Evaluation of genotype performance of yield traits under the influence of the chemical mutagen EMS for first mutational generation of bread wheat cultivars (*Triticum aestivum* L).

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Abstract.

This study was conducted at AL- Baiji Research Station, affiliated with the College of Agriculture, Tikrit University, located 40 km from the city center of Tikrit, during the 2023-2024 growing season. Fifteen bread wheat genotypes were used: Mawada, Ozkan, Tammuz 2, Buhouth 22, Sulaimani 2, Sham 6, Jihan, Al-Rashid, Al-Wafiya, Alaa, Babylon, Baghdad, Al-Fayyad, IPA 99, and Adna 99. One hundred seeds from each genotype were treated with the chemical mutagen (Ethyl Methane Sulfonate) EMS at a concentration of 0.5 mmol/100 mol of distilled water. An additional 100 seeds from the same genotype were used for comparison with the mutagenic seeds. The fifteen genotypes were grown in a randomized complete block design (RCBD) with three replicates. The genetic parameters for six traits were estimated: number of spikes per plant (spikes plant^{-1}), number of grains per spike (Grain. spike $^{-1}$), 1000 grain weight (g), biological yield (g), grain yield (g), harvest index. The results were as follows: There were highly significant differences at the 1% probability level between the genotype for all studied traits and the mutation treatments. These differences were significant for the number of spikes per plant and the 1000 grain weight. The interaction between the genotype and the mutation treatments was significant only for the 1000 grain weight. In the first environment (0 mmol), the Buhouth22 genotype was excelled in the number of spikes per plant, number of grains per spike, and biological yield. The Sham6 genotype was superior in the 1000 grain weight and grain yield. In the second environment (0.5 mmol), which is the effect of the EMS chemical mutagen, the results show that the Buhouth22 × 0.5 mmol mutation treatment was superior in the number of grains per spike and biological yield, as was the Sham6 × 0.5 mmol mutation treatment. 0.5/mmol in the weight of 1000 grains. The values of heritability in the broad sense were high for the number of grains per spike and the biological yield and moderate for the rest of the traits in the first environment 0/mmol. The values of heritability in the broad sense were moderate for the number of grains per spike only and high for the rest of the traits in the second environment 0.5/mmol., the values of expected genetic improvement from selection and as a percentage ranged from low to moderate to high in the two environments.

Keywords: Bread wheat, chemical mutagens, cereal yield, genetic markers.

1- Introduction.

Wheat (*Triticum aestivum* L.) is one of the most important grain crops, providing a staple food source for about one-third of the world's population. Iraq ranks first globally in terms of cultivated area, with wheat occupying approximately 32% of the total area cultivated with grains worldwide. In 2023, the area cultivated with wheat in Iraq reached approximately 1.668.077 hectares, with an average production of approximately 4.247.726 tons/hectare, compared to a global production of 807.400.000 tons/ hectare[1].

Despite Iraq being the original home of wheat, it still suffers from low bread wheat productivity due to the genetic deterioration of

ISSN 2072-3857

local cultivars and poor crop management practices. To overcome these factors, it was necessary to work on increasing vertical expansion in wheat cultivation by evaluating new genetic combinations. This aims to expand genetic variation and utilize these combinations in breeding and improvement programs, comparing them with local genotypes and selecting the superior ones to obtain a new variety characterized by high productivity and quality[2] The use of chemical mutagens is considered one of the modern methods for inducing Genetic variation in the quantitative and qualitative traits of wheat is a key factor. Scientific data indicates that using this method is an effective way to achieve the highest percentage of genetic variation and is considered one of the methods of plant breeding. The term "plant mutation breeding" was first used by [3]. There are two types of mutagens: chemical and physical. Research on chemical and physical mutagens in plant breeding continued until the period between 2000 and 2009, during which a significant leap forward occurred in breeding using mutations. This was achieved through the introduction of robots and computers in modeling the phenotype and genetic makeup of numerous genotypes and mutant isolates[4]. Random point mutations arise primarily through the effect of the chemical mutagensis (EMS) by replacing one nitrogenous base with another. Both coding and non-coding regions are subject to the effect of mutations through modifications to amino acids, stop codons, or displacement mutations. In rare cases, mutations can modify protein structure or increase or decrease gene expression regulation. Oats, barley, corn, and wheat are just a few examples. On crops where EMS mutations were successfully applied[5].

This study aims to:

1- Determine the IPA response to the chemical mutagenant (EMS) in the first mutational generation (1M) of the studied traits.

2- Estimate the variation in yield traits and components in the first mutational generation (1M).

3- Estimate the genetic parameters.

2- Materials and Methods:

This study was conducted at Al-Baiji Research Station, affiliated with the College of Agriculture, Tikrit University, located 40 km from the center of Tikrit city, during the 2023-2024 growing season. Fifteen bread wheat genotypes were obtained from various sources, as shown in Table (1). The experiment involved cultivating seeds of these fifteen genotypes after treatment with the mutagenic agent EMS during the 2023-2024 growing season. One hundred seeds were taken for each genotype, and a concentration of (0.5) mmol 100 mol of the mutagenic agent EMS was used, as per the study conducted by [6]. The seeds were soaked in distilled water for (12-20) hours, then placed in a strainer to drain. They were then soaked in distilled water with the required concentration of EMS added for approximately 8 hours. Afterward, the seeds were washed with distilled water for direct sowing in the field. Additionally, one hundred seeds were taken from each genotype without exposure to the agent. To use the mutant as a control for comparison with the mutant genotype, the experimental land was prepared by perpendicular plowing, smoothing, leveling, and dividing according to the recommended scientific guidelines. NPK fertilizer (15-15-15) was added at a rate of 300 kg ha^{-1}, and urea fertilizer was added at a rate of 200 kg ha^{-1} in three applications during the crop growth stages[7]. The experiment was implemented with a randomized complete block design (RCBD) and three replicates, where each replicate contained 30 experimental units, 15 of which were treated with the chemical mutant EMS and 15 were not treated with the chemical mutant and were considered as a control. The seeds were planted in rows 2 m long, with 20 cm between rows and 10 cm between plants.

ISSN 2072-3857

2-1- EMS (Ethyl Methane Sulfonate)

Name: Ethylmethane Sulfonate

Chemical Formula: CH3SO3C2H5

Molecular Formula: C3H8O3S

Molecular Weight: 124.16 g/mol

Density: 1.1452 g/cm³ at 22°C

Boiling Point: 85-86°C

A colorless, transparent to oily liquid, soluble in water. It is widely used in genetic research to induce point mutations by substituting the thymine (T) base for the cytosine (C) base in DNA, resulting in a G:C transition mutation that transforms into A:T. It is an important organic compound with a wide range of applications in various fields, including genetic and biological research. In genetic research: As efficient mutants, they are widely used in genetic research by manipulating experimental materials such as plant seeds and microbial cells. A large number of random mutations can be generated to study the relationship between gene function, genetic variation, and phenotype. This method provides a powerful tool for uncovering the genetic laws of organisms and analyzing complex genetic traits.

In molecular biology research: They can be used to prepare cell lines or strains with specific gene mutations. These mutants can be used to study biological processes such as the regulation of gene expression, protein functions, and signaling pathways. By comparing differences between wild-type and mutated species, we can gain a deeper understanding of the interactions and regulatory mechanisms between biomolecules[8].

Table (1) lists the names and sources of the genotypes used in the study.

Symbol	genotypes	Source
1	Mawada	Accredited/General Authority for Agricultural Research
2	Ozkan	Accredited/Private Sector Companies
3	Tammuz 2	Accredited/General Authority for Agricultural Research
4	Buhuth 22	Accredited/General Authority for Agricultural Research
5	Sulaimani 2	Accredited/Seed Testing and Certification Department/Sulaimaniyah
6	Sham 6	Accredited/General Authority for Agricultural Research
7	Jihan	Accredited/Private Sector Companies
8	Al-Rashid	Accredited/General Authority for Agricultural Research
9	Al-Wafiya	Accredited/Private Sector Companies
10	Alaa	Accredited/General Authority for Agricultural Research
11	Babel	Accredited/General Authority for Agricultural Research

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12	Baghdad	Accredited/General Authority for Agricultural Research
13	Al-Fayyad	Accredited/Tikrit University - College of Agriculture
14	IPA 99	Accredited/General Authority for Agricultural Research
15	Adna 99	Accredited/Private Sector Companies

Table (2) Some chemical and physical properties of the experimental soil before cultivtion.

1	**Traits**	**values**	**units**
2	**PH**	**6.9**	**———————**
3	**EC electrical conductivity**	**2.1**	**DS.m^{-1}**
4	**dissolved ions**		
5	**N Available Nitrogen**	**39.4**	**mg.kg^{-1} soil**
6	**P Available Phosphorus**	**12.2**	**mg.kg^{-1} soil**
7	**K Available Potassium**	**85.3**	**mg.kg^{-1} soil**
8	**Organic Matter**	**1.8**	
9	**Soil separators**		
10	**Sand**	**492**	**g.kg^{-1} soil**
11	**Silt**	**254**	
12	**Clay**	**109**	
13	**Soil texture**	**silty sandy**	

ISSN 2072-3857

2.2 Study Factors:

The experiment included studying the effect of two factors:

2.2.1. First Factor: Using fifteen bread wheat genotypes as shown in Table (1).

2.2.2. Second Factor: Using a concentration of the chemical mutagen EMS, which included two treatments:

Treatment 1: Using 0 mmol of EMS (no treatment)

Treatment 2: Using 0.5 mmol per 100 ml of distilled water of EMS

2.3. Studied Traits:

1. Number of spikes per plant (spikes.plant^{-1}): The average number of viable spikes was calculated for ten fully mature plants from each experimental unit.

2. Number of grains per spike (grains.spikes^{-1}): The average number of grains was manually calculated for viable spikes randomly selected from ten plants from each experimental unit.

3- Weight of 1000 grains (g): A random sample of harvested ears of grain was taken and counted using a grain counter calibrated to count 1000 grains. The weight was then calculated using a sensitive balance[9].

4- Biological yield (g. plant^{-1}): Ten plants of each genotype were harvested at full maturity and weighed (straw + spike). The average yield was calculated.

5- Yield per plant (g. plant^{-1}): The average yield of ten plants of each genotype was calculated at full maturity after cleaning the grains of impurities. The grains were then weighed using a sensitive electronic balance.

6- Harvest Index %: Calculated using the following equation mentioned previously[10].

Harvest Index = (Individual Plant Yield / Biological Yield) × 100

2-3- Statistical Analysis:

The experimental data for all studied traits were analyzed according to a two-factor using a Randomized Complete Block Design (RCBD) with three replicates, according to the following mathematical model equation:

$yijk = \mu + Rk + Ai + Bj + ABij + eijk$ {i=1,..a ; j=1,..b ; k=1,..r}

Where:

Yijk is the observation value

u is the overall mean for the trait

Rk is the replicate effect

Ai is the treatment effect

Bj is the genotype effect

ABij is the interaction effect between treatments and genotype

eijk is the experimental error effect

ISSN 2072-3857

Table (3) shows the analysis of variance for the experimental design.

S.O.V	d.f	SS	MS	Cal.F
Reps	**r-1=2**	**SSr=R-CF**	**MS_r**	**F_r**
A	**a-1=14**	**SS_A=A-CF**	**MS_A**	**F_A**
B	**b-1=1**	**SS_B=B-CF**	**MS_B**	**F_B**
AB	**(a-1) (b-1)=28**	**SS_{AB}=AB-A-B+CF**	**MS_{AB}**	**F_{AB}**
Error	**(ab-1) (r-1)=58**	**SS_e=ABR-AB-R+CF**	**MS_e**	
Total	**Abr-1=90**	**SST=ABR-CF**		

Where:

R = replicates

A = Genotype

B = Mutation Coefficients

AB = Interference between Mutation Coefficients and Genotype

2-4-Genetic Analysis:

2-4-1-Estimation of Variance Components:

The phenotypic (σ^2P), genetic (σ^2G), and environmental (σ^2E) variance components were estimated from the Analysis of Variance Table (Table 3). The significance of the variances was tested against zero using Method 8 by calculating the variance of each of these variances and then extracting the square root of each to obtain the standard errors, as follows:

$$\sigma^2_P = \sigma^2_G + \sigma^2_E$$

$$(MS_b - MS_e)/ R = \sigma^2_G$$

$$MSe = \sigma^2_E$$

σ^2_P = Phenotypic variance
σ^2_G = genotypic variance
σ^2_E = environmental variance
MS_b = Average of genotype squares
MS_e = Mean squared experimental error
R = replicates

To test the significance of phenotypic, genetic, and environmental variations, the following equations were used:

$$S.E(\sigma^2 P) = \sqrt{\frac{2msp^2}{N}}$$

ISSN 2072-3857

$$S.E(\sigma^2 \text{G}) = \sqrt{\frac{1}{r^2}[\frac{2msg^2}{k+2} + \frac{2mse^2}{k+2}]}$$

$$S.E(\sigma^2 \text{E}) = \sqrt{\frac{2mse^2}{k+2}}$$

Where k represents the degrees of freedom for each source of variation.

N represents the sum of the degrees of freedom for error and the degrees of freedom for genotype.

-2-4-2Estimation of Phenotypic Variance coefficients **%, Genotypic Variance** coefficients **%, and Environmental Variance** coefficients**%**

The phenotypic, Genotypic and environmental variation coefficients and their ranges were calculated to the method mentioned by [11] as follows: less than (10)% is low, between (10-30)% is medium, and more than (30)% is high. according to the following equations:

$$P.C.V\% = \frac{\sqrt{\sigma^2 P}}{\overline{X}} \times 100$$

$$G.C.V\% = \frac{\sqrt{\sigma^2 G}}{\overline{X}} \times 100$$

$$E.C.V\% = \frac{\sqrt{\sigma^2 E}}{\overline{X}} \times 100$$

Where x represents the overall mean for the trait

2-4-3- Broad-sense heritability:

Broad-sense heritability was estimated along with the categories into which it was divided, according to the method outlined by (12) and as expressed in the following equation:
and was classified into the following categories: low (< 20%), moderate (20–50%), and high (> 50%).

$$\mathbf{h^2_{b.S}} = \frac{\sigma^2 \text{G}}{\sigma^2 \text{p}}$$

$h^2_{b.s}$ = Degree of inheritance in the broad sense.

2-4-4- Expected Genetic Improvement:

The expected genetic improvement under the selection intensity mentioned in [13] was estimated according to the following equation:

$G.A = h^2_{b.S} .K. \sigma p$
Where:
G.A = Expected genetic improvement.
$h^2_{b.S}$ = heritability in the broad sense.
σ_P =phenotypic standard deviation.
K = The intensity of selection factor equals 1.40 when the intensity of selection (20)%
Estimate the expected genetic improvement as a percentage of the overall average for the trait using the following equation:

$$G.A(\%) = \frac{G.A}{\overline{X}} \times 100$$

G.A(%) = Expected genetic improvement as a percentage of the overall average for the trait
$\bar{x}$ =The overall average of the trait.

3- Results:

1- Analysis of Variance:

The data in Table (4), "Analysis of Variance for Yield Traits and Components," indicate highly significant differences at the 1% probability level between genotypes for the traits of number of spikes per plant, number of grains per spike, 1000-grain weight, biological yield, grain yield, and harvest index. The effect of mutational treatments was significant at the 1% probability level for the traits of number of spikes per plant, 1000-grain weight, and biological yield, but did not reach significance for the traits of number of grains per spike, grain yield, and harvest index. The interaction between genotype and mutational treatments was significant for the trait of 1000-grain weight, while the interaction for the remaining traits did not reach significance. These results are consistent with [14 , 15].

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Table (4) Analysis of Variance for Yield Traits and Components in Bread Wheat.

Sources of difference	degrees of freedom	Average of squares					
		Number of spikes of grain on the plant	Number of grains per spike	Weight of 1000 Grains	Biological Yield	Grain Yield	Harvest index
replicates	2	1.677	4.844	0.433	18.300	1.811	3.403
genotype	14	24.034 **	995.820 **	55.736 **	2790.190 **	556.777 **	128.133 **
Mutation treatments	1	15.211 **	1.111 ns	177.662**	40.000**	5.377 ns	30.079 ns
genotype × Mutation treatments	14	0.615 ns	2.230 ns	32.310 **	5.761 ns	12.377 ns	38.926 ns
experimental error	58	0.516	2.097	1.042	2.656	9.845	12.320

, * at probability levels of 0.01 ≥p and 0.05 ≥p respectively, **ns is not significant.

3-2- Effect of genotype, chemical mutagens, and their interaction on yield traits and components of bread wheat:

Table (5), "Effect of genotype, mutagens, and their interaction on yield traits and components," shows that the Buhouth22 genotype was superior in the number of spikes per plant trait, with an average of 17.50 spikes.plant^{-1}. The lowest average for this trait was recorded by the Sulaimani2 genotype, with an average of 10.50 spikes per plant this did not differ significantly from the genotype of Babylon, with an average of 11.16 spikes. Plant^{-1} , Regarding the mutagens, the 0/mmol treatment was excelled, recording the highest average of 14.08 spikes.plant^{-1}, followed by the 0.5/mmol treatment with the lowest average of 13.26 spikes.plant^{-1}, regarding the interaction between genotype and mutational treatments, the interaction treatment (22 × 0/mmol) showed the highest average yield of 18 spikes, while the treatment (2 × 0.5/mmol) gave the lowest average yield of 10 spikes.plant^{-1} and correspond to what was obtained [16]. From the same table, the results for the number of grains per spike trait indicate the superiority of the Buhouth22 genotype with an average of 119.16 grains.spike^{-1}, while the lowest average for the trait was recorded by the Tammuz2 genotype with an average of 74.83 grains.spike^{-1}. However, the mutation rates did not reach the level of significance. Regarding the interaction between genotype and mutational treatments, the interaction treatments Buhouth22 × 0.5/mmol and Buhouth22 × 0/mmol were superior, with the highest averages of 120 and 118 grains.spike^{-1}, respectively this did not differ significantly from the treatment with 6 x 0/ mmol, with an average of 113.33 grains. spike^{-1} while the Tammuz2 × 0.5/mmol treatment gave the lowest average for the trait at 75. The results for the grains.spike^{-1} are consistent with those obtained [17]. Regarding the weight of 1000 grains, Table (5) shows that the Sham6 genotype had the highest average weight of 45.83 g, while the Babel genotype recorded the lowest average weight of 34.59 g. As for the mutational treatments, the 0/mmol treatment showed the highest average weight of 42.13 g, while the 0.5/mmol treatment had the lowest average weight of 39.32 g. Regarding the interaction between genotype and mutational treatments, the Sham6 × 0.5/mmol interaction treatment showed the highest average weight of 47 g, while the Babel × 0.5/mmol treatment had the lowest average weight of 31 g. These results are consistent with those obtained [18]. For the biological yield trait, the results in Table (5) indicate highly significant differences at the 1% level between the genotypes for this trait.

ISSN 2072-3857

The Buhouth22 genotype exhibited the highest average yield of 216 g.plant^{-1}, while Mawada genotype recorded the lowest average yield of 150.50 g.plant-1. Regarding the mutational treatments, the 0/mmol treatment resulted in the highest yield of 183 g.plant-1, followed by the 0.5/mmol treatment with the lowest average yield of 181.66 g.plant-1. As for the interaction between genotype and mutational treatments, the Buhouth22 × 0/mmol and Buhouth22 × 0.5/mmol treatments resulted in the highest yields of 217 and 215 g.plant-1, respectively. Conversely, the Mawada × 0/mmol and Mawada × 0.5/mmol treatments recorded the lowest average yields of 151 and 150 g.plant-1, respectively. Similarly, Tammuz2 in the 0.5/mmol treatment also recorded an average yield of 150 g.plant-1, consistent with the results obtained [19]. Table (5) shows highly significant differences at the 1% level for grain yield between genotypes for this trait. The Sham6 genotype recorded the highest average yield of 87.16 g.plant^{-1}, followed by the Jihan genotype, which did not differ significantly with an average of 83.83 g.plant^{-1}. The lowest average yield for the trait was recorded by the Tammuz2 genotype at 53.33 g.plant^{-1}. As for the mutation treatments, they did not reach the level of significance، Regarding the interaction between genotype and mutational treatments, the Sham6 × 0/mmol and Sham6 × 0.5/mmol treatments were superior, recording the highest average yields of 86.33 and 88 g.plant^{-1}, respectively. The successive treatment followed by the interaction treatment, Jihan × 0/mmol, did not differ significantly, with an average of 84.66 g.plant^{-1}. The lowest average for the trait was recorded in the Tammuz2 × 0/mmol and Tammuz2 × 0.5/mmol treatments, at 53.66 and 53 g.plant^{-1}, respectively. These results are consistent with those of studies[20 , 21]. For the harvest index trait, the results in Table (5) show highly significant differences at the 1% level between genotypes for this trait. The Jihan genotype had the highest average at 51.10%, while the Adna99 genotype had the lowest average at 33.90%. As for the mutation treatments with the genotype, there were no significant differences. The treatments 0 mmol/Jihan and 0.5 mmol/Jihan were superior, with average yields of 50.32% and 51.88%, respectively. These results are consistent with[22].

Table (5) shows the effect of genotype, chemical mutagens, and their interaction on yield traits and components.

genotype	Number of spikes per plant			Number of grains per e spike ar			Weight of 1000 grains		
	Mutation treatments		Average effect of genotype	Mutation treatments		Average effect of genotype	Mutation treatments		Average effect of genotype
	0 mmol	5 mmol		0 mmol	5 mmol		0 mmol	5 mmol	
Mawada	17 ab	16 Lm	16.50 b	101.33 cd	103 De	102.16 d	40.33 hij	41 ghij	40.66 D
Ozkan	14.66 cd	14 def	14.33 cde	93.66 def	93 I	93.33 f	44 cde	44 cde	44 bc
Tammuz 2	11.66 f-i	12 ghi	11.83 fg	74.66 hij	75 N	74.83 j	37 m	38 klm	37.5 f
Buhouth 22	18 a	17 Ab	17.50 a	118.33 a	120 A	119.16 a	42 fgh	45 bc	43.50 bc
Sulaimani 2	11 ij	10 J	10.50 h	85 fg	84 L	84.50 h	39.66 ijk	40 jk	39.83 de
Sham 6	16.66 abc	15 Cd	15.83 b	113.33 ab	115 B	114.16 b	44.66 bcd	47 A	45.83 a
Jihan	12	12	12	106	105	105.50	45.33	44	44.66

ISSN 2072-3857

	e-i	ghi	gh	bc	Cd	c	abc	cde	ab
Al-Rashid	15 bcd	15 Cd	15 c	101 cd	100 F	100.50 d	41.33 fghi	39.25 jkl	40.29 de
Al-Wafiya	15 bcd	14 def	14.50 cd	79.33 ghi	80 M	79.66 i	45.66 abc	34.70 N	40.18 de
Alaa	12.33 e-h	12 ghi	12.16 f	100.33 cd	101 Ef	100.66 d	43 def	38 klm	40.50 d
Babel	11.33 f-i	11 Ij	11.16 gh	85 fg	85 Kl	85 h	38 klm	31.18 P	34.59 g
Baghdad	14.66 cd	13 fgh	13.83 de	88 efg	87 Jk	87.50 g	45 bc	33 O	39 e
Al-Fayyad	13.33 def	12 ghi	12.66 f	97 cde	99 Fg	98 e	46 ab	40 ij	43 c
IPA 99	14 de	13 fgh	13.50 e	94 def	95 hi	94.50 f	42.66 efg	37.66 lm	40.11 de
Adana 99	14.66 cd	13 fgh	13.83 de	80.66 gh	79 m	79.83 i	37.33 M	37.16 M	37.24 f
Average Mutation treatments	14.08 a	13.26 B		94.51 a	94.73 a		42.13 A	39.32 B	

Table (5) continues with the effect of genotype, chemical mutagens, and the interaction between them on traits of the yield and its components.

genotype	Biological yield			Grain yield			Harvest index		
	Mutation treatments		Average effect of genotype	Mutation treatments		Average effect of genotype	Mutation treatments		Average effect of genotype
	0 mmol	5 mmol		0 mmol	5 mmol		0 mmol	5 mmol	
Mawada	151 m	150 m	150.50 l	59.33 hi	57 ij	58.16 f	37.24 f-j	38 e-j	37.81 cde
Ozkan	199.33 e	200 de	199.66 cd	74 cde	68 fg	71 c	37.11 f-j	34 hijk	35.55 e
Tammuz 2	153.66 l	150 m	151.83 l	53.66 j	53 j	53.33 f	34.90 g-k	35.48 f-k	35.19 e
Buhouth 22	217 a	215 a	216 a	62 hi	64 gh	63 d	44.84 abc	29.87 k	37.35 cde
Sulaimani 2	154.33 l	155 l	154.66 k	64 gh	62 hi	63 d	41.45 defg	40 defghi	40.72 c
Sham 6	200.66 de	198 e	199.33 d	86.33 a	88 a	87.16 a	48.14 Bcd	44.61 bcde	46.37 b
Jihan	163.33 j	160 k	161.66 j	84.66 a	83 ab	83.83 a	50.32 Ab	51.88 a	51.10 a
Al-Rashid	181.66 g	182 g	181.83 f	65 gh	64 gh	64.50 d	36.66 f-k	35.16 g-k	35.91 de
Al-Wafiya	187 f	186 f	186.50 e	75.33 cd	73 cdef	74.16 c	32.83 Jk	39.25 d-j	36.04 de
Alaa	179.33	175	177.16	73	74	73.50	40.70	42.29	41.49

ISSN 2072-3857

	g	h	g	cdef	cde	c	defgh	cdef	c
Babel	172.66 h	172.66 h	170.83 i	62 hi	69 efg	65.50 d	36.05 f-k	40.83 defgh	38.44 cde
Baghdad	204 bc	205 bc	204.50 b	75 cd	75 cd	75 bc	44.22 bcde	36.59 f-k	40.40 cd
Al-Fayyad	205.33 bc	206 b	205.66 b	79 b	77 cd	78 b	38.48 d-j	37.38 f-j	37.93 cde
IPA 99	202.66 cd	200 de	201.33 c	72.33 def	73 cdef	72.66 c	35.05 g-k	36.50 f-k	35.77 de
Adana 99	173 h	174 h	158.50 h	59.66 hi	58 ij	58.83 e	34.48 g-k	33.33 Ijk	33.90 e
Average Mutation treatments	183 a	181.66 b		69.68 a	69.20 a		39.50 a	38.34 a	

3-3- Genetic Parameters:

Genetic variation is an important objective for plant breeders, as it is the primary basis upon which selection is built. Selection usually occurs through phenotypic traits. Therefore, estimating genetic, environmental, and phenotypic variations, their coefficients of variation, and wide-range heritability are among the most important genetic parameters that lead to achieving the expected genetic improvement as a percentage, which indicates the importance of selecting for a particular trait[26].

3-3-1- Components of Phenotypic Variation and Genetic Parameters for the Studied Traits in the First Environment (0 mmol/no treatment)

The results in Table (7) indicate that the values of genotypic , environmental, and phenotypic variation for all studied traits differed from zero. This highlights the importance of estimating these variations for the studied traits. The values of genetic variation were higher than the values of environmental variation for the following traits: number of spikes per plant (3.524), number of grains per spike (157.427), weight of 1000 grains (8.811), biological yield (455.205), grain yield (87.649) and harvest index (23.547). This indicates that these traits, where the genetic variance was higher than the environmental coefficient, are genetically determined, and genetic factors contribute significantly in their inheritance. This variation between genotypes provides an opportunity for selection towards excelled traits. These results are consistent with those obtained in studies [27 , 28].

The environmental coefficient of variation was low for all studied traits. The values of the genotypic and phenotypic coefficients of variation were Closely aligned for the following traits: number of spikes per plant (13.325 and 14.840), number of grains per spike (13.276 and 13.443), biological yield (11.659 and 11.712), grain yield (13.434 and 14.907), and harvest index (12.285 and 17.041, respectively). These results are consistent with the findings of studies [29 , 30]. Broad-sense heritability values were high for the number of spikes per plant (0.806), number of grains per spike, 1000-grain weight (0.805), biological yield (0.991), and grain yield (0.812), and moderate for the harvest index (0.520). This indicates a greater role for genetic variation, which was reflected in the increased phenotypic variance of the studied traits compared to environmental variation. These traits can be improved through genetic factors, and high broad-sense heritability values were obtained for the studied traits. The expected genetic improvement values from selection were high for biological yield (37.166), moderate for number of grains per

spike (21.684) and grain yield (14.765), and low for number of spikes per plant (2.950), 100-grain weight (4.662), and harvest index (6.122). The expected genetic improvement values as a percentage were moderate for all studied traits. Results with what was found in [31].

Table (7) Components of phenotypic variance and genetic parameters of the first environment 0/mmol for all studied traits.

genetic parameters	Traits					
	Number of spikes of grain on the plant	Number of grains per spike	Weight of 1000 Grains	Biological Yield	Grain Yield	Harvest index
$^{2}\sigma G$	3.524 ±1.347	157.427 ±56.131	8.811 ±3.368	455.205 ±161.434	87.649 ±33.400	23.547 ±10.970
$^{2}\sigma E$	0.847 ±0.155	3.998 ±0.730	2.128 ±0.389	4.195 ±0.766	20.265 ±3.700	21.763 ±3.973
$^{2}\sigma P$	4.371 ±0.729	161.425 ±26.904	10.939 ±1.823	459.400 ±76.567	107.914 ±17.986	45.310 ±7.552
GCV%	13.325	13.276	7.045	11.659	13.434	12.285
ECV%	6.533	2.116	3.462	1.119	6.460	11.810
PCV%	14.840	13.443	7.850	11.712	14.907	17.041
h^2.b.s%	0.806	0.975	0.805	0.991	0.812	0.520
GA	2.950	21.684	4.662	37.166	14.765	6.122
GA%	20.938	22.943	11.065	20.309	21.188	15.498

3-3-2- Components of phenotypic variance and genetic parameters for the studied traits in the second environment: 0.5/mmol.

Table (8) shows that the values of genetic, environmental, and phenotypic variance for all studied traits were not zero. Genetic variance was higher than environmental variance for all studied traits: number of spikes per plant, 1000-grain weight, biological yield, grain yield, and harvest index. The exception was the number of grains per spike, where environmental variance was higher than genetic variance. This indicates that these traits are genetically determined and that genetic factors play a significant role in their inheritance. The values of the genetic and phenotypic coefficients of variation were moderate for all studied traits. The environmental coefficient of variation was moderate for the number of grains per spike and low for all other studied traits, consistent with the findings of [32].

The values of heritability in the broad sense were moderate for the number of grains per spike (0.459) and high for the remaining traits: number of spikes per plant (1000), 1000-grain weight (0.951), biological yield (1000), and grain yield ([Reference 32]). The expected genetic improvement values from selection were 1.000 and 0.976 for the harvest index. The values of expected genetic improvement from selection were high for the biological yield (66.087) and moderate for the number of grains per spike, 1000-grain weight, grain yield, and harvest index. As a percentage, the expected genetic improvement values were high for the number of spikes per plant, 1000-grain weight, biological yield, grain yield, and harvest index, and moderate for the number of grains per spike. This indicates that the use of

ISSN 2072-3857

the chemical mutagenesis at a concentration of 0.5/mmol affected some yield traits by altering the genes responsible for these traits in the desired direction of increased production, as evidenced by the high broad-sense heritability values. These results are consistent with those obtained in study [33].

Table (8) shows the components of phenotypic variance and genetic parameters for the second environment at 0.5/mmol for all studied traits.

genetic parameters	traits					
	Number of spikes of grain on the plant	Number of grains per spike	Weight of 1000 Grains	Biological Yield	Grain Yield	Harvest index
Genetic variance	10.914 ±1.286	137.081 ±24.563	58.484 ±7.013	1426.142 ±168.072	285.942 ±33.699	82.793 ±9.837
Environmental variance	0.001 ±0.000	161.679 ±29.518	3.001 ±0.548	0.001 ±0.000	0.001 ±0.000	2.001 ±0.365
Phenometric variance	10.915 ±1.819	298.760 ±49.793	61.485 ±10.247	1426.143 ±237.690	185.943 ±47.657	84.794 ±14.132
Coefficient of genetic variation	25.412	12.324	19.449	20.788	24.507	23.733
Coefficient of environmental variation	0.243	13.385	4.406	0.017	0.046	3.690
Coefficient of phenotypic variation	25.413	18.194	19.942	20.788	24.507	24.018
Broad sense heritability	1.000	0.459	0.951	1.000	1.000	0.976
Genetic improvement expected from selection	5.781	13.879	13.052	66.087	29.592	15.734
Genetic improvement expected as a percentage	44.469	14.609	33.195	36.380	42.887	41.039

ISSN 2072-3857

Discussion.

In light of the information in Table (5), we observe the superiority of the genotype "Buhouth22" in the traits of number of spikes per plant, number of grains per spike, and biological yield. The increase in the number of spikes per plant is attributed to differences in the genotype and its ability to form fertile and efficient spikes, in addition to the influence of the environment and the effects of competition between plants for light and nutrients, as well as the genetic factor. The reason for its superiority in the number of grains per spike is the appropriate cultivation time, which leads to the completion of the pollination and fertilization of the grains, thus resulting in the spike being full of grains, which in turn leads to an increase in the number of grains. All of this leads to an increase in biological yield, consistent with[23]. The genotype "Sham6" is excelled in the trait of 1000-grain weight and grain yield. The increase in 1000-grain weight depends primarily on the efficiency of the flag leaf and its ability to transport nutrients to the grains, thus filling the grains and increasing their weight. Ultimately, this leads to an increase in grain yield, which is an important trait for plant breeders. This aligns with the findings [24], which indicated that the weight of 1000 grains is considered This is an important trait that contributes to productivity, as it can be used as a criterion for selecting high-yielding genotypes. This trait is considered to be heritable to a reasonable degree and less affected by the environment.

Ethylmethanesulfonate (EMS) is a potent and widely used chemical mutagen that primarily acts as a chelating agent to induce random point mutations. Research confirms that EMS acts as a chelating agent by transferring an ethyl group to nitrogenous bases in DNA (especially guanine), leading to a base pairing error during replication where the G:C pair is transformed into A:T. This type of mutation often alters the function of encoded proteins without completely destroying the chromosome. It is widely used in crop breeding and improvement to create genetic diversity and is frequently employed in techniques targeting induced loci in the genome to generate new phenotypes. EMS is a chemical mutagen that produces a high mutation rate in plants[25]. EMS induces changes in the plant genome, chromosomes, and gene sequence by substituting one nitrogenous base for another. For example, it replaces the cytosine-guanine base with the adenine-thymine base, leading to a change in a gene responsible for plant traits. This gene change may be either In the desired direction and improvement in a particular trait or in the undesirable direction and deterioration in an important trait[16]. Mutations occur in both coding and non-coding regions and can lead to an increase or decrease in the regulation of gene expression or a change in the stability of messenger RNA (mRNA) or changes in protein structure by introducing changes in amino acids or stop codons or, in rare cases, frameshift mutations. EMS-induced mutations have been successfully applied to many crops[34]. The use of the chemical mutagen EMS at a concentration of 0.5 mmol, through grain soaking and absorption by embryo cells, directly affected plant biological processes, resulting in a noticeable change in plant morphology and impacting certain yield traits. We observed the superiority of the genotype "Buhouth22" in the traits of number of grains per spike and 1000-grain weight, while "Sham6" showed superior grain yield, and "Jihan" demonstrated superior harvest index. This indicates the genotype's susceptibility to the chemical mutagen concentration, inducing desired changes in the genes responsible for yield traits[21, 34]

4- Conclusions

ISSN 2072-3857

• The genotype's performance was significant for all studied traits. Mutagenesis coefficients were significant for the traits of number of spikes per plant, 1000-grain weight, and biological yield, but not for the remaining traits. The interaction was significant for the 1000-grain weight trait and not significant for the other traits. • The genotype *Buhouth22* showed the highest average values for the number of spikes per plant, the number of grains per spike, and the biological yield, while the genotype *Sham6* showed the highest values for 1000-grain weight and grain yield.

• Regarding the mutational treatments, the 0/mmol treatment showed the highest values for the number of spikes per plant, 1000-grain weight, and biological yield.

• As for the interaction between genotype and mutational treatments, the results show that the treatment (Buhouth22 × 0/mmol) showed the highest values for the number of spikes per plant and biological yield, while the treatment (Buhouth22 × 0.5/mmol) showed the highest values for the number of grains per spike. The interaction treatment (Sham6 × 0.5/mmol) showed the highest values for 1000-grain weight and grain yield.

• Genetic variance was higher than environmental variance for all traits in both environments, except for the number of grains per spike in the second environment, where environmental variance was higher than genetic. The values of the genetic and environmental coefficients of variation were moderate for all traits in both environments.

• The broad-sense heritability was high for the number of grains per spike and the biological yield in the first environment (0/mmol). In the second environment (0.5/mmol), the broad-sense heritability was moderate for the number of grains per spike and high for the other traits.

• The expected genetic improvement from selection in the first environment (0/mmol) was low for the number of spikes per plant, 1000-grain weight, and harvest index; moderate for the number of grains per spike and grain yield per plant; and high for the biological yield. In the second environment (0.5/mmol), the expected genetic improvement from selection was low for the number of spikes per plant, high for the biological yield, and moderate for the remaining traits. • The expected genetic improvement values, expressed as a percentage, were moderate for all traits in the first environment (0 mmol/hr), while in the second environment (0.5 mmol/hr), the values were moderate for the number of grains per spike and high for all studied traits.

• The effect of a 0.5 mmol/hr concentration of the chemical mutagen EMS per 100 mL of distilled water significantly impacted some yield traits and components.

5- Recommendations.

• Utilize the genotypes Research 22 and Sham 6, as they possess desirable traits and can be used to induce changes and improve traits through further mutagen experiments.

• Using a 0.5 mmol/hr concentration of the chemical mutagen EMS is considered acceptable for inducing changes in yield traits; therefore, we recommend conducting further experiments in the field of mutagen.

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ISSN 2072-3857