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INDUCED MUTATIONS FOR IMPROVED YIELD AND ITS COMPONENTS IN BREAD WHEAT USING GAMMA RADIATION

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ABATRACT

Mutations induced by irradiation are widely used for developing new varieties of plants. This study was conducted during the four winter seasons from 2015/2016 through 2018/2019 at the experimental station of Plant Research Department, Nuclear Research Center, Atomic Energy Authority, Inshas, Egypt. The aim of this study was to estimate the magnitude of genetic variability in yield and its attributes, practice visual selection for yield and its components in irradiated bread wheat (line10) with 300Gy and 350Gy of gamma rays in the M_2 and M_3 generation and evaluation of bread wheat mutations for yield and its components in the M_4 generation. The results showed that gamma irradiation dose of 300Gy was more effective in creating genetic variation in quantitative traits in the M_2 population of bread wheat (Line 10) as compared to irradiation treatment of 350Gy. High values of genotypic coefficient of variability, heritability and expected genetic advance were found for number of spikes/plant and medium values for 100-grain weight and no. of grains/spike. Positive and significant correlation coefficient (r=776*) was found between yield and No. of spikes/ plant, positive but not significant correlation coefficients between grain yield and No. of grains/spike and 100-grain weight. Results indicated that yield components could be considered useful selection criteria for improving grain yield in wheat. In the M_3 progeny test, data indicated that some of the selected plants (high yielding) expressed the traits of their M_2 selections. Therefore, they were considered breed true. In M_4 generation, family 1 was characterized by a reduced plant height (79.3cm), Family 2 by high number of spikes/ plant, long spike, heavy 100-grain weight (6.0g), high number of grains/spike and high grain yield/plant, Family 3 by high number of spikes/plant, heavy 100-grain weight (6.25g) and high grain yield/plant, Family 4 by high number of spikes/plant, heavy 100-grain weight (6.03g), high number of grains/spike and high grain yield/plant,but heading was late. Family 5 was characterized by a heavy 100-grain weight (6.27g). These new families well be tested in further experiments.

Key words: ***Gamma irradiation, Triticum aestivum, Mutation breeding, Genetic variability, Yield attributes, Correlation analysis***

INTRODUCTION

Increasing the yield potential of wheat has been a major focus of most wheat breeding programs around the world. Grain yield is a complex trait and highly influenced by many genetic factors, environment and their interaction. In plant breeding programs, direct selection for yield could be misleading. A successful selection depends upon information on the genetic variability and association of morpho-agronomic traits with grain yield (Ashraf and Mohamed 2014). Correlation analysis is an important statistical method which can help wheat breeders in selection for higher yields. Some of the researchers indicated the positive correlation between grain yield and its components in wheat such as spikes number per plant (Mondal and

Khajuria 2001), grains number per spike (Kashif and Khaliq 2004) and 1000-kernel weight (Akbar *et al* 1995).

Globally, more than 3200 mutant varieties have been directly or indirectly derived through mutation induction, including 256 bread wheat varieties (International Atomic Energy Agency, IAEA, 2018). A wide range of genetic variability has been induced by mutagenic treatments for use in plant breeding and crop improvement programs (Celik and Atake 2017). The most part of mutant varieties have been obtained by using gamma irradiation (about 85 percent from general number) (IAEA, 2018). Induced mutations have been applied to produce mutant varieties by changing the plant characteristic for a significant increase in productivity and improved quality (Ahloowalia *et al* 2004 and Shu 2013).

The aim of this study was to estimate the magnitude of genetic variability in yield and its attributes, practice visual selection for yield and its components in irradiated bread wheat (Line 10) with 300 and 350Gy of gamma rays in the M_2 and M_3 generations and evaluation of bread wheat mutations for yield and its components in the M_4 generation.

MATERIALS AND METHODS

Grains of the bread wheat line 10 (F_6) derived from hybridization between the cultivar Gemmeiza10 and wheat mutant ($LSWM_9$) were irradiated with gamma rays at doses of 300 and 350Gy. Line10 was characterized by high number of grains/spike and heavy 100-grain weight but reduction in number of spikes/plant. The source of irradiation was installed at gamma unit, the Cyclotron project, Nuclear Research Center, Inshas, Egypt. Irradiated and non-irradiated grains were sown on November 2015 at the experimental farm of the Plant Research Department, Nuclear Research Center, Inshas. Separate plots were used to obtain M_1 plants of each bulk. Each plot consisted of 30 rows, each row was 3m long and 30cm wide, spaces between each two plants were 10cm in each row. Ten grains were harvested at random from each M_1 plant (M_2 seed). These samples were sown on November, 2016 to raise M_2 plants and obtain M_3 seeds. Each plot consisted of 10 rows, 3m long and 30cm wide. A single grain was planted in each hill at 10cm distance between hills. A randomized complete block design was used with three replications. The common procedures for wheat production were followed. At harvest, thirty individual plants were taken at random from each treatment to determine the effect of gamma rays on plant height, spike length (cm), number of spikes/plant, 100 grain weight (g), number of grains /spike and grain yield/plant.

Additionally, M_2 irradiated populations were screened in order to select high yielding variants. As a result, 12 elite plants (8 plants from 300Gy and 4 plants from 350Gy) were selected. The selectants, exceeded the average of the best 3 plants (control) by 16% or more. Seeds of the selectants as well as the best 3 plants in control were kept separately in paper bags for sowing of the next season.

The twelve selectants from M_2population along with their control were grown on November, 2017 as single plant progeny to assess the breeding value of the selected variants. In M_3 generation, selectants were screened among and within progenies in order to select high yielding variants. At harvest, 10 individual plants from each progeny were used to determine the best progenies as compared to the control. As a result, 6 elite progenies (5 progenies from 300Gy and one progeny from 350Gy) were selected. Seeds of the six M_3 progenies selectants as well as the best control plant were kept separately for sowing in the next season. Seeds of the selected plants within each M_3 progeny (six progenies) were bulked and grown in M_4generations in November 2018 to evaluate of bread wheat mutations for yield and its components in the M_4 generation.

Statistical analysis

The data obtained were subjected to the proper statistical analysis of variance for RCBD according to Gomez and Gomez (1984). Least significant differences (L.S.D) were computed to compare means (Waller and Duncan 1969). Genetic and phenotypic variance (Burton and Devane 1953), heritability in broad sense (Hanson *et al* 1955) were computed. Phenotypic correlation coefficients were calculated among studied traits by using the formula given by Singh and Chaudhary (1999).

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance of the tested 3 populations of bread wheat (two irradiated and one non-irradiated with gamma rays) in M_2 generation in

2015/2016 season is presented in Table (1). Results indicated that mean squares due to populations (mutagenic treatments) were significant ($p \leq 0.05$ or $P \leq 0.01$) for all studied traits, except spike length and 100-grain weight.

Table 1. Mean squares for the studied traits in M_2 populations of bread wheat resulted via treatment by different doses of gamma rays.

SOV	df	Plant height	Spike length	No. of spikes/plant	No. of grains/spike	100-grain weight	Grain yield/plant
Replication	2	2.12	0.234	1.26	24.59	0.054	5.58
Populations	2	15.45*	1.23	8.79*	15.58*	0.053	264.1**
Error		2.76	0.481	0.71	12.55	0.070	5.57

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

Genetic parameters in M_2 generations

Phenotypic (VP) and genotypic (VG) variance, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2_b) and expected genetic advance (GA) from selection were determined. These estimates are presented in Table 2.

Relatively higher phenotypic than genotypic variance values for number of grains per spike and grain yield per plant were recorded for the mutagenic treatment 300Gy. The genotypic variance for these traits were also high, indicating that the genotype could be reflected by the phenotypic variances. Thus, selection based on the phenotypic performance for these traits is effective. Moreover, phenotypic variance was higher than genotypic variance for all traits studied in the mutagenic treatment 350Gy. The GCV ranged from 6.24% for spike length to 22.52% for number of spikes per plant, whereas PCV ranged from 6.95% for plant height to 25.93% for grain numbers per spike in the mutagenic treatment 300Gy. For the treatment 350Gy, GCV ranged from 4.26% for plant height to 14.60% for 100 grain weight, however, PCV ranged from 4.81% for plant height to 16.50% for 100-grain weight (Table 2).

Table 2. Estimates of phenotypic (PV) and genotypic (GV) variance, phenotypic (GCV) and genotypic (GCV) coefficient of variation, heritability (H) and expected genetic advance (GA) for 6 characters of bread wheat (line 10) in M2 populations.

Mutagenic treatment	Genetic parameters	Plant height	Spike length	No. of spikes/ plant	No. of grains/ spike	100-Grain weight	Grain yield/plant
Control (not irradiated)	PCV%	2.30	3.68	16.95	13.28	7.67	17.86
300Gy	PV	34.20	1.83	9.73	252.25	0.56	133.20
	GV	30.43	1.40	7.34	122.36	0.39	75.67
	PCV%	6.95	7.12	25.93	17.54	13.66	19.27
	GCV%	6.56	6.24	22.52	12.22	11.43	14.52
	H (%)	88.96	76.78	75.39	48.51	70.01	56.81
	GA	10.89	9.62	34.41	14.98	16.83	19.27
350GY	PV	17.75	1.25	3.14	135.91	0.78	67.03
	GV	13.97	0.82	0.74	6.02	0.61	9.50
	PCV%	4.81	6.15	14.66	13.68	16.50	14.20
	GCV%	4.26	4.99	7.13	2.88	14.60	5.35
	H (%)	78.72	65.99	23.64	4.43	78.32	14.18
	GA	6.66	7.14	6.10	1.07	22.75	3.54

Deshmukh *et al* (1986) classified PCV and GCV values as high (>20%), medium (10-20%) and low (<10%). Accordingly, high PCV and GCV were observed in number of spikes/plant, also, medium PCV and GCV were observed in grain yield/plant, No. of grains/spike and 100 grain weight in the mutagenic treatment 300Gy. Medium PCV and GCV were observed in 100 grain weight in the mutagenic treatment 350Gy. The high PCV and GCV indicated that selection may be effective and phenotypic expression would be good indication of the genotypic potential (Singh *et al* 1994) induced genetic variability *via* gamma rays for yield and its attributes in bread wheat as previously reported by Sobieh and Ragab (2000) and El-Degwy and Hathout (2014).

The heritability estimates ranged from 48.51% for number of grains per spike to 88.96% for plant height for the mutagenic treatment 300Gy, and ranged from 4.43% for number of grains/spike to 78.72% for plant height in the mutagenic treatment 350Gy. Pramoda and Gangaprased (2007) suggested that heritability estimates can be low (<40%), medium (40-59%), moderately high (60-79%) and very high (≥ 80%).Accordingly, in the present study, heritability estimate was very high for plant height (88.96%) and spike length (76.78%). Number of spikes/plant (75.36%) and 100-grain weight (70.01%) showed moderately high heritability, indicating that these characters, may respond effectively to selection pressure. These findings agreed with those reported by Abdel-Daym (2017). Medium heritability estimates were recorded for grain yield/plant (56.81%) and number of grains/spikes (48.51%). Results may indicate the influence of the environment on the polygenic nature of these traits, after treating with 300Gy. On the other hand, plant height (78.72%), spike length (65.99%) and 100-grain weight (78.32%) showed a moderately high heritability, after treating with 350Gy.

Expected genetic advance in M_2 populations was high for number of spikes/plant and medium for grain yield/plant, 100-grain weight and No. of grains/spike in the mutagenic treatment with 300Gy. Whereas, it was medium for 100-grain weight after the irradiation treatment 350Gy. Johnson and Hernandez (1980) reported that high genotypic coefficient of variation with high heritability and high expected genetic advance provide better information than each parameter separately. High genotypic coefficient of variation, high heritability and high expected genetic advance were found in number of spikes/plant and medium values for these parameters in 100-grain weight, No. of grains/spike and grain yield/plant, after treatment with 300Gy. Results indicated that these traits could be used useful selection criteria for high grain yield. These findings agreed with those reported by Vidhyapeeth (2013).

Correlation analysis

Correlation analysis (Table 3) revealed that the association between yield and its attributes was positive and significant for only number of spikes/plant. This trait may be considered an effective trait to select for higher yielding genotype.

Table (3). Phenotypic correlation coefficients among yield and its attributes in bread wheat M2 populations.

Traits	Plant height	Spike length	No. of spikes/plant	No. of grains/spike	100-Grain weight
Spike length	**0.159**				
No. of spikes/plant	**0.558**	**0.699**			
No. of grains/spike	**-0.314**	**0.190**	**-0.061**		
100 grain weight	**-0.554**	**-0.239**	**-0.058**	**0.159**	
Grain yield/plant	**0.099**	**0.536**	**0.776***	**0.397**	**0.449**

The traits spike length, number of grains/spike and 100-grain weight also exhibited positive, but not significant association with yield (0.54, 0.40 and 0.45, respectively). Present findings are in agreement with Ahmed *et al* (2010) and Singh *et al* (2012) who found strong associations of yield with its component traits. Among the associations only number of spikes/plant exhibited a negative correlation with number of grains/spike (-0.061) and 100 grain weight (-0.058). Number of grains/spike had a slight association with 100- grain weight (0.16). To achieve quantum jum in wheat productivity, attempts are being made to modify the wheat plant by breaking some of the negative correlations among the yield and its components, namely number of productive tillers/plant, number of grains/spike and 100-grain weight (Singh *et al* 2001).

M_3 progeny test

The mean values of different traits of M_3 progenies as compared to the values of their parent selectants are presented in Table (4). The results of M_3 selected progenies number 4,5,6,10,11 and 12 showed low grain yielding potentially as compared to their M_2 selectants or even to their respective controls. This obviously indicated the high yielding capacity of these M_2 selectants which may be due to environmental conditions and not to genetic effects. This in turn means that the response of these materials to selection would be very weak and consequently they were neglected and did not subjected to further evaluation due to their negative breeding value.

Table 4. Means of yield and its attributes for 12 M_2 selectants plant as well as means of their M3 progenies.

M_2 selectant No.	Gamma-rays treatment (Gy)	Days to maturity		Plant height(cm)		Spike length (cm)		No. of spikes/plant	
		M_2 selectants	M_3 progenies	M_2 selectants	M_3 progenies	M_2 selectants	M_3 progenies	M_2 selectants	M_3 progenies
Control	0	135	136.0	84	83.0	17	17.0	9	9.3
1	300	140	135.7	81	83.7	20	20.3	12	13.0
2	300	137	136.0	89	93.3	20	18.7	13	20.0
3	300	135	136.0	90	88.3	18	18.7	12	11.7
4	300	138	135.7	90	86.0	20	18.7	11	12.3
5	300	137	135.3	82	86.3	18	17.3	17	15.0
6	300	135	137.7	90	87.7	17	18.7	13	11.3
7	300	136	135.7	80	87.0	17	18.7	12	13.7
8	300	135	137.0	89	83.7	18	18.7	13	9.0
9	350	135	137.3	87	96.0	18	19.0	12	16.3
10	350	141	138.7	83	87.0	20	18.3	15	13.3
11	350	135	137.7	89	95.7	19	18.0	13	12.7
12	350	136	138.3	75	91.7	18	18.0	11	16.3
L.S.D 5%			1.13		11.2		2.79		4.40

M_2 selectant No.	Gamma-rays treatment (Gy)	No. of grains/spikes		100 grain weight (g)		Grain yield/plant (g)	
		M_2 selectants	M_3 progenies	M_2 selectants	M_3 progenies	M_2 selectants	M_3 progenies
Control	0	81	84.3	5.4	5.40	51.3	51.5
1	300	103	118.7	5.5	5.43	72.4	68.37
2	300	95	82.7	5.4	5.07	71.3	72.03
3	300	85	87.3	6.9	6.70	60.2	59.57
4	300	85	84.0	7.0	4.67	64.9	51.53
5	300	76	70.0	6.0	4.80	75.3	52.63
6	300	80	69.0	5.6	5.17	60.1	52.27
7	300	106	98.0	7.0	6.07	74.7	77.47
8	300	86	110.0	5.9	6.03	67.1	63.27
9	350	91	75.7	5.8	6.20	63.7	72.93
10	350	75	71.7	5.5	5.07	70.2	53.13
11	350	70	77.0	6.0	5.67	62.9	52.60
12	350	97	72.3	6.2	5.57	66.2	52.47
L.S.D 5%			14.47		0.880		6.46

In contrast, the remainder six M_3 progenies retained the features of their M_2 parents (selectants No. 1, 2,3,7,8 and 9) meaning that they were breed true. These M_3 progenies showed an increase in grain yield ranging from 15.67% to 50.43%, as compared to respective parental value (Table 3). In this respect, Nasarudding *et al* (2018) found that the wheat mutant No. 300 4.3.6 (1.92t per hectare) gave the highest growth and production and was significantly different from all other mutants and check varieties. It is obvious from the above results that selected mutants with high yielding potentiality must be evaluated in the next generation to confirm their superiority and to get rid of the deleterious effect of irradiation.

M_4 generation

In M_4 generation, the analysis of variance exhibited that all the six families varied significantly ($P \leq 0.05$) for days to heading, plant height, number of spikes/plant, 100 grain weight, number of grains/spike and grain yield/plant as shown in Table (5).

Table 5. Mean performance for yield and its attributes of six wheat families and their parent in the (M4) generation.

Genotypes	Days to heading	Plant height (cm)	Spike length (cm)	No. of spikes/plant (cm)	100-Grain weight (g)	No. of grains / spike	Grain yield/ plant (g)
Line 10	81.00	87.00	18.67	7.00	5.00	102.33	35.96
Family 1	81.67	79.33	17.83	9.29	5.47	88.33	38.34
Family 2	82.00	96.67	18.50	9.67	6.00	99.33	56.08
Family 3	81.00	91.00	17.67	11.00	6.23	77.00	53.07
Family 4	91.33	100.00	18.33	10.33	6.03	90.67	60.22
Family 5	80.33	83.00	17.00	7.00	6.27	86.67	37.42
Family 6	81.33	88.00	17.67	7.33	4.83	91.00	32.20
L.S.D.0.05	1.45	1.64	Ns	2.31	0.73	12.00	12.35

Ns = Not significant.

Family 1 is characterized by a reduced plant height (79.3 cm). Family 2 is characterized by high number of spikes/plant, long spike, heavy 100-grain weight (6.0 g), high number of grains/spike and high grain yield/plant. Family 3 is characterized by a high number of spikes/plant, heavy 100-grain weight (6.23 g) and high grain yield/plant. Family 4 is characterized by a high number of spikes/plant, heavy 100-grain weight

(6.03 g), a high number of grains/spike and high grain yield/plant, but date to heading was late. Family 5 is characterized by a heavy 100-grain weight (6.27 g). Family 6 has the lowest 100–grain weight and grain yield/plant. These new families will be tested for further evaluation.

CONCLUSION

Genetic variability is very essential for the success of any breeding program. Cultivars possessing desirable traits are selected from variable populations. Wide variation among tested family lines was observed for different parameters. Family 1 was characterized by a reduced plant height than parent. Family 2 and family 3 were characterized by high number of spikes / plant, heavy 100-grain weight, high number of grains / spike and high grain yield / plant than parent. Family 4 was characterized by a high number of spikes/plant, heavy 100-grain weight, high number of grains/spike and high grain yield/plant, but heading was late than parent. Family 5 was characterized by a heavy 100-grain weight than parent. This study showed positive effects in the use of mutation in inducing improvement for some desirable traits.

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استحداث طفرات للمحصول العالى ومكوناته في قمح الخبز باستخدام أشعة جاما

صبيح السيد سليمان صبيح و خالد فؤاد العزب
قسم البحوث النباتية – مركز البحوث النووية – هيئة الطاقة الذرية – أنشاص – ج.م.ع

الطفرات المستحدثة بالإشعاع تستخدم بتوسع لتطوير أصناف نباتية جديدة. أجري هذا البحث خلال المواسم الشتوية الأربعة ٢٠١٥ / ٢٠١٦ , ٢٠١٦ / ٢٠١٧ , ٢٠١٧/٢٠١٨ و ٢٠١٨/٢٠١٩ بالمزرعة التجريبية لقسم البحوث النباتية – مركز البحوث النووية – أنشاص – مصر بهدف تحديد التباينات الوراثية وتحليل الارتباط للمحصول ومساهماته والانتخاب في العشائر المشععة في الجيل الثاني والثالث في قمح الخبز (سلالة ١٠) بالجرعات ٣٠٠ جراي و ٣٥٠ جراي بأشعة جاما وتقييم طفرات قمح الخبز للمحصول ومكوناته في الجيل الرابع.أظهرت النتائج ان المعاملة الإشعاعية ٣٠٠ جراي كانت أكثر فعالية في استحداث تباينات وراثية في الصفات الكمية في عشائر الجيل الطفري الثاني في قمح الخبز سلالة ١٠ مقارنة بالمعاملة الإشعاعية ٣٥٠ جراي. كانت قيم معامل التباين الوراثي وكفاءة التوريث والتحسين الوراثي المتوقع بالانتخاب مرتفعة لصفة عدد السنابل في النبات وكانت القيم متوسطة لصفات وزن ١٠٠ حبة وعدد الحبوب في السنبلة. كان الارتباط موجب ومعنوي (r=776) بين محصول الحبوب وعدد السنابل بالنبات وموجب وغير معنوي بين محصول الحبوب وعدد الحبوب في السنبلة ووزن ١٠٠ حبة. وتشير النتائج إلي إمكانية استخدام هذه الصفات كمعايير انتخابية لتحسين محصول قمح الخبز. يوضح اختبار النسل في الجيل الإشعاعي الثالث ان بعض النسل (المرتفع في المحصول) استعاد صفات النباتات المنتخبة في الجيل الإشعاعي الثاني وتعتبر هذه النباتات مواد صادقة التربية. في الجيل الرابع ، تميزت العائلة رقم ١ بطولها المنخفض (٧٩,٣سم) وتميزت العائلة رقم ٢ بارتفاع عدد السنابل في النبات وطول السنبلة، ووزن الـ١٠٠ حبة (٦٠ جم) وعدد الحبوب في السنبلة ومحصول النبات. وتميزت العائلة رقم ٣ بارتفاع عدد السنابل في النبات ووزن الـ١٠٠ حبة (٦,٢٣ جم) ومحصول النبات. وتميزت العائلة رقم ٤ بارتفاع عدد السنابل في النبات ووزن الـ ١٠٠ حبة (٦,٠٣ جم) وعدد الحبوب في السنبلة ومحصول النبات الفردي ولكن كانت متأخرة في ميعاد الطرد. وتميزت العائلة ٥ بارتفاع وزن الـ١٠٠ حبة (٦,٢٧جم). وسيتم اختبار هذه العائلات الجديدة مع مزيد من التقييم.*

المجلة المصرية لتربية النبات ٢٤(٤): ٩١٥- ٩٢٦ (٢٠٢٠)