The Comparative Effects Of Chemical Mutagen And Hybridization To Get Genetic Variation In Bread Wheat (*Triticum aestivum* L.).

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ABSTRACT

In an attempt to develop for high yield genotypes of bread wheat, two procedures, *i.e.* mutation breeding and hybridization were used to induce new genetic variations. Three field experiments were conducted during the seasons 2017/2018, 2018/2019 and 2019/2020, at the Experimental Farm, Faculty of Agriculture, Al-Azhar University Assiut Branch. The results showed that, hybridization and treated plants by 2000 ppm of hydrazine hydrate were the more effective than other treatment of hydrazine hydrate, as well as the hybrids were more responsible than the other genotypes for induction of stable promising mutants according to final results at F_2 and F_2M_2 generation especially grain yield /plant. The F_2 and M_2 populations of these genotypes exhibited differences in the magnitude of phenotypic (PCV) and genotypic (GCV) coefficient of variation and heritability for studied traits under this study. The highest expected gain from selection (GA%) for grain yield/plant was obtained from Sids-14, Gemmiza 11 and Sids 14 x Giza 171 when treated by 2000 ppm from Hydrazine hydrate reached to 77.80, 57.70 and 55.71 %, respectively., more than those of the untreated F_2 populations.

KEYWORDS: wheat, mutation breeding, hybridization, phenotypic and genotypic of variability, heritability, genetic advance.

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most widely grown cereal crop in the world and one of the central pillars of global food security. About 651 to 730.3 million tons of wheat was produced from 217 million hectares in 2010 and 2017/2018 with productivity level of 3 t/ha (FAO (2010)). Wheat is an important food crops of the world. It is a dietary mainstay for millions of people as it provides 50% caloric and protein requirements to a major population of the world.

The prime strategy in mutation breeding has been to upgrade the well adapted plant varieties by altering one or two major traits which limit their productivity or enhance their quality. The genetic variability resulted from micro- mutation allows breeding of quantitative characters (Brojevic (1965)). Sarkar (1986) indicated that estimated variation of the quantitative characters were higher for the M_3 generation than those of the M2 generation. Chemical mutagenesis is regarded as in effective and important tool in improving the yield and quality characters of crop plants .In alkylating agents are very effective mutagens in higher plants. Lately, the importance of mutagenesis in increasing the recombinations rate with possibility of adding induced variability to the inheritance in a cross has been realized and heterozygous genotypes of different crop species have been exposed to mutagens. Artificial induction of mutations by using of chemical mutagens such as radiation and chemicals are considered to be one of the useful tools for plant improvement by increasing of genetic variability in many plant species, especially the self-fertilized plants. (Sakin 2002), Srivastava *et al* (2011). Fatima and Al-Shamma (2015), Okaz *et al* (2016) and Al-Shamma and Mohammed (2018).

Hybridization is the principal breeding procedure for inducing genetic variability in wheat. The chief role of hybrid to cross divers genotypes to create hybrid populations with wide genetic variation from which new recombinations of genetic selected (Singh (2000), Khadr and shukry (1972) and Gupta and Virk (1997)) reported that the variations induced by irradiation ,EMS and hybridization were not always cumulative.

The main objective of the present investigation is to comparative effect of (HZ) and hybridization to create genetic variation in bread wheat.

2. MATERIALS AND METHODS

The present study was carried out at the Experimental Farm Faculty of Agriculture, Al-Azhar University Assiut Branch, during the successive growing seasons of 2017/2018, 2018/2019 and 2019/2020. Three bread wheat (*Triticum aestivum* L.)

cultivars were used. The name and pedigree of this parents are showed in Table1. In the 2017/2018 season two crosses were made among the parents to produce F_1 hybrid grains.

Table 1. Pedigree and origin of cultivars and /or lines used in the two bread wheat crosses in this study.

	Parent	Pedigree	Origin
P1	Sids- 14	BOW"S"/Vee"S"//Bow"S"/TSI/3/Beni Sweef 1 SD293-1SD-2SD-4SD- Osd	Egypt
P2	giza-171	Sakha93 / Gemmiza 9	Egypt
P2	Gemmiza 11	BOW"S"/KVZ"S"//7C/SERI-82/3/GIZA 168/SAKHA 61 GM7892-2GM-1GM-2GM-1GM-0GM	Egypt

In the 2018/2019 season some F_1 and parental seeds were planted. Self-pollination was made for F_1 crosses. The seeds of all studied populations (P_1, P_2 and F1) were randomly divided in two equal groups. The first group and F_2 was normally planted without any treatment. The second group of seeds was soaked for 24 hours before planting in 1000 and 2000 ppm solution from (HZ) for two F_1 crosses namely ., Sids 14 x Gemmiza11 and Sids 14 x Giza 171. These treated populations represented the M_1 generations. The genotypes were treated as follows:

Two control F_2 (Sids14 x Gemmiza 11 and Sids14 x Giza 171), four F_2M_2 (Sids14 x Gemmiza 11 (1000ppm HZ), Sids14 x Gemmiza 11(2000ppm HZ), Sids14 x Giza 171(1000ppm HZ) and Sids14 x Giza 171 (2000ppm HZ), six treated parents *i.e.* Sids 14(1000ppm HZ), Sids 14(2000ppm HZ), Gemmiza 11(1000ppm HZ) , Gemmiza 11(2000ppm HZ), Giza

171 (1000ppm HZ) and Giza 171 (2000ppm HZ) which were grown during season 2019/2020. From each population was grown in a plot size of 12.5m x 5m. From each population about 100 plants were randomly selected for recording observations on six quantitative characters viz., days to 50% heading (D.F), plant height (PH) (cm), number of spikes / plant (S/P) , number of kernels / spike (K/S), 100-kernel weight (100-Wg) (g) and grain yield / plant (G.Y/P) (gm) . Plants which have grain yield higher than the control treatments by 20 – 50% considered as mutant (M_1). The data were subjected to statistical analysis and various genetic parameters such as phenotypic (PCV) and genotypic (GCV) coefficient variation, heritability (h_b), genetic advance were calculated According Johnson *et al* (1955) and Allard (1960).

Table 2. The analysis of variance and expected mean squares:-

Source of variance	D.F	M.S	Expected mean square	
			Variance	Covariance
Replications	r–1	M_3	$\sigma^2e + g\sigma^2r$	
Genotypes	g-1	M_2	$\sigma^2e + r\sigma^2g$	Cov.e + r Cov.g
Error	(r-1)(g-1)	M_1	σ^2e	Cov.e

Where: r and g are number of replications and genotypes, respectively.
σ^2e and cov.e are error variance and covariance, respectively and σ^2g and cov.g are genetic variance and covariance, respectively.
*** Heritability in broad sense was calculated as follow:
Heritability in F_2 and M_2 (H) = (σ^2g / σ^2p) x100

2.1. Expected gain from selection (GA%)

The expected genetic advance (GA) expressed as a percentage of the mean value with an assumed 5% intensity of selection pressure was computed by the formula given by Johnson *et al* (1955) and Allard (1960).

as**:** $(GA\%) = k. H \sqrt{\sigma^2 P}$

Where: k = 2.06 constant for 20% selection intensity (*i.e.* the highest-performing 5% are selected), respectively.
H = broad-sense heritability and σ^2P = Phenotypic variance of the population.
The phenotypic and genotypic coefficients of variation are computed as follow Burton (1952).

$$PCV = (\sqrt{VP} / \overline{X})100$$
$$GCV = (\sqrt{VG} / \overline{X})100$$

Where: PCV, GCV are phenotypic and genotypic coefficients of variation, respectively; VP, VG are corresponding variances; and $\overline{X}$ is the population mean the relative values of these two types of coefficients give an idea about the magnitude of

variability presented in a population. Interpretation of variability in terms is given below (Singh and Singh, 1975).

3. RESULTS AND DiISSECTION

The obtained results of the present investigation well be presented in three parts as follows:

1- Means and variances of the different studied characters for the untreated and HZ treated groups. Each group included P_1، P_2، F_1 and F_2 populations of an inetrspecific cross between the three bread wheat varieties (Sids ١٤, Gemmiza ١١ and Giza 171).

2-PCV , GCV and heritability estimates .

3-The response to selection with respect to the studied characters.

3.1. Means and coefficient of variations in first seasons.

It's clear from C.V% values, presence of great variations among obtained data, as indicator to effect treatments on genotypes. Means of the P_1, P_2, F_1 and F_2 populations in the two seasons for the characters studied are presented in Table 3. With respect to HZ treatments, there are clear differences among all population means for all traits except for days to 50 % to heading, all populations means were late or equal with untreated parents means. In connection with remain studied characters, populations means gave significant or noticed differences.

These results are in according with those Ahmad (2011), Khan and verma (2015) and Ahmad (2019).

Table 3. Estimates of genetic parameters for difference quanetitive characters in M_1, F_1 and F_1M_1 populations in bread wheat.

Traits / Genotypes	Days to heading 50% mean	Cv%	Plant height mean	Cv%	Number of spike/ plant Mean	Cv%
Sids 14(1000)	88.2	2.25	128.3	5.45	14.7	12.85
Sids 14(2000)	90.45	2.11	122.85	5.50	11.3	20.39
Giza 171 (1000)	96.50	9.00	114.1	7.07	12.3	15.44
G 171 (2000)	101.40	3.53	104.30	13.66	11.35	34.6
Sids 14 X G 171	89.85	2.06	118.12	5.60	13.55	16.84
Sids 14 X Giza 171(1000)	90.4	1.61	120.60	5.95	13.35	18.58
Sids 14 X G 171(2000)	95.45	3.96	116.95	6.48	12.65	12.59
Gemmiza 11 (1000)	86.15	2.41	107.65	4.23	5.20	19.79
Gemmiza 11 (2000)	88.8	1.15	120.8	4.47	10.05	26.60
Sids 14 X Gemmiza 11	88.5	3.67	109.65	9.81	12.90	19.20
Sids 14 X Gemmiza 11(1000)	95.37	7.48	99.6	5.68	7.45	19.67
Sids 14 X Gemmiza11(2000)	101.72	1.53	101.9	17.54	9.17	43.31
Sids 14	88.15	2.06	110.05	2.49	12.65	10.68
Giza 171	90.10	8.00	114.31	4.53	10.95	10.98
Gemmiza 11	86.35	2.40	108.55	3.98	11.7	9.00

Table 3. Continued.

Traits / Genotypes	Number of kerlines/ spike Mean	Cv%	100-grain wheight mean	Cv%	Grain yield / plant mean	Cv%
Sids 14(1000)	74.10	19.94	5.18	13.25	50.37	28.02
Sids 14(2000)	64.60	16.42	5.05	9.42	49.62	34.18
Giza 171 (1000)	62.20	13.63	5.64	13.09	40.88	18.84
G 171 (2000)	73.30	15.60	6.08	9.66	45.36	28.56
Sids 14 X G 171	60.50	14.45	4.28	9.24	51.00	16.59
Sids 14 X Giza 171(1000)	70.95	13.36	5.50	8.31	43.70	29.15
Sids 14 X G 171(2000)	74.47	20.76	5.31	9.31	51.13	13.35
Gemmiza 11 (1000)	68.65	15.17	5.55	12.47	40.12	26.63
Gemmiza 11 (2000)	70.10	10.46	6.05	8.78	54.37	23.25
Sids 14 X Gemmiza 11	57.40	13.57	5.13	10.40	36.65	22.97
Sids 14 X Gemmiza 11(1000)	83.10	16.00	5.22	8.39	50.85	33.63
Sids 14 X Gemmiza11(2000)	79.10	10.27	5.04	11.17	49.97	33.38
Sids 14	64.40	8.04	4.93	4.06	38.59	2.79
Giza 171	56.75	8.41	4.39	8.80	30.90	7.82
Gemmiza 11	57.05	8.75	3.96	4.54	36.78	9.08

3.2. M₂ generation

Analysis of variance and means in second seasons.

The significant of variance components obtained from the analysis of variance for all the studied characters in the bread wheat mutated populations of the M₂ generation is presented in Table 4.

With respect to days to 50% heading, the genotype Giza171 (1000and 2000 ppm) was the earliest populations.

Also, HZ treatments increased clearly the amount of variation (as a percentage) of plant height of all the studied genotypes, but number of spikes per plant had changed significantly of Sids 14(1000), Gemmiza 11 (2000) and Sids 14 X Gemmiza .

Concerning number of kernels per spike, appearance and genetic changes were clear and noticed on all genotypes except cross Sids 14 X Gemmiza 11.

In connection with 100 - grain weigh, all genotypes were high except Sids 14(2000), G 171 (1000), Sids 14 X G 171and Sids 14 X Gem 11(1000).

With respect to grain yield per plant, all genotypes gave noticed high means except Sids 14(1000) and Sids 14(2000). These results are in according with those Sakin (2002), Ahmad (2011), Khan and verma(2015), Balkan (2018) and Ahmed (2019).

The phenotypic coefficient (PCV) of variability values were higher than (GCV) for all studied traits in the two crosses (Table 4). The phenotypic and genotypic coefficient variabilities were low for days to 50% heading in all derived populations.

For plant height, it is clear in Table 4, there are many variations in plant height of genotypes .The effect of 1000ppm and 2000 PPM from HZ was highly as compared with control. All genotypes gave average values except G 171 (2000) and Sids 14 X Giza 171(1000) were short. This results coincides with Hanafy *et al* (2006), Ahmad (2011), Hawash and Al-Shamma (2016), and Al-Shamma and Mohammed (2018) found that the lowest plant height was obtained when exposed the seedlings to external electric field , sodium azide and heat shock.

The PCV and GCV were low for plant height in all derived populations except Giza 171(2000ppm) had highest values. The obtained results are in accordance with those obtained by Sakin (2002), Zaazaa *et al* (2012) and Balkan (2018).

With respect to number of spikes /plant, The highest number of spikes /plant (13.26 and 12.87) were obtained from Sids 14 (HZ), (1000ppm) and x Gemmiza 11 (HZ), (2000 ppm) . This results

coincides with Ahmad (2011) and Hawash and Al-Shamma (2016) when used electric shock on wheat.

There were high to moderate phenotypic and genotypic coefficient variabilities for number of spike /plant in all derived populations. Mutant Sids 14 hydrazine hydrate (1000 ppm) surpassed original plants in number of spike per plant with 21.5%. This considered genetic variability accompanied with high heritability estimates, this occurred in the 1000ppm concentrate M2 populations of Sids 14 The obtained results are in accordance with those obtained by Sobieh (1999) and Khan and Verma (2015) when used gamma rays on wheat.

Concerning number of kernels per spike, the differences in the mean values due to genotypes effect were high in F2M₂ and M₂ generation. The treatments of HZ were effective either from 1000 ppm or 2000pp except untreated cross Sids 14 X Gemmiza 11.

There were moderate phenotypic and genotypic coefficient variabilities for number of kernels per spike in all derived populations (Table 4). The obtained results are in accordance with those obtained by Khan and Verma (2015) and Balkan (2018) when used gamma rays on wheat.

All plants which maintain the mutations until M2 were surpassed untreated plants in 100-grain weight. The highest 100-grain weight (5.82, 5.63 and 5.47g) was obtained from Gemmiza 11 (HZ 2000ppm), Sids14 x Gemmiza 11 (HZ 2000ppm) and Sids 14 x Giza 171 (HZ 2000ppm) but untreated plant Sids 14 x Giza 171 gave 4.43g Sids14 x Gemmiza 11 gave 4,91g. So, the increasing percentage from untreated plants was 18.53, 14.66 and 13.25%, respectively. The phenotypic and genotypic coefficient variabilities were moderate for 100-grain weight in all derived populations except Giza 171 (2000ppm) was low. The obtained results are in accordance with those obtained by Balkan (2018).

Regarding grain yield / plant, all plants which maintain the mutations until M₂ were surpassed untreated plants. The highest value of means was (41.91g)) obtained from Sids14 x Gemmiza 11 (HZ 2000ppm) So, the increasing percentage from untreated plants was 22.18%, but the F₂ (Sids14 x Giza 171) population was higher than the all treatments of F₂M₂ and M₂ populations. This result coincides with Dhole *et al.* (2003), Ahmad (2011), Al-Shammaa (2014), Okaz *et al.* (2016) and Ahmed (2019). On the other hand, Sobieh (1999) found that no significant effect on mean values of yield and most of its components in M₂ generation when used gamma rays in wheat.

The PCV was generally higher than the GCV for all genotypes. High PCV and GCV values were observed for grain yield/plant and yield components

in F_2, M_2, and F_2M_2 population .These results indicate that both hybridization among parents and HZ treatments are capable of creating genetic variability in grin yield per plant , 100- grain weight, number of spike /plant and number of kernels/ spike which could be used to improve this important characters. Therefore, these traits were highly affected by environmental factors. The obtained results are in accordance with those obtained by Khan and Verma (2015) and Zaazaa *et al* (2012). It can say the effectiveness of selection based on the phenotype performance for the characters in the early mutant generations. Zaazaa *et al* (2012) obtained the lowest number of grains /spike in value PCV and GCV coefficient variabilities. Mahantashivayogayya *et al.* (2003) found that the highest genetic advance from selection was observed in EMS treated populations for grains per spike and 1000-grain weight.

Khadr and Shukry (1972) reported that the relative magnitude of induced variation compared with that from hybridization depended on the particular mutagen and characters, and averaged less than 50 % percent of that from hybridization. . Heritabilities and expected genetic gains were not much lower in mutagenic populations than in hybrid populations. The induced variation was not accompanied by any shift in the population mean in most cases, variation was equally distributed around the population mean. Reddy and Revathi (1992) found that the mutation frequency increased with duration, concentration of the mutagen treatment, and it was higher when treating seeds of barley and wheat individually and in combination with gamma ray, 0.5 ethyl methane sulphonate (EMS) and sodium azide.

Heritability values are categorized as low (0-30%), moderate (30-60%) and high (60% and above) as stated by Robinson *et al*. (1949). Heritability estimates indicate that the progress from selection for plant characters is relatively easy or difficult to make in breeding program. Heritability estimates in broad sense and genetic advance are presented in Table 4. The heritability values in broad sense was high for all studied traits in all populations.

The heritability values in broad sense was moderate for number of kernels /spike in F_2 untreated cross1 (Sids 14 x Giza 171).

These results are in accordance with the findings of El- Aref *et al*. (2011), Amin (2013), Abd El- Rady (2018) , Balkan (2018), El-Gammaal and Yahya (2018) and El Massry and El-Nahas (2018). On the other hand, Sakin (2002). Sakin and Yildrim (2004) estimated that the high heritability for mutant

populations demonstrated that induced variation was maintained in the M_2 and M_3 generations. Johnson *et al.* (1955) advocated that heritability estimates along with genetic advance are usually more helpful than the heritability value alone in predicting the resultant effects of selection. Sobieh and Ragab (2000) reported that high magnitudes of GCV, h_b^2. and GA for number of spikes/plant and number of grains/spike were obtained, but moderate magnitude for the weight of grains /spike was found. The high h_b^2 and GA indicated the effectiveness of selection for these traits.

According to Johnson *et al*. (1955) genetic advance as percent of mean classified as low (<10%) moderate (10-20%) and high (>20%). Expected genetic advance calculated from the M_2 generation were moderate to high compared to the controls of both treatments (Table 4). The expected genetic advance values was low in F_2M_2, M_2 and F_2 untreated population for days to 50% heading. The expected genetic advance value was moderate to high in all populations for plant height, but highest values were Giza 171 (2000), Sids 14 X Giza 171(2000) and Sids 14 X Gemmiza11(2000) .

The expected genetic advance was moderate to higher in hybrid material after mutagen treatments in all derived populations for traits number of spike / plant, number of kernels / spike, 100-kernel weight (gm) and grain yield / plant (gm). These results are in accordance with the findings of Kattab *et al* (2010), El- Aref *et al*. (2011), Amin (2013), Abd El- Rady (2018) and El Massry and El-Nahas (2018).Hassan (1993) and Shafey *et al* (1993) found that the highest genetic advance was obtained for plant height, weight of 1000 grains and grain yield /plant. On the other hand, Balkan (2018) found that the high heritability and genetic advance for plant height , number of grains per spike and grain yield /plant in three mutant generations. Grain yield /plant had the lowest heritability estimate with a relatively low value for genetic advance. Kashif and Khaliq (2004) and Al-Azab (2013) found that the highest genetic advance was obtained for grain yield / plant (gm) in M_2 generation when used gamma rays and hybridization.

In conclusion, HZ and hybridization were equally effective for inducing genetic variation in the quantitative traits of wheat. Both agents produced approximately the same amount of heritable variability and were similar for predicted

Table 4. Estimates of genetic parameters for difference quanetitive characters in M_2, F_2 and F_2M_2 populations in bread wheat.

Genotypes	D.F						
	Mean	VP	VG	PCV	GCV	h_b	GA%
Sids 14(1000)	98.16	3.45	3.27	1.89	1.84	94.62	3.69

Genotypes	Mean	VP	VG	PCV	GCV	Hb	GA%
Sids 14(2000)	93.95	21.61	21.15	4.94	4.89	97.84	9.97
Giza 171 (1000)	88.45	5.32	5.09	2.60	2.55	95.66	5.14
Giza 171 (2000)	89.80	14.126	13.75	4.18	4.12	97.33	8.39
Sids 14 X Giza 171	91.85	9.45	9.15	3.34	3.29	96.74	6.67
Sids 14 X Giza 171(1000)	100.25	19.97	19.52	4.45	4.40	97.62	8.97
Sids 14 X Giza 171(2000)	97.92	22.35	21.88	4.82	4.77	97.88	9.73
Gemmiza 11 (1000)	107.91	5.016	4.79	2.07	2.02	95.53	4.08
Gemmiza 11 (2000)	108.16	9.44	9.14	2.84	2.79	96.74	5.66
Sids 14 X Gemmiza 11	95.82	1.037	0.935	1.06	1.00	90.18	1.97
Sids 14 X Gemmiza11(1000)	106.17	23.68	23.19	4.58	4.53	97.94	9.34
Sids 14 X Gemmiza11(2000)	99.49	2.69	2.11	1.51	1.46	93.36	2.91

				PH			
Genotypes	Mean	VP	VG	PCV	GCV	Hb	GA%
Sids 14(1000)	113.91	14.80	14.18	3.37	3.30	95.80	6.66
Sids 14(2000)	119.35	62.94	62.05	6.64	6.60	98.58	13.49
Giza 171 (1000)	113.26	57.15	56.28	6.67	6.62	98.47	13.53
Giza 171 (2000)	103.98	167.65	166.52	12.45	12.41	99.32	25.47
Sids 14 X Giza 171	108.35	110.10	109.08	9.68	9.64	99.06	19.76
Sids 14 X Giza 171(1000)	101.15	56.05	55.18	7.80	7.33	98.45	15.01
Sids 14 X Giza 171(2000)	107.39	129.10	128.04	10.58	10.53	99.17	21.61
Gemmiza 11 (1000)	108.05	21.46	20.78	4.28	4.21	96.82	8.55
Gemmiza 11 (2000)	120.52	41.36	30.62	4.64	4.59	97.61	9.34
Sids 14 X Gemmiza 11	114.38	86.03	85.05	6.10	8.06	98.88	16.51
Sids 14 X Gemmiza11(1000)	118.51	67.44	66.54	6.93	6.88	98.65	14.08
Sids 14 X Gemmiza11(2000)	112.65	137.02	135.94	10.39	10.34	99.21	21.23

Table 4. Continued.

				S/P			
Genotypes	mean	VP	VG	PCV	GCV	h_b	GA%
Sids 14(1000)	13.26	7.49	6.96	20.64	19.90	93.01	39.55
Sids 14(2000)	10.08	5.69	5.20	23.67	22.63	91.42	44.58
Giza 171 (1000)	10.48	6.18	5.69	23.73	22.76	94.94	44.96
Giza 171 (2000)	9.35	13.96	13.35	39.97	39.08	95.62	78.73
Sids 14 X Giza 171	10.91	11.94	11.35	31.67	30.88	95.07	62.03
Sids 14 X Giza 171(1000)	9.16	13.17	12.57	39.62	38.70	95.42	77.89
Sids 14 X Giza 171(2000)	7.44	2.62	2.22	21.78	20.04	84.67	37.99
Gemmiza 11 (1000)	10.00	10.00	9.43	31.62	30.72	94.37	61.47
Gemmiza 11 (2000)	12.87	5.31	5.83	17.90	17.08	90.96	33.56
Sids 14 X Gemmiza 11	12.16	12.59	11.99	29.18	28.48	95.26	57.27
Sids 14 X Gemmiza11(1000)	10.74	6.63	6.12	23.97	23.04	92.34	45.61
Sids 14 X Gemmiza11(2000)	11.35	8.18	7.65	25.21	24.32	96.82	57.27

				K/S			
Genotypes	mean	VP	VG	PCV	GCV	h_b	GA%
Sids 14(1000)	75.44	164.64	163.51	17.00	16.95	99.31	34.79
Sids 14(2000)	76.43	172.66	171.51	17.19	17.13	99.33	35.18
Giza 171 (1000)	75.99	65.98	65.08	10.69	10.61	98.63	21.72
Giza 171 (2000)	66.79	97.76	96.77	14.80	14.72	98.98	30.18
Sids 14 X Giza 171	63.93	56.32	27.97	11.73	8.27	48.66	12.01
Sids 14 X Giza 171(1000)	73.14	90.00	61.65	12.97	10.73	68.51	18.30
Sids 14 X Giza 171(2000)	74.26	154.65	153.53	16.74	15.13	81.66	28.17
Gemmiza 11 (1000)	72.79	109.96	108.94	14.40	14.33	99.06	29.40
Gemmiza 11 (2000)	71.01	67.02	66.12	11.52	11.54	98.65	29.44
Sids 14 X Gemmiza 11	58.12	48.62	35.08	11.99	10.19	72.15	17.86
Sids 14 X Gemmiza11(1000)	77.26	233.49	220.01	19.77	19.19	94.22	38.39
Sids 14 X Gemmiza11(2000)	77.99	7.14	57.66	10.81	9.73	81.05	18.05

Table 4. Continued.

Genotypes	100-Wg						
	mean	VP	VG	PCV	GCV	h_b	GA%
Sids 14(1000)	5.46	0.308	0.253	10.17	9.20	82.00	17.17
Sids 14(2000)	4.86	0.190	0.146	8.96	7.86	77.07	14.23
G 171 (1000)	4.83	0.450	0.383	13.88	12.81	85.09	24.34
G 171 (2000)	5.44	0.283	0.230	9.78	8.82	81.22	16.73
Sids 14 X G 171	4.43	0.316	0.259	12.68	11.50	82.21	21.48
Sids 14 X G 171(1000)	5.02	0.517	0.445	14.31	13.28	86.10	25.39
Sids 14 X G 171(2000)	5.47	0.402	0.339	11.59	10.64	84.23	20.11
Gem 11 (1000)	5.07	0.302	0.247	10.82	9.78	81.80	18.23
Gem 11 (2000)	5.82	0.582	0.506	13.11	12.22	86.89	23.47
Sids 14 X Gem 11	5.35	0.363	0.303	11.25	10.27	84.41	19.33
Sids 14 X Gem 11(1000)	4.91	0.388	0.326	12.68	11.62	83.95	21.93
Sids 14 X Gem 11(2000)	5.63	0.540	0.467	13.05	12.13	86.40	23.22
Genotypes	S.Y/P						
	mean	VP	VG	PCV	GCV	h_b	GA%
Sids 14(1000)	28.41	44.59	36.36	23.50	21.22	81.54	39.48
Sids 14(2000)	29.25	138.05	125.82	40.16	38.94	94.03	77.80
G 171 (1000)	37.32	70.31	61.03	22.46	20.93	86.80	40.17
G 171 (2000)	34.16	94.91	86.68	28.51	27.25	91.32	53.64
Sids 14 X G 171	47.96	143.45	135.22	24.97	24.24	94.26	48.49
Sids 14 X G 171(1000)	31.66	80.03	70.74	28.25	26.56	88.39	51.44
Sids 14 X G 171(2000)	41.30	91.94	82.65	23.21	22.01	89.89	42.98
Gem 11 (1000)	32.99	62.44	57.87	23.34	23.04	92.25	45.66
Gem 11 (2000)	36.93	122.96	114.73	30.02	29.00	93.30	57.70
Sids 14 X Gem 11	36.13	64.61	59.98	22.24	21.43	92.83	42.53
Sids 14 X Gem 11(1000)	34.30	94.78	90.15	28.38	27.68	95.11	55.61
Sids 14 X Gem 11(2000)	41.91	143.14	138.51	28.54	28.08	96.76	55.71

genetic gain from selection. In recent years the techniques of seed treatment with HZ have been greatly refined to give positive results for mutation programs. Besides, this chemical is easier to handle in the lab than irradiation. For these reasons ،HZ seed treatment should be recommended as an alternative to irradiation in inducing genetic variability for wheat breeding purposes.

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مقارنة تأثير المطفر الكيميائى (هيدرازين هيدريت) والتهجين فى قمح الخبز

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فى محاولة لإستنباط تراكيب وراثية من قمح الخبز عالية المحصول استخدم طريقتان هما التربية بالطفرات والتربية بالتهجين لإستحداث تباينات وراثية . تم إجراء ثلاث تجارب حقلية بكلية الزراعة جامعة الأزهر فرع أسيوط خلال المواسم من ٢٠١٧/ ٢٠١٨ إلى ٢٠١٩/٢٠٢٠. أكدت النتائج أن التهجين والمعاملة بالهيدرازين هيدرات بتركيز ٢٠٠٠ جزء في المليون أفضل من استخدام المعاملة بالهيدرازين هيدرات بتركيز ١٠٠٠ جزء في المليون . أكدت النتائج أن الهجينين سدس ١٤ × جيزن ١٧١ وسدس ١٤ × جميزة ١١ جميزة ١١ كانوا أكثر إستجابة لإستحداث تراكيب وراثية جديدة عن التراكيب الأخري فيما يتعلق بمحصول الحبوب على النبات .عشائر الجيل الثانى وعشائر الجيل الطفرى الثانى لهذه التراكيب أظهرت فروقا معنوية من حيث معاملات التباين المظهرى والوراثى ودرجة التوريث للصفات تحت الدراسة.

تراوحت قيم التقدم الوراثى (٧٧,٨٠ و ٥٧,٧٠ و ٥٥,٧١%) فى كلا من الصنفين سدس ١٤ وجميزة ١١ والهجين سدس ١٤ × جميزة ١١ المطفرين بالهيدرازين هيدريت بتركيز ٢٠٠٠ جزء في المليون فيما يتعلق بصفة المحصول . تشير النتائج بإمكانية إجراء الإنتخاب فى الأجيال المبكرة وتحسين هذه الصفات .