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RESPONSE OF DIFFERENT GENOTYPES TO GROWTH AND YIELD CHARACTERISTICS OF BREAD WHEAT AT DIFFERENT LEVELS OF NITROGEN FERTILIZER

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ABSTRACT

The experiment was carried out during the 2023/2024 agricultural season in the village of Al-Qubba, affiliated with the Tel Kaif district, which is 17 km north of Mosul. The aim is to evaluate the performance of bread wheat genetic compositions and to determine the crop response to nitrogen fertilisation in plant growth and yield traits, using a complete randomised block design. In a split-plot Replaced by design and three sectors, the experiment included two factors: the first has three levels of nitrogen fertilization, urea 46% (0, 120, 240 kg/ha), distributed in the main sectors, and the second factor has been ten genetic compositions of soft wheat (BAASH-14, AZAD-2, BAOBAB-1, ASEEL-1, Ibaa99, Buhuth22, Mawaddah, Baghdad1, Jihan99, Adana99) . It is important to state that the results of the variance analysis showed that nitrogen fertilisation levels were significant at the 1% probability level for all studied traits. The genotypes have been significant at the 1% probability level for all traits except flag leaf area cm^2 and harvest index%, which have been significant at the 5% probability level. The interaction between genetic compositions and fertilization was significant at the 1% level for all traits except for the trait of leaf area and flag, where it was significant at 5%, exceeding the nitrogen level of 120 kg/ha with the highest average for most traits, which are (weight of a thousand grains/g, biological yield g/m^2, grain yield g/m^2, harvest index%).

INTRODUCTION

Bread wheat (Triticum aestivum L.) is a strategic crop worldwide, given its vital role in providing food for more than 40% of the world's population. Despite the availability of the agricultural resources necessary for its successful cultivation, wheat production rates in Iraq remain low compared to available potential (Al-Jobouri and Alabar 2021). This is likely due to two reasons: the first is the reliance on old wheat varieties, and the second is farmers' lack of experience with advanced wheat production technology (FAO, 2023). Nitrogen fertilization is one of the most important Ways to treat the shortage of produce. Nitrogen is an essential plant element, greatly needed for its participation in many physiological processes and in forming chlorophyll, nucleic acids, carbohydrates, and proteins. Consequently, it increases yield and its qualitative and quantitative components. Among the studies conducted in this field, Abbas *et al.* (2023) indicated that when using different levels of nitrogen (0, 140, 220) kg/ha-1, the results showed that the 220 kg/ha^{-1} level was superior for all studied traits. In another study conducted by (Al-Falahy *et al*., 2022), when using different levels of nitrogen (0،75،150،200) kg/ha, the 200 level and gave the highest grain yield of 23 grams from plant of the genetic composition Apast 36. (Baber *et al*,2024) also noted when studying seven levels of nitrogen fertilization (0, 80, 100, 120, 140, 160, 180 kg/h) that the level of 180 kg/h was superior to the average for the characteristics of plant height (cm), number of tillers/m^2, biological yield (g/m^2), biological yield (g/m^2), and number of days from maturity. The study aimed to evaluate the performance of ten soft wheat genes for the traits proposed for study at three nitrogen levels (0, 120, 240 kg/ha) and the interaction between them.

MATERIALS AND METHODS

The experiment was conducted during the 2023/2024 agricultural season in the village of Al-Qubba, in the Tel Kaif district, 17 km north of Mosul. It is located at latitude 36.451° north of the equator, and longitude 43.352° east. The experiment used a complete randomized block design with a split-plot design. It included two factors, the first factor being nitrogen levels of urea 46% N (0, 120, 240) kg/ha distributed in the main sectors, one batch during land preparation before planting, and urea in two batches, the first half of the quantity after the emergence of the seedlings and the other half in the tillering stage .The second factor, the ten genetic structures of bread wheat, shown in Table (1), are distributed in the split plots. Each sector includes 30 experimental units after matching the workers' levels. Each secondary experimental unit includes two lines, each three meters long. The distance between lines is 0.20 m at a seed rate of 120 kg/ha (adjusted for genetic compositions according to the average weight of 1000 seeds). Agricultural operations have been carried out, including irrigation and pest control, as needed, and samples were taken from ten plants randomly from the lines to conduct measurements of plant growth, yield, and its components.

Table (1): Names of genetic structures and their source

Lineage	**Genetic name**	**Sequence**
MLAN/PASTOR	BAOBAB-1	1
MLAN/PASTOR	BAASHA-14	2
MLAN/PASTOR/3/SHAMISS-3	ASEEL-1	3
PFAU/MILAN	AZD-2	4
Source	**Class**	
Seed Inspection and Certification / Nineveh	Mawadda	5
Seed Inspection and Certification / Nineveh	Buhuth22	6
Seed Inspection and Certification / Nineveh	Ibaa99	7
Seed Inspection and Certification / Nineveh	Baghdad1	8
Seed Inspection and Certification / Nineveh	Adana99	9
Seed Inspection and Certification / Nineveh	Jihan99	10

The studied traits included

Plant height (cm), which was measured from the soil surface to the tip of the spike excluding the awns; flag leaf area (cm²), calculated using the formula; length × maximum width × correction factor (0.95); number of spikes per square meter; number of grains per spike; and 1000-grain weight (g), determined using a precision balance after drying. Additionally, grain yield (g/m²) was estimated based on the weight of grains harvested from a known area, biological yield (g/m²) was obtained by weighing the total above-ground biomass (straw + grains) from the central rows and converting it to per square meter, and finally, harvest index (%) was calculated by dividing grain yield by biological yield and multiplying by 100.

Statistical analysis of the studied characteristics

Data for the studied traits were analysed using a computer program (SAS and SPSS 2002), using a randomised complete block design and a split-panel split-plot design. Differences between means were tested using Duncan's multiple range test.

The analysis has been conducted for nitrogen fertilization levels as levels of a quantitative factor and for all the traits under study. For this purpose, the mean squares of this factor were divided into linear (first degree) and quadratic (second degree) relationships to identify the nature of the response of each trait to nitrogen fertilisation levels, and through this to know the best level of nitrogen fertiliser that gives the best average performance for the trait, as follows:

1. For the characteristics that showed a linear response to nitrogen fertiliser, the desired point at the end of the regression line was determined from which the best level of fertiliser with the best average performance was determined.
2. As for the traits that showed a second-order (quadratic) response, the values of the parameters of their regression equations have been adopted, which are in the form: $\hat{y} = \beta 0 + \beta 1\ x + \beta 2\ 2\ x$, in calculating the best fertiliser level (x) that gave the best average for the trait (y) as follows :The best fertiliser level is ($\beta 22/\beta 1$). by substituting this value into the regression equation, the best average for the trait is obtained.

RESULTS AND DISCUSSION

Table (2) shows the results of the variance analysis for grain yield traits and their components in wheat. It is noted that the mean squares of fertilization levels and genotypes showed significant differences at a 1% probability level for all studied traits, except flag leaf area (cm^2) and harvest index (%) for the genotypes. The interaction between the two factors also showed significant differences at a 1% probability level for all studied traits, except flag leaf area (cm^2), which was significant at a 5% probability level. This means that the varieties behaved differently at the levels of added nitrogen fertiliser, and these results are consistent with Baber *et al.* (2024) and Rekani (2017). As for the results of the trend analysis, it is noted that the mean squares of the linear relationship were significant for all traits except for the trait of number of spikes/m^2.It did not reach the limit of statistical significance, the quadratic relationship was significant for the following traits: number of spikes/m^2, weight of 1000 grains (g), biological yield (g/m^2), grain yield (g/m^2)and harvest index%.

Table (2): Results of analysis of variance for the studied traits

		Mean of squares							
harvest index (%)	grain yield (g /m)	biological yield (g/ m)	weight of 1000 grains (g)	Number of grains spike^{-1}	number of spikes m^{-2}	flag leaf area (cm^2)	Plant height (cm)	D. F	Sources of difference
112.914	32467.676	35724.033	7.644	88.707	11235.14	33.845	291.647	2	Block
**1092.963	**227642.309	**103326.633	**73.677	**102.014	**53732.211	**319.710	**378.091	2	Fertilization levels
**726.70	**152800	**75757	*33.750	**180.267	15843.7	**584.381	**744.833	1	Linear relationship
**1459.22	**302484	**130896	**113.606	23.762	**91620.7	55.039	11.350	1	Quadratic relationship
66.179	8963.671	7818.116	3.477	4.590	2705.161	9.922	39.717	4	Experimental error A
*137.040	**28081.181	**47398.982	**25.912	**49.970	**7586.080	*32.319	**181.131	9	Genetic structures
**239.082	**11669.816	**44846.275	**19.060	**48.679	**2181.902	*30.379	**90.918	18	Genetic structures × Fertilization levels
54.720	4628.163	6808.015	7.088	15.294	902.809	14.463	28.7200	54	Experimental error B

(*or**) significant at 1% and 5% probability levels, respectively

The results of Table (3), which include the averages of genetic compositions and fertilization levels in the trait of plant height, indicate that the genetic composition Ibaa 99 outperformed the rest of the genetic compositions with the highest average of 105.733 cm. As for the comparison between the averages of nitrogen fertilisation, it showed that the level of 240 kg/ha outperformed with the highest average of (102.507 cm) .These genetic differences between the genetic structures may be due to the variation in the lengths of the internodes, especially the upper internodes, which increases the plant height. These results are consistent with (Alaamer *et al.*, 2024; Mohammad, 2024) .Concerning the results of Table (5) of the regression analysis, it was obvious that the first-degree equation is appropriate for predicting plant height at any fertiliser level, which determines the response of the trait to these levels, which was appropriate with a coefficient of determination of (49.7%), and the best reading for plant height reached (102.7654 cm) at the best fertiliser level (240 kg/ha^{-1}or more) .The comparison of the averages of the compatibility between the genetic compositions and the nitrogen fertilisation levels in Table (3) shows the presence of significant differences, as the genetic composition Ibaa 99 at the level (240 kg/ha) gave the highest average, reaching 118.334 cm, with a significant difference from the rest of the genetic compositions, and this is consistent with (Al-Sebahi *et al.*, 2015 and Abbas, 2023). They indicated the importance of nitrogen in increasing plant growth, cell division and expansion, and increasing the meristematic activity, in addition to the interaction of the genetic compositions with fertilisation in a different way through the growth characteristics.

Table (3): Averages of genetic compositions, fertilization levels, and their compatibility for the trait (plant height/cm)

Mean	Fertilization levels (kg/ha)			Genetic name
	240	120	0	
101.078 AB	96.867 DEF	107.50 BCD	98.867 B-E	BAOBAB-1
99.533 BC	101.667 B-E	103.133 B-F	93.800 EFG	BAASHA-14
4.356 CD	99.00 B-E	87.467 FGH	96.600 EF	ASEEL-1
91.556 D	97.533 C-F	94.400 EFG	82.733 H	AZD-2
102.800 AB	109.067 B	101.800 B-E	97.533 D-G	Mawadda
102.622 AB	103.333 B-E	102.867 B-E	101.667 B-E	Buhuth22
105.733 A	118.333 A	97.733 C-F	101.133 B-E	Ibaa99
100.978 AB	97.600 C-F	107.733 BC	97.600 C-F	Baghdad1
99.489 BC	101.600 B-E	98.600 B-E	98.267 CDE	Adana99
94.200 CD	100.067 B-F	96.133 EFG	86.400 GH	Jihan99
	102.507 A	99.737 AB	95.460 B	Average

Table (4) shows that the genetic composition (Mawadda) has the highest average of 50.651 cm over the rest of the genetic compositions. This is due to the effects of genetic and environmental factors on plant growth. Each genetic composition has limited characteristics that affect the size of the flag leaf because it is due to the genes responsible for the growth of the leaf and its adaptation to the surrounding conditions.

Table (4): Averages of genetic compositions, fertilization levels, and their compatibility for the trait (flag leaf area/cm^2)

Mean	Fertilization levels (kg/ha)			Genetic name
	240	120	0	
49.614 AB	52.063 A-D	49.157 B-G	47.621 C-F	BAOBAB-1
46.532 ABC	53.192 ABC	44.455 E-H	41.949 GH	BAASHA-14
46.086 BC	55.215 AB	43.900 E-H	39.142 H	ASEEL-1
48.715 AB	52.619 ABC	44.931 D-H	48.594 B-G	AZD-2
50.651 A	57.432 A	51.030 A-E	43.490 E-H	Mawadda
44.019 C	45.718 C-H	43.533 E-H	42.806 FGH	Buhuth22
48.715 AB	49.012 C-G	48.156 B-G	48.810 B-G	Ibaa99
47.462 AB	48.973 B-H	50.161 B-G	43.252 FGH	Baghdad1
47.120 ABC	49.238 C-G	44.677 D-G	47.447 C-G	Adana99
48.003 ABC	50.138 C-F	45.800 C-F	48.070 B-G	Jihan99
	51.359 A	46.580 B	45.118 B	Average

As for the nitrogen fertilisation levels only, the level (240 kg/ha) showed superiority with the highest average of (51.359 cm) and a significant difference from the rest.The comparison of the averages indicated the compatibility between the genetic compositions and the nitrogen fertilisation levels, as the genetic composition (Mawda) recorded the highest average at the fertilisation level (240 kg/ha) and reached (57.432 cm) .The results of the trend analysis for this trait show that a first-degree relationship was appropriate at the best rate for the trait, which is)50.992 cm) and at the best nitrogen fertilizer, which is (240 kg/ha or more), with a coefficient of determination of (78.3%). The results agree with (Naas *et al*., 2024).

Table (5): The degree of response of different traits to nitrogen fertilizer levels and the best rate for the trait at the best level

determination %	Calculated F	Regression equation	Best rate of trait	Best amount of nitrogen fertilize	Characteristics
49.7	** 6.92	$Y1 = 95.71+ 0.02936\ X$	102.7564	more 240	Plant height(cm^2)
78.3	** 25.19	$Y2= 44.57+ 0.02601\ X$	50.9924	more 240	flag leaf area (cm^2)
76.3	** 16.51	$Y6= 230.5 + 1.263\ X -0.0047\ X^2$	315.349	134.361	number of spikes/m^2
45.1	** 5.75	$Y7= 41.73 + 0.01444\ X$	45.1956	more 240	Number of grains/spike
83.5	** 23.34	$Y8= 34.33+0.04597\ X- 0.000166\ X^2$	37.512	138.463	weight of 1000 grains
66.8	** 7.65	$Y9= 924.6+ 1.644\ X- 0.005618\ X^2$	1044.871	146.315	biological yield (g/m^2)
81.9	** 18.01	$Y10= 3302+24.70\ X - 0.0854\ X^2$	508.7978	144.613	grain yield (g/m^2)
81.7	17.85	$Y11= 36.71 + 0.1714\ X -0.000593\ X^2$	49.095175	144.519	harvest index (%)

Table (6) shows that the genetic composition ASEEL-1 has the highest average of (338.44 spikes/m^2), significantly different from the rest of the genetic compositions. As for the fertilisation levels, the level (120 kg/ha) shows the superiority with the highest average of (314.40 spikes/m^2), with a significant difference from the rest. The interaction between fertilization levels and genetic compositions showed significant differences, with the ASEEL-1 composition outperforming the fertilisation level of 120 kg/ha, with the highest average reaching 385.33 spikes/m^2. The difference in the number of spikes/m^2 among wheat genetic compositions is due to the difference in fertilisation levels, depending on the response of these genetic compositions to fertilisation levels. Some structures may benefit more from nitrogen than others, leading to increased spike count, while others may appear less responsive. Other factors like nutrient availability and soil characteristics may also play a role in this difference. As for the trend analysis, Table (5) shows that the appropriate second-degree equation is found, and the best rate for the trait is (315.349 spikes/m^2) at the best nitrogen fertiliser quantity of (134.361 kg/ha^{-1}) with a coefficient of determination of (76.3%). These results are consistent with (Patel *et al*,2025).

Table (6): Averages of genetic compositions, fertilization levels and their compatibility for the trait (number of spikes/m^2)

Mean	Fertilization levels (kg/ha)			Genetic name
	240	120	0	
237.11 D	198.67 J	291.00 C-F	221.67 IJ	BAOBAB-1
284.78 BC	266.00 E-J	370.67 AB	217.67 IJ	BAASHA-14
338.44 A	344.00 A-C	385.33 A	286.00 D-G	ASEEL-1
246.56 D	229.00 HIJ	296.00 CDE	214.67 IJ	AZD-2
269.22 BCD	259.33 E-J	321.33 BCD	227.00 G-J	Mawadda
259.33 BCD	262.33 F-J	285.00 D-H	230.67 HIJ	Buhuth22
253.89 CE	232.67 F-J	294.00 CDE	235.00 F-J	Ibaa99
263.44 BCD	297.33 CDE	267.00 D-I	226.00 HIJ	Baghdad1
287.89 B	266.00 E-J	368.00 AB	229.67 G-J	Adana99
252.11 D	274.33 E-J	265.67 E-J	216.33 IJ	Jihan99
	262.96 B	314.40 A	230.47 B	Average

Table (7) indicates that the genetic composition of Mawaddah is superior, with its highest average of 47.222 grains/spike. As for the fertilisation levels, the level (240 kg/ha) is superior, with the highest average of 45.563 grains/spike, with a significant difference from the rest of the levels (Ibraheem,2018). The results of the interaction between the genetic compositions and the fertilisation levels show that the genetic composition of Adana99 is superior and reached (55.400 grains/spike) at the level (240 kg/ha^{-1} or more). This is due to the availability of nitrogen in the stages of growth and development of the crop, which consequently led to raising the efficiency of the photosynthesis process and the results and increase of food building products, as this contributed to increasing the number of ears and their creation, which consists of grains that provided a suitable opportunity to reduce the failure of pollination in the flowers. Therefore, the number of grains in one spike increases, and these results are consistent with (Al-Jaboury, and Al abar, 2021; Abdulla *et al.*, 2024).

Table (7): Averages of genetic compositions, fertilization levels, and their compatibility for the trait: Number of grains per spike

Mean	Fertilization levels (kg/ha)			Genetic name
	240	120	0	
41.867 BC	45.400 B-E	41.733 B-F	38.467 EF	BAOBAB-1
41.511 BC	45.200 B-E	39.067 DEF	40.267 C-G	BAASHA-14
43.644 ABC	43.667 B-E	48.000 CD	39.267 DEF	ASEEL-1
42.067 BC	39.200 DEF	41.133 B-F	45.867 B-E	AZD-2
47.222 A	47.800 BC	45.267 B-E	48.600 B	Mawadda
43.778 AB	44.800 B-E	42.933 B-F	43.600 C-G	Buhuth22
45.189 AB	46.700 BCD	40.333 C-F	48.533 B	Ibaa99
43.422 ABC	48.933 B	42.267 B-F	39.067 DEF	Baghdad1
46.444 A	55.533 A	42.667 B-F	41.133 B-F	Adana99
39.522 C	38.400 FG	44.000 B-E	36.167 F	Jihan99
	45.563 A	42.740 B	42.096 B	Average

The results of trend analysis show that the equation is linear of the first degree for this trait at the best rate of the trait, which reaches (45.1956), and at the best amount of fertiliser (240 kg/ha or more), with a coefficient of determination.(%45.1)

Table (8) shows that the genetic composition of Abaa99 is superior, with the highest average, reaching 39.111 grains/g. (Kadum et al,2017; Al-Hachami and Frhan,2017) As for the fertilisation levels, the level (120 kg/ha) is superior with the highest average, reaching (37.466 grains/g) over the rest of the nitrogen levels. The increase in the average weight of 1000 grains may be due to the major role of nutritional elements in improving the efficiency of the photosynthesis process, which leads to the accumulation of dry matter in the grains. The interaction between genetic compositions and fertilisation levels shows that the genetic composition Aba99 is superior, with its highest average of (42.667 grains/g) at the level (120 kg/ha). The trend analysis results show that the equation is of the second degree with a coefficient of determination of 83.5%, and at the best rate for the trait of 37.512 grains/g and the best level for the trait of 138.463 kg/ha. These results are consistent with (Imdad *et al*,2018; Al-Rifai *et al.,* 2023)

Table (8): Averages of genetic compositions, fertilization levels, and their compatibility for the trait (weight of 1000 grains/g)

Mean	Fertilization levels (kg/ha)			Genetic name
	240	120	(0	
35.111 BCD	35.333 CDE	40.000 ABC	30.000 F	BAOBAB-1
35.889 BCD	36.000 B-E	37.000 B-E	34.667 DEF	BAASHA-14
35.444 BCD	36.333 B-E	36.000 B-E	34.000 DEF	ASEEL-1
37.444 AB	38.000 A-D	38.667 A-D	35.667 B-E	AZD-2
37.000 ABC	34.000 DEF	40.000 ABC	37.000 B-E	Mawadda
33.222 D	37.667 A-D	30.000 F	32.000 EF	Buhuth22
39.111 A	36.667 B-E	42.667 A	38.000 A-D	Ibaa99
34.333 CD	35.667 B-E	33.667 DEF	33.667 DEF	Baghdad1
34.778 BCD	33.667 DEF	36.000 B-E	34.667 DEF	Adana99
36.444 BC	35.000 C-F	40.667 AB	33.667 DEF	Jihan99
	35.833 B	37.466 A	34.333 C	Average

Table (9) shows that the ASEEL-1 genotype is superior, with its highest average reaching 1110.22 g/m^2. Fertilisation levels show superiority over the 120 kg/ha level and the highest average reaching (1041.07 g/m^2) with a significant difference from the rest of the nitrogen levels. This is consistent with (Dhahi and Baktash, 2018; Tahir *et al*,2021). As for the interaction between the genotypes and fertilisation levels, the Mawaddah genotype is superior, with the highest average reaching (1229.33 g/m^2) at the level (120 kg/h).

The results of the trend analysis showed that the symmetry equation for this trait is quadratic of the second degree with a coefficient of determination (66.8%) at the best rate for the trait (1044.871 g/m^2), and at the best fertilisation rate of (146.315 kg/ha).

Table (9): Averages of genetic compositions, fertilization levels, and their compatibility for the trait (biological yield, g/m^2).

Mean	Fertilization levels (kg/ha)			Genetic name
	240	120	0	
971.89 CD	917.33 E-I	1139.33 ABC	859.00 IJ	BAOBAB-1
970.67 CD	918.67 F-I	945.33 F-I	1048.00 B-G	BAAS-14
1110.22 A	1102.67 A-E	1041.33 B-G	1186.67 AB	ASEEL-1
862.22 E	930.67 F-I	929.33 F-I	726.67 JK	AZD-2
1065.00 AB	965.67 D-I	1229.33 A	1000.00 C-I	Mawadda
940.22 DE	1116.67 A-D	1074.67 A-F	629.33 K	Buhuth22
1000.00 BCD	1077.33 A-E	896.00 GHI	1026.67 B-H	Ibaa99
916.44 DE	873.33 HI	958.33 C-I	890.67 GHI	Baghdad1
1038.44 ABC	981.33 E-I	1139.33 ABC	994.667 FGH	Adana99
996.22 CD	1073.33 A-F	1030.67 B-G	884.67 GHI	Jihan99
	995.70 B	1041.07 A	924.63 B	Average

Table (10) shows that the ASEEL-1 genotype has the highest average (531.23 g/m^2), significantly different from the other genotypes. As for the fertilisation levels, it exceeds (120 kg/ha), with a significant difference from the rest of the levels, and reaches (503.65 g/m^2). High nitrogen levels enhance the ability of plants to produce grains in larger quantities ,which leads to an improvement in the grain yield (g/m^2). Among the genetic compositions and fertilisation levels, the ASEEL-1 genetic composition excels with the highest average, reaching (670.18 g/m^2) at 120 kg/ha. As for the results of the regression analysis, the predictive equation for this trait is quadratic of the second degree, with a coefficient of determination (81.7%) at the best rate for the trait, which reaches (508.797 g/m^2), and at the best amount of nitrogen fertilizer, which reached (144.613 kg/ha). These results are consistent with(Fresew *et al*, 2018; Sadeqi *et al*,2025) .

Table (10): Averages of genetic compositions, fertilization levels, and compatibility between them for the trait: Grain yield (g/m^2)

Mean	Fertilization levels (kg/ha)			Genetic name
	240	120	0	
350.81 E	321.87 I-L	477.45 B-H	253.12 L	BAOBAB-1
422.37 B-E	434.51 C-I	531.56 B-E	301.03 JKL	BAASHA-14
531.23 A	547.56 BCD	670.18 A	375.16 G-L	ASEEL-1
386.76 DE	344.57 I-L	470.34 B-I	345.37 H-L	AZD-2
469.58 AB	421.13 D-K	586.19 AB	401.40 E-J	Mawadda
376.67 E	443.76 C-I	370.23 G-L	316.02 JKL	Buhuth22
449.19 BCD	408.16 E-K	511.07 B-F	428.35 D-I	Ibaa99
397.81 BCD	520.77 B-G	378.96 F-L	293.71 KL	Baghdad1
461.51 BC	494.75 B-G	566.30 ABC	323.50 I-L	Adana99
370.65 E	374.22 G-L	474.19 B-H	263.55 L	Jihan99
	431.13 B	503.65 A	330.20 C	Average

Table (11) shows that the two genetic combinations ASEEL-1 and AZAD-2 had the highest average, reaching 48.484% and 45.424%, respectively. The two levels (240 and 120 kg/ha) show the highest average (48.731 and 43.669%), respectively. The interaction between the genetic compositions and fertilisation levels shows that the ASEEL-1 genetic composition has the highest average (64.130%) at the level (120 kg/ha) .The trend analysis results show that the predictive equation for this trait is quadratic of the second degree with a coefficient of determination of 81.9%. At the best quantity of the trait it is (49.095%) and at the best quantity of nitrogen fertiliser it was (144.519 kg/ha) when these results agree with (Hassanein *et al.*,2018; Kumar *et al*,2023)**.**

Table (11): Averages of genetic compositions, fertilization levels, and their compatibility for the trait: harvest index (x).

Mean	Fertilization levels (kg/ha)			Genetic name
	240	120	0	
35.816 C	35.129 E-I	41.898 D-H	30.422 IG	BAOBAB-1
44.369 AB	47.925 B-F	56.403 ABC	28.779 I	BAASHA-14
48.484 A	49.670 B-E	64.130 A	31.651 GHI	ASEEL-1
45.424 A	37.447 D-I	50.953 A-D	47.873 B-F	AZD-2
43.973 AB	43.826 C-H	47.881 B-F	40.210 D-I	Mawadda
41.782 ABC	39.994 D-I	35.175 E-I	50.177 BCD	Buhuth22
45.498 A	37.857 D-I	56.825 ABC	41.812 D-I	Ibaa99
43.851 AB	59.590 AB	38.461 D-I	33.502 F-I	Baghdad1
44.228 AB	50.421 BCD	49.627 B-E	32.635 HJI	Adana99
36.940 C	34.835 F-I	45.958 B-G	30.029 HI	Jihan99
	43.669 A	48.731 A	36.709 B	Average

CONCLUSIONS

1. The genotype (ASEEL-1) was characterized by good performance averages, with the highest number of traits, reaching five (number of tillers, number of spikes, biological yield, grain yield, and harvest index).
2. It was found that the nitrogen fertilization level (240 kg/ha) was superior in most traits, and the increase in the fertilization rate was accompanied by a significant increase in (plant height, leaf area, number of tillers, number of spikes, spike length, number of grains per spike, and protein content).
3. The two-way interaction between the two study factors showed a significant effect on most of the studied traits, and the best combinations between the genotypes were with the high fertilization rate (240 kg/ha).

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CONFLICT OF INTEREST

Author declares no conflicts of interest regarding he publish this article.

استجابة تراكيب وراثية مختلفة لصفات نمو وحاصل حنطة الخبز عند مستويات مختلفة من السماد النيتروجيني

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الخلاصة

أجريت التجربة خلال الموسم الزراعي 2024/2023 في قرية القبة التابعة لقضاء تلكيف والتي تبعد 17 كم شمال مدينة الموصل. الهدف هو تقييم أداء التراكيب الوراثية حنطة الخبز وتحديد استجابة المحصول للتسميد النيتروجيني في نمو النبات وصفات الحاصل، باستخدام تصميم القطاعات العشوائية الكاملة. في تصميم القطع المنشقة بثلاثة قطاعات، تضمنت التجربة عاملين: الأول بثلاثة مستويات من التسميد النيتروجيني، اليوريا 46٪ (0، 120، 240 كجم / هـ$^{-1}$)، موزعة في القطاعات الرئيسية، والعامل الثاني كان عشرة تركيبات وراثية من حنطة الخبز BAASH-14، AZAD-2، BAOBAB-1، ASEEL-1، Ibaa99، Buhuth22، Mawaddah، Baghdad1، Jihan99، Adana99 اظهرت نتائج تحليل التباين أن مستويات التسميد النيتروجيني كانت معنوية عند مستوى احتمال 1% لجميع الصفات المدروسة. وكانت التراكيب الوراثية معنوية عند مستوى احتمال 1% لجميع الصفات باستثناء صفة مساحة الورقة (سم^{2}) ومعامل الحصاد (%)، حيث كانت معنوية عند مستوى احتمال 5%. وكان التداخل بين التركيب الوراثي والتسميد معنويًا عند مستوى احتمال 1% لجميع الصفات باستثناء صفة مساحة الورقة (سم^{2}) ومعامل الحصاد (%)، حيث كان معنويًا عند مستوى احتمال 5%، متجاوزًا مستوى النيتروجين البالغ 120 كجم/هكتار بأعلى متوسط لمعظم الصفات، وهي (وزن ألف حبة/جم، الغلة البيولوجية (جم/م^{2})، محصول الحبوب (جم/م^{2})، معامل الحصاد (%).

الكلمات المفتاحية: التراكيب الوراثية للحنطة، السماد النيتروجيني، الحاصل ومكوناتها.

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