Moursy and Ismail (2019), and Ahmed and Ahmed (2020).

Table (8): Mean performance for investigated characters of M2 and M3 for genotype Shandweel 1 of bread wheat (*Triticum aestivum* L.).

Character / Treatment	Number of spikes/plant		Number of grains/spikelet		1000 grains weight (g)		Grains yield/plant (g)	
Generation	M2	M3	M2	M3	M2	M3	M2	M3
Control	22.00	30.40	4.63	4.81	36.58	40.64	43.09	77.09
SA$_1$	22.06	21.09	4.80	4.63	36.08	39.88	34.51	68.63
SA$_2$	17.92	20.07	4.11	4.75	43.01	51.86	40.07	71.99
SA$_3$	17.17	18.53	4.50	5.02	44.67	52.15	50.50	74.56
SA$_4$	20.17	17.11	4.93	5.00	44.47	49.84	54.62	70.58
Mean	19.33	19.20	4.58	4.85	42.06	48.44	44.93	71.44
HZ$_1$	18.68	18.22	4.26	5.09	47.97	50.28	57.25	70.39
HZ$_2$	19.33	24.64	4.00	5.32	38.72	41.92	33.48	80.11
HZ$_3$	19.67	17.16	5.31	5.57	42.04	49.47	50.81	67.56
HZ$_4$	22.93	16.04	5.28	5.91	44.94	50.94	66.02	69.09
Mean	20.15	19.02	4.71	5.47	43.42	48.15	51.89	71.79
E$_1$	21.26	20.16	4.98	4.60	44.30	50.52	68.34	71.26
E$_2$	23.33	20.69	4.51	4.78	39.85	49.02	59.27	78.99
E$_3$	19.63	20.36	4.53	4.89	43.62	52.41	61.49	75.92
E$_4$	17.33	19.09	4.80	4.70	40.53	52.78	50.10	69.77
E$_5$	19.61	19.64	4.74	4.60	41.27	49.89	56.41	70.86
E$_6$	19.47	20.11	4.69	4.93	44.80	49.62	53.91	73.66
Mean	20.11	20.01	4.71	4.75	42.40	50.70	58.25	73.41
R$_{10}$	30.00	30.28	4.67	4.69	37.49	40.63	53.12	82.69
Mean	30.00	30.28	4.67	4.69	37.49	40.63	53.12	82.69
LSD$_{0.01}$	5.10	7.46	0.53	0.43	2.83	3.68	15.31	9.33
LSD$_{0.05}$	3.79	5.54	0.39	0.32	2.10	2.74	11.37	6.93
C.V	11.00	15.93	5.07	3.86	3.00	3.40	13.10	5.67

3.2.3 Genotypic response to mutagens

Results in Table (9) explain that the means of all characters showed significant increase. For the number of spikes per plant, the mean value in M2 was 20.66 then increased in M3 to 20.85. The mean number of grains per spikelet increased from 4.67 in M2 to 4.96 in M3 generation. The mean weight of the 1000 grains was 41.90 in M2 generation then increased to 48.24 in M3 generation. For mean of grain yield per plant increased from 52.06 in M2 generation to 73.32 in M3 generation.

3.2.4 Phenotypic (PCV) and genotypic (GCV) coefficients of variability

The results in Table (9) indicated that the high PCV value was for number of spikes/plant in M3 generation. The moderate PCV and GCV were estimated for number of spikes/plant in M2, GCV for number of spikes/plant in M3 generation and grain yield/plant in M2 generation. The results are in agreement with Awaad *et al.* (2018). This indicated that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters in early mutated generations. Low estimates of the PCV and GCV were recorded for

number of grains/spikelet, 1000 grain weight in both M2 and M3 generations and grain yield /plant in M3 generation.

3.2.5 Heritability in a broad sense

The results in Table (9) explain that the heritability was estimated for all characters studied in both generations that were high except spikes/plant and grain yield/plant in M3 were moderate. The results in agreement with Sakin and Yildirim (2004). This indicated that selection might be effective for these characters.

3.2.6 Genetic advance

The estimated genetic advance as present of mean Table (9) were high for number of spikes/plant in both generations as well grain yield/plant for M2 generation. Moderate estimates were number of grains/spikelet and 1000 grain weight in M2 and M3 generation. Low estimates for grain yield/plant in M3 generation.

3.3 The best families for each genotype

Results in table (10) shown the best of ten families for Gemmiza 11 genotype. The best family for grain yield/plant was obtained from SA_3 treatment with value 94.13, while for 1000 grain weight was obtained from E_6 with value 57.22, for number of grains/spikelet obtained from E_2 with value 7.22 and the best family for number of spikes/plant was found in SA_1 treatment with value 27.11. Table (11) exhibits the best of ten families for genotype Shandweel 1.

Table (9): Means, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2_{bs} %), and expected gain (GA) from selection for the studied traits in both M2 and M3 generations for genotype Shandweel 1 of bread wheat (*Triticum aestivum* L.).

Characters	Generation	Grand mean	PCV	GCV	h^2_{bs} (%)	GA	GA (%)
Number of spikes/plant	M_2	20.66 ± 1.31	15.05	13.64	82.18	4.50	21.76
	M_3	20.85 ± 1.92	20.12	17.90	79.11	5.84	28.02
Number of grains/spikelet	M_2	4.67 ± 0.14	7.79	7.22	85.88	0.55	11.77
	M_3	4.96 ± 0.11	7.43	7.09	90.99	0.59	11.90
1000 grain weight (g)	M_2	41.90 ± 0.73	8.20	8.01	95.52	5.77	13.78
	M_3	48.24 ± 0.95	9.54	9.34	95.77	7.76	16.08
Grain yeild /plant (g)	M_2	52.06 ± 3.94	19.48	17.95	84.94	15.16	29.12
	M_3	73.32 ± 2.40	6.12	5.18	71.46	5.65	7.70

Table (10): The best of ten families for genotype Gemmiza 11 of bread wheat.

Grain yield /plant		1000 grain weight		Number of grains /spikelet		Number of spikes /plant	
Control	71.18	Control	51.16	Control	4.70	Control	22.56
1 SA_3	94.13	4 E_6	57.22	1 E_2	7.22	5 SA_1	27.11
5 SA_4	93.27	2 HZ_4	56.61	4 E_2	6.78	5 R_{10}	25.22
1 R_{15}	93.06	2 E_6	56.10	2 HZ_4	6.67	1 R_{15}	25.11
5 R_{10}	91.76	5 E_3	55.20	5 E_2	6.56	2 R_{15}	24.00
5 HZ_1	91.03	3 HZ_4	55.05	1 HZ_4	6.44	3 R_{15}	23.56
4 E_4	88.94	1 E_5	55.03	2 E_2	6.13	5 SA_2	23.11
4 HZ_1	88.69	3 E_4	54.86	3 E_2	5.89	5 SA_4	23.11
5 R_{15}	88.08	3 E_6	54.86	5 SA_3	5.67	1 SA_2	22.89
5 SA_1	87.38	5 E_1	54.77	3 SA_2	5.33	5 HZ_1	22.89
1 R_{10}	86.04	5 HZ_2	54.76	5 R_{15}	5.33	5 R_{15}	22.56

Table (11): The best of ten families for genotype Shandweel 1 of bread wheat.

Grain yield /plant		1000 grain weight		Number of grains /spikelet	
Control	77.09	Control	40.64	Control	4.81
3 HZ_4	98.26	3 E_3	54.17	5 HZ_4	7.44
4 R_{10}	91.94	4 E_4	53.89	2 HZ_3	7.22
2 E_2	88.36	2 E_4	53.88	4 HZ_4	6.78
2 E_4	88.35	3 HZ_3	53.72	5 HZ_2	5.44
2 SA_3	87.99	4 SA_3	53.60	3 HZ_2	5.43
1 HZ_2	87.57	2 HZ_4	53.42	4 HZ_2	5.38
1 R_{10}	87.30	3 E_5	53.28	2 HZ_1	5.33
1 E_3	85.92	3 SA_3	53.10	2 HZ_2	5.33
5 E_2	85.55	1 E_2	52.90	5 SA_4	5.33
2 SA_2	82.41	3 SA_2	52.89	1 E_6	5.22

The best family for grain yield/plant and number of grains/spikelet were obtained from HZ_4 treatment with values 98.26 and 7.44 respectively, while the best family for1000 grain weight was obtained E_3 with value 54.17. Gemmiza 11 was more responsive to mutagens for number of spikes/plant, number of grains/spikelet and grain yield/plant than Shandweel 1. While Shandweel 1was more response to mutagens for 1000 grains weight than Gemmiza 11.

4. Conclusion

Using of different mutagen treatment were effective tool to obtain new wheat genotypes which could be used as new genotypes in wheat breeding program to improve the genetic background of wheat for grain yield and its components.

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