KIRKUK UNIVERSITY JOURNAL
FOR AGRICULTURAL SCIENCES

Study of thermal aggregation of growth traits in the branching and elongation phases of a group of genotypes in Coarse wheat (*Triticum durum* Desf.)

Niaz Farq Radha [1]

niaz.farq@gmail.com

Khalid Khalil Ahmed [2]

Khalid_khalil@uokirkuk.edu.iq

[1]Department of field crops, College of Agriculture, Kirkuk University– Kirkuk, Iraq.

[2]Department of Medicinal and industrial plants, College of Agriculture-Haweja, Kirkuk University– Kirkuk, Iraq

• Date of research received 20 /03/2023 and accepted 02/04/2023**.**

Abstract

This study was conducted during the agricultural season 2021-2022 at the Agricultural Research and Experiment Station (Sayada area) belonging to the College of Agriculture at the University of Kirkuk, using a randomized complete block design (R.C.B.D) and with three replications, each block included twenty experimental units, the number of genotypes of durum wheat is (DW38, Bejah-6/SLA, Halio, Mikki, Guayacan, Amedakul s, Fadda98, Icarasha 2, Sham 5, Lahnaucan, Sardar, Bagdad, DW10, Axad5, Simito, Crezo, Corvilla , Iraq Oasis, Surat Kul,Um Rabie), Where the results showed that there are significant differences between the genotypes at the probability level of 1% for the number of branches and the stage of elongation, and the existence of significant differences between the genotypes at the level of probability 1% for the studied traits, where the genetic structure of Sardar exceeded the trait (the number of total fragments, the number of effective fragments, the number of days for the number of branches, 50% spikes parcel) with the highest average, as their average reached (583.20 branches, 526.37 branches, 103.00 days, 16.73 branches, 116.66 days) And the highest average number of branches in the stage (Z21, Z23, Z24, Z25, Z26, Z27, Z28 and Z29) where their average was (1.20, 7.10, 8.46, 9.90, 12.43, 14.36, 15.60, 16.73) and the superiority of the two genetic structures Mikki and Crezo for the characteristic of the area of the flag leaf with the highest average, as their average reached (42.35, 42.18) respectively, while the composition um Rabie

with the highest average average plant height, with an average of 83.82, and the genetic makeup of Corvella with the highest average chlorophyll content of the flag paper, with a peak of 47.28 The genetic structure Lahnaucan gives the highest average number of branches in the stage (Z22, Z23, Z24 and (Z25), where their average was (4.20, 7.40, 8.46, 9.60) and the genetic structure Fadda98 gave the highest average number of branches in the stage of Z24) and (Z25, where the average of they are (7.83, 9.70) and the genotype Bejah-6/SLA gives the highest average number of branches in the stage (Z29), where it averaged (16.00) and the superiority of the genetic structure Surat Kul in the elongation stage (for the first decade, the second decade, the third decade, the fourth decade and the fifth decade) The highest average in the number of days, which reached (80.00, 86.66, 92.66, 99.33 and 99.33) and the genetic structure Fadda98 in (the fourth and fifth decade), the highest average in the number of days, reaching (99.33), plants needed to enter the branching stage to the accumulated temperature of 379.0 m0, while plants of all genotypes entered the stage of the maximum number of branches requiring thermal collection of 707.0 m0, and thermal collection required to complete the elongation stage 635.5 m0.

Keywords: thermal aggregation, buckwheat, branching and elongation.
Citation: Niaz F. Radha; Khalid K. Ahmed. " Study of thermal aggregation of growth traits in the branching and elongation phases of a group of genotypes in Coarse wheat (*Triticum durum* Desf.)". *Kirkuk University Journal For Agricultural Sciences*, 14, 2, 2023, 22-34. doi: 10.58928/ku23.14203
Correspondence Author: Niaz Farq Radha - niaz.farq@gmail.com

Introduction

Scale It is a relatively recent measure for diagnosing the growth of cereal crops. It was created by a Dutch botanist, It is currently widely used in agricultural research, the decimal growth scale is based on ten major growth stages classified from 0 to 9, each primary growth stage is divided into secondary stages, thus the scale extends from 00 to 99.[1]

Durum wheat or what is called durum wheat or bulgur wheat is one of the types of wheat that is widely cultivated in different parts of the world, and is mainly involved in the production of pasta [2].

Coarse wheat constitutes 8% of the world's cultivated areas, and the uses of its grains vary in the manufacture of groats, bulgur and semolina and may be used in some countries instead of rice in meals [3] The percentage of total protein in coarse wheat ranges from 6% to 20% depending on the rank and variety Environmental conditions as well as agricultural operations The period of the growing season, as rainfall during the ripening stage of the grain leads to a decline in the percentage of total protein, either high temperatures during The stage of maturity of the grain leads to a high protein content [4].

Branching in cereal crops, including wheat, is a characteristic of them. Being the first important growth stage, and a major component of the yield, so it is an important goal to improve and increase the grain yield, and that a good understanding of the performance of the primary branches leads us to understand how to improve the grain yield as it is essential and gives a complete perception of the performance of the plant or the good or not good genetic structure of its functions through its contribution to the grain yield and other traits, as well as it is one of the adaptive mechanisms in grain crop plants such as wheat to maintain the balance between the source and the mouth. [5].

Wheatgrass plants are characterized by the formation of branches that produce fertile ears, compared to most field crop plants [6] and that setting the appropriate planting date means that the plant obtains the required temperatures to give the maximum number of branches to plants by promoting leaf development, which can affect the amount of yield [7].

Materials and methods of work

This study was conducted in the agricultural season 2021-2022 at the Agricultural Research and Experiments Station (Sayada Area) belonging to the Faculty of Agriculture, University of Kirkuk, using the design of simple complete random sectors (R.C.B.D) and with three replicates, each sector contains twenty experimental units that guarantee the genetic structures of coarse wheat are (DW38, Bejah-6/SLA, Halio, Mikki, Guayacan, Amedakul s, Fadda98, Icarasha 2, Sham 5, Lahnaucan, Sardar, Baghdad, DW10, ACSAD 5, Simito, Crezo, Corvilla, Iraq Oasis, Sura Kul, um Rabi). The experiment was applied by designing complete random sectors (R.C.B.D) and with three sectors, and each plot included 20 experimental units, on which the 20 genetic structures were randomly distributed, and the experiment was carried out and planted on November 15, 2021, the experiment land was plowed, then the division and settlement process was the experimental field, and then the land was divided. The cultivation was done in a line method, each experimental unit contained four lines with a length of 3 m and the distance between one line and another 25 cm using the amount of seed 280 grains. m-2 for each line that the experimental field is Fertilizing it with 320 kg.E-1 Dab

fertilizer (N% 18, P2O5) and then (200) kg urea was added as the second batch in the branching stage, and agricultural operations were carried out from irrigation and control of thin leaf bushes on 8/3/2022 using Topek pesticide by 250 ml, then diluted by 100 liters of water and broad bushes on 2/3/2022 using D.2.4 pesticide by 125 ml, then diluted by 100 liters of water, as well as manual control of all bushes and as needed during the season, The field was covered with a net to protect it from bird and animal damage. All agricultural operations of the crop were carried out from soil service and all crops from germination to maturity and then harvesting. The thermal collection was calculated by taking the daily temperatures (DD) from the beginning of the planting date until harvest, and the base temperature was retained as (4) for wheat and according to the following equation:

$$\text{GDD } \frac{(max.t+min.t)}{2} - base.temp.(0c)$$

Whereas:
GDD= Daily Temperatures
Max.t = Maximum Temperature
Min.t = Minimum Temperature
Base temp.(0c)= Base Temperature

The data was analyzed statistically using a computer using the ready-made SAS (Statistical Analysis System) program according to the design of the complete random sectors and the genetic averages were compared based on the multi-range Duncan test.

Results and discussion

Between Table (1) stages of branching according to the scale of Zadok variation of genetic structures in the values of branching, the genetic structure Sardar was the most number of branching, as the value of 1.20, unlike the genotypes Simito, Iraq Oasis, um Rabie and Icarasha2, as their peak reached 1.00 each for the stage of Zadok (21), but in the stage (22), the genetic structure was Lahnaucan, as its value was 4.20, unlike the genetic structure Guayacan, which reached its peak of 1.53 ,In stage (23), the genetic structures Lahnaucan and Sardar, with an average value of 7.40 and 7.10, respectively, may be the opposite of the Guayacan genotype, which reached a peak of 3.03, and in the stage (24), the genotypes may be Lahnaucan, Sardar and Fadda98, as they reached their peak of 8.46 and 7.83, respectively, opposite the genetic structure Guayacan, where it reached its peak of 3.93, but in the stage (25), the genotypes may be Fadda98, Lahnaucan and Sardar, with an average peak of 9.70, 9.60 and 9.90, respectively, unlike the genetic structure Guayacan. It peaked at 5.20، In stage (26) the genetic structure Sardar, where it reached a peak of 12.43, unlike the genotype Guayacan, Amedakuls and DW10, where their average peak reached 7.56, 7.60 and 7.26 respectively, the genetic structure Sardar has the most number of branches, as it reached a peak of 14.36, unlike the genetic structure DW10, where it reached a peak of 8.16 for stage (27), while in stage (28), the genetic structure Sardar has the most number of branches, as it reached a peak of 15.60, unlike the genetic structure DW10, where its peak reached 9.20 ،In the stage (29) genotypes Bejah-6/SLA and Sardar, where their peaks averaged 16.00 and 16.73 respectively, unlike the genotypes Icarasha and sham 5, where their peaks averaged 10.60 and 010.63 respectively, and it is noted in the table of genetic structures significant for the number of branches for each stage at the probability level 5%. This is consistent with [8].

Table (1) shows the number of branches of the genotypes for all stages.

Genotypes	Branching stage according to Zaddock scale								
	Stage 21	Stage 22	Stage 23	Stage 24	Stage 25	Stage 26	Stage 27	Stage 28	Stage 29
Dw38	1.10 b	2.33 c-f	4.23 fg	6.96 b	8.46 b	10.16 c-e	14.20 ab	14.66 ab	15.40 ab
Bejah-6/SLA	1.03 bc	2.46 c-e	4.93 d-f	6.16 b-e	7.23 cd	10.30 b-e	13.56 a-c	14.43 ab	16.00 a
Halio	1.10 b	2.56 cd	5.73 cb	6.43 b-d	8.00 bc	9.86 c-e	10.63 g-i	11.23 f-j	11.43 f-h
Mikki	1.03 bc	1.86 h	3.93 g	5.10 f-h	6.10 f-h	9.00 d-f	10.83 f-i	11.56 e-j	12.33 ef
Guayacan	1.03 bc	1.53 i	3.03 h	3.93 i	5.20 h	7.56 g	9.76 i	10.86 h-j	11.53 f-h
Amedakuls	1.03 bc	2.10 f-h	3.73 g	4.40 hi	5.50 gh	7.60 g	11.03 e-i	12.46 c-e	12.73 d-f
Fadda98	1.03 bc	2.46 c-e	6.26 b	7.83 a	9.70 a	11.16 bc	12.23 c-f	12.73 c-f	13.40 c-e
Icarasha 2	1.00 c	2.16 e-h	4.46 e-g	5.43 e-g	6.63 d-f	8.46 fg	9.90 hi	10.26 i-k	10.60 h
Sham5	1.06 bc	2.23 e-g	5.56 b-d	6.70 bc	7.53 b-d	8.93 ef	10.03 hi	10.20 jk	10.63 h
Lahnaucan	1.10 b	4.20 a	7.40 a	8.46 a	9.60 a	11.56 ab	12.80 b-d	13.26 b-d	14.16 b-d
Sardar	1.20 a	3.23 b	7.10 a	8.46 a	9.90 a	12.43 a	14.36 a	15.60 a	16.73 a
Bagdad	1.06 bc	2.63 c	4.70 ef	5.76 c-f	7.46 cd	10.36 b-d	12.80 b-d	13.66 bc	14.23 bc
DW10	1.06 bc	2.56 cd	5.06 c-e	5.53 d-g	6.20 e-g	7.26 g	8.16 j	9.20 k	10.83 gh
ACSAD 5	1.03 bc	2.00 gh	3.90 g	4.63 g-i	5.53 gh	9.43 d-f	11.33 d-h	11.93 d-h	13.10 c-e
Simito	1.00 c	2.43 c-e	5.00 c-f	6.13 b-e	7.16 c-e	9.63 d-f	10.96 e-i	11.73 e-i	12.66 ef
Crezo	1.03 bc	1.86 h	4.36 e-g	5.40 e-g	6.63 d-f	9.76 d-f	11.90 d-g	12.80 c-e	13.43 c-e
Corvilla	1.06 bc	2.40 c-f	5.06 c-e	6.00 c-f	6.90 d-f	9.03 d-f	10.83 f-i	10.96 g-j	12.13 e-g
Iraq Oasis	1.00 c	2.26 d-g	4.90 d-f	5.76 c-f	6.86 d-f	8.43 fg	11.00 e-i	12.20 c-h	14.30 bc
Sura Kul	1.06 bc	2.60 c	5.10 c-e	5.83 c-f	6.96 d-f	8.96 ef	11.16 e-i	12.00 d-h	13.40 c-e
um Rabi	1.00 c	2.10 f-h	4.76 ef	6.33 c-f	7.60 b-d	10.30 b-e	12.43 c-e	13.63 bc	15.53 ab

Table (2) shows the stage of elongation according to the Zadok scale, where the genetic structure surpassed Surat Kul at the first decade with an average of 80.00 days, unlike the genetic structure Sardar, as it averaged 69.00 days, while in the second decade, the genetic structure was Surat Kol, where its average peak was 86.66 days, unlike the genetic

structure Halio, Sardar, Simito and Crezo, with an average of 79.66, 79.00, 79.66 and 79.66 days, respectively .In the third decade, Surat Kol genotype, with an average of 92.66 days, reversed the genetic structure Halio, Amedakuls, Sardar, Simito, Crezo and um Rabie, with an average of 86.00, 86.33, 86.00, 86.00, 86.00 and 87.00 days, respectively, while in the fourth decade, the genetic structure Surat Kol, with an average of 99.33 days, reversed Simito, with an average of 91.00 days .In the fifth decade, the two genotypes Surat Kul and Fadda98, where the highest average number of days was 99.33 days, and the reverse of the genotype Bejah-6/SLA, where the lowest average number of days was 96.00 days, and it is noted in the table of significant genotypes for the number of days for the first, second, third, fourth and fifth decade at the probability level of 5%.[9].

Table (2) shows the genetic structures and the number of days required for the stages of elongation.

Genotypes	Elongation stage according to the Zaddock scale				
	First nodes	Second nodes	Third nodes	Fourth decade	Fifth decade
Dw38	74.00 fg	81.33 gh	89.00 d	96.33 ef	96.33 de
Bejah-6/SLA	74.33 f	81.66 gh	89.00 d	96.00 f	96.00 e
Halio	73.00 fg	79.66 i	86.00 e	91.33 hi	98.33 b
Mikki	76.00 e	82.66 fg	90.00 c	97.33 cd	97.33 bc
Guayacan	78.66 a-c	85.66 ab	91.66 b	98.33 b	98.33 b
Amedakul s	79.00 ab	84.00 c-f	86.33 e	96.33ef	96.33de
Fadda98	77.00 df	84.00 c-f	91.33 b	99.33 a	99.33 a
Icarasha 2	77.00 df	83.66 d-f	91.33 b	98.33 b	98.33 b
Sham5	77.33 c-e	84.00 c-f	91.33 b	97.66 b-d	97.66 bc
Lahnaucan	78.33 b-d	85.33 a-c	91.66 b	98.00 bc	98.00 bc
Sardar	69.00 h	79.00 i	86.00 e	91.66 hi	98.33 b
Bagdad	76.66 e	83.33 d-f	91.00 b	97.00 de	97.00 cd
DW10	77.33c-e	84.66 b-e	91.00 b	97.66 b-d	97.66 bc
ACSAD 5	77.33 c-e	83.33 ef	89.66 cd	97.66 b-d	97.66 bc
Simito	72.66 g	79.66 i	86.00 e	91.00 i	98.00 bc
Crezo	73.00 fg	79.66 i	86.00 e	92.00 h	98.33 b
Corvilla	78.33 b-d	85.33 a-c	91.33 b	98.00 bc	98.00 bc
Iraq Oasis	78.66 a-c	85.00 b-d	91.33 b	98.00 bc	98.00 bc
Sura Kul	80.00 a	86.66 a	92.66 a	99.33 a	99.33 a
um Rabi	74.00 fg	80.33 hi	87.00 e	93.33 g	98.33 b

Table (3) shows the studied traits that the genetic structures varied in the characteristics of the genetic structure um Rabie gave the highest value of the height of the plant as it reached a peak of 83.82 cm, unlike the genetic structure of the oasis of Iraq gives the lowest peak, as its peak reached 68.59 cm [10],[11], either in the characteristic of the area of the flag paper, we note the genetic structure Mikki and Crezo gave the highest value, as their peak reached 42.35 and 42.18, respectively, and the opposite of the genetic structure Corvella and Amedakuls, as it reached Their averages are 33.14 and 32.81 respectively [12],[13].

Table (3) shows the effect of genotypes on vegetative growth traits.

Genotypes	Studied qualities							
	Plant height (cm)	Flag leaf area (cm^2.sheet^{-1})	Chlorophyll content of flag leaf	Number of total shoots (1 sheet)	Number of active shoots (1 sheet)	50% Expel Sanabel	Number of days for number of branches	
							Number of days	Number of branches
Dw38	79.70 fg	40.20 c-f	43.54 cd	426.88 ij	353.62 i	121.33 de	106.66 b-e	15.40 ab
Bejah-6/SLA	80.25 e-g	39.14 e-g	35.13 k	444.23 hi	394.36 g	120.66 ef	105.33 f-h	16.00 a
Halio	82.03 bc	38.22 g	41.36 f	482.47 fg	443.63 d	118.00 g	106.33 c-f	11.43 f-h
Mikki	73.38 k	42.35 a	38.84 ij	468.92 g	414.85 f	122.00 cd	107.66 ab	12.33 ef
Guayacan	73.87 k	39.82 d-f	39.30 hi	495.92 ef	428.22 e	123.33 ab	107.00 a-d	11.53 f-h
Amedakuls	76.69 i	32.81 i	45.08 b	378.84 kl	324.90 j	120.66 ef	108.00 a	12.73 d-f
Fadda98	81.46 b-e	38.44 g	40.89 fg	361.60 lm	322.77 j	121.66 d	105.66 e-h	13.40 c-e
Icarasha 2	78.09 h	39.85 d-f	42.84 de	506.77 de	455.68 d	120.66 ef	105.33 gh	10.60 h
Sham5	81.10 c-e	41.95 ab	40.90 fg	438.20 hi	357.70 i	122.66 bc	106.33 c-f	10.63 h
Lahnaucan	78.04 h	39.40 e-g	38.19 j	501.02 de	455.26 d	123.00 ab	104.33 h	14.16 b-d
Sardar	80.74 d-f	39.23 e-g	41.17 f	583.20 a	526.37 a	116.66 h	103.00 i	16.73 a
Bagdad	80.52 ef	40.81 b-d	43.33 c-e	526.45 c	491.52 b	121.33 de	106.00 d-g	14.23 bc
DW10	81.90 b-d	40.35 c-e	40.14 gh	411.47 j	356.66 i	122.00 cd	107.66 ab	10.83 gh
ACSAD 5	80.80 d-f	36.99 h	43.01 c-e	517.02 cd	470.35 c	123.00 ab	106.66 b-e	13.10 c-e
Simito	79.20 g	41.37 a-c	39.10 ij	369.44 k-m	313.03 j	123.33 ab	107.66 ab	12.66 ef
Crezo	75.57 j	42.18 a	33.28 l	353.52 m	314.64 j	123.66 a	107.33 a-c	13.43 c-e
Corvilla	80.81 d-f	33.14 i	47.28 a	558.31 b	479.90 bc	117.66 g	107.00 a-d	12.13 e-g
Iraq Oasis	68.59 l	39.09 fg	42.52 e	382.07 k	315.11 j	120.00 f	107.00 a-d	14.30 bc
Sura Kul	82.46 b	36.93 h	38.52 ij	445.54 h	381.52 h	122.00 cd	108.00 a	13.40 c-e
um Rabi	83.82 a	40.65 cd	43.85 c	476.88 g	398.59 g	122.66 bc	106.66 b-e	15.53 ab

In the characteristic of chlorophyll content, the genotype Corvella gave the highest value, reaching 47.28, unlike the genetic structure crezo, giving the lowest peak, reaching a peak of 33.28, while in the characteristic of the total number of fragments, the genetic structure Sardar, which reached a peak of 583.20, unlike the genotype Crezo, as it gave the lowest value, reaching a peak of 353.52 [14],As for the number of active fragments, the Sardar genotype gave the highest value, reaching a peak of 526.37 branches, unlike the genotypes Amedakul S, Fadda98, Simito, Crezo and the oasis of Iraq gives the lowest peak, with their values reaching 324.90, 322.77, 313.03, 314.64 and 315.11 respectively. The Crezo genotype gave the highest rate of 50% spikes with a peak of 123.66 days, unlike the Sardar genotype gave the lowest value of 116.66 days for this trait [15] , while in the number of days for the number of branches, the genotype Bejah6/SLA and Sardar gave the highest value for the number of branches, as their values reached 16.00 and 16.73 and needed 105.33 and 103.00 days respectively, unlike the genotype Icarasha 2 and Sham5 gives the lowest peak, as their values reached 10.60 and 10.63 and needed 105.33 and 10.6.33 days respectively, The table shows the significant genetic structures of the studied traits at the probability level of 5%.

Table (4) shows the values of thermal collection and notes in it from planting until the end of the season and the plants needed to enter the branching stage to the accumulated heat of 379.0 m0 while the plants of all genotypes entered the stage of the maximum number of branches requiring thermal collection 707.0 m0, and thermal collection required to complete the elongation stage 635.5 m0. [16].

Table (4) shows the temperatures for the growing months.

Months	Daily cumulative temperatures					Total
November	12.0	10.5	10.0	9.0	9.5	176.5
	13.0	12.0	12.0	11.0	10.5	
	11.0	10.5	10.5	11.0	11.5	
	12.5					
December	13.5	5.5	55.	6.5	8.0	202.5
	10.0	9.5	12.5	8.5	8.5	
	7.0	6.5	6.5	6.5	11.0	
	11.0	9.0	7.5	7.5	8.5	
	4.5	1.5	4.0	2.5	1.0	
	2.0	1.5	3.5	4.5	4.0	
	4.5					
January	4.5	3.5	3.0	2.0	3.5	116.0
	2.0	4.0	4.0	5.5	7.5	
	8.5	9.0	8.5	8.0	4.5	
	2.5	0.5	-1.0	0.5	5.0	
	3.5-	3.5-	-1.0	4.5	5.5	
	4.5	4.5	2.5	1.5	2.5	
	2.0					
February	4.5	4.5	6.0	7.5	4.5	212.0
	4.0	4.0	4.0	6.5	7.5	
	6.0	7.5	8.0	8.0	6.5	
	7.0	8.0	8.5	12.5	7.5	
	8.0	11.5	10.5	11.5	11.5	
	9.0	8.5	9.0			
March	9.5	12.5	11.5	11.0	5.5	236.5
	4.5	8.5	8.0	7.5	8.5	
	8.5	5.5	6.0	8.5	4.5	
	1.5	3.5	4.5	7.5	4.5	
	4.0	9.0	12.5	7.5	8.0	
	6.5	8.0	6.0	10.0	11.5	
	12.0					
Aprile	14.0	16.5	20.0	17.0	17.0	472.5
	16.5	19.0	19.0	16.0	9.5	
	19.5	16.0	11.5	10.0	11.5	
	13.5	15.0	18.5	19.0	20.5	
	16.0	10.0	17.0	18.5	18.5	
	10.0	9.0	18.5	19.5	16.0	
May	19.0	15.5	17.0	21.5	18.5	604.5
	16.0	7.0	9.0	9.0	16.0	
	17.5	17.5	16.5	19.5	21.5	
	21.0	21.5	22.0	23.5	23.5	
	20.5	21.0	20.5	21.5	19.5	
	21.5	24.0	27.0	22.5	27.5	
	26.5					
June	29.0	30.0				59.0

References

[1] Zadoks , J.C. , T. T.T. Change , and C.F. Knozak . 1974. A decimal code for growth stages of cereals. Weed Res., 14 : 415-421.

[2] Food and Drug Administration, (1996). Code of Fedral Regulation, Titk 21 Ch.1, sub part B, Part 139, resvised Aprils U.S. Govermment Printing Office, Washington, D.C.

[3] Awwad, Haifa Ali.2000. A study of the relationship between physical and chemical properties and qualitative characteristics of some Iraqi wheat cultivars. Master Thesis. faculty of Agriculture. Baghdad University. Department of food industries.

[4] California wheat commission. 2001. Description of durum semolina quality factors. P.O. Box 2267, woodland CA 9577-2267 (530) 661-1292Fax: (530) 661-1332. E-mail: info@california wheat. org.

[5] Evres, J.B., J. Vos, C. Fournier,B. Andrieu., M. Chelle., P.C Struik, (2004). A3D Approach for modeling tillering in wheat (*Triticum aestivum*-L). 4TH International Workshop on functional structural plant models, 7// June -Montpellier,France:210-215.

[6] Al-Fahdawi, Hamada Musleh Matar and Muhammad Hamada Musleh (2018). Testing the Susceptibility of Soft Wheat Genotypes to Formation of Stem, Iraqi Journal of Desert Studies, 7801-1994 : ISSN 20188: (1) 8, 1-5.

[7] Oakes, J., R. Heiniger, C. Crozier, J. Murphy, and G. Wilkerson.(2016). Phyllochron interval and yield responses to planting date and fertility in wheat. Crop, Forage, & Turfgrass Manage. 2:2016-03-0026. Doi:10.2134/cftm 2016 .03 .0026.

[8] Al-Jubouri, Jassem Muhammad Aziz and Tariq Raad Thaer Al-Mafarji (2020). Pattern and branching ability of fifteen cultivars of bread wheat (Triticum aestivum L.) and their relation to grain yield. Kirkuk University Journal of Agricultural Sciences, Volume (11) Issue (4) 2020.

[9] Asaoud, Abd Al-Razzaq, Mamoun Khaiti, Osama Al-Shablaq, and Sana Al-Suleiman (2019). Effect of drought on some morphological traits and grain yield of genotypes of durum wheat (Triticum durum L.). Syrian Journal of Agricultural Research 6(1): 151-167

[10] Al-Ajabi, Nasser Abdel-Hassan Dahash (2014). Response of genotypes of durum wheat (Triticum durum Desf.) to sowing dates. Master's thesis - College of Agriculture - Al-Muthanna University.

[11] Hussein, Muhammad Ali, Murad Jan Muzaffar, and Rizan Issa Musa (2020). Yield and its components for coarse wheat grown under different levels of irrigation and nitrogen fertilizer. Kirkuk University Journal of Agricultural Sciences, 2020, Volume 11, Issue 4, Pages 136-149.

[12] Al-Khattab, Imad Muhammad (2011). Evaluation of the productive efficiency of some inputs of durum wheat (Triticum (Durum L) in rain-fed conditions in the central region of Syria. Al-Rafidain Agriculture Journal, 39 (4): p. 11.

[13] Al-Samarrai, Anis, Reem Subhi Kazem, and Ahmed Hawas Abdullah (2020). Determination of zinc nanoparticle requirements for durum wheat (Triticum durum Desf). Kirkuk University Journal of Agricultural Sciences 2020, Volume 11, Issue 4, Pages 101-113.

[14] Al-Kikani, Khalil Ibrahim Khalil, Fakhr Al-Din Abdul Qadir Siddig and Ahmed Salih Khalaf (2021), Effect of seed size and estimation of seeding rate using different equations on the vegetative growth characteristics of two cultivars of bread wheat (Triticum aestivum L). Kirkuk University Journal of Agricultural Sciences, 2021, Volume 12, Issue 1, 163-177.

[15] Shi, C., Zhao, L., Zhang, X., Lv, G., Pan, Y., and Chen, F. (2019). Gene

regulatory network and abundant genetic variation play critical roles in heading stage of polyploidy wheat. BMC Plant Biology, 19(1): 1-16.

[16] Al-Hassan, Muhammad Fawzi Hamza (2007). The pattern and ability of branching of five varieties of wheat influencing the planting date and its relationship to grain yield and its components, a master's thesis submitted to the Council of the College of Agriculture at the University of Baghdad.

دراسة التجميع الحراري لصفات النمو في مرحلتي التفريع والاستطالة لمجموعة من التراكيب الوراثية في الحنطة الخشنة (*Triticum durum* Desf.)

نياز فارق رضا [1]
niaz.farq@gmail.com

خالد خليل احمد [2]
Khalid_khalil@uokirkuk.edu.iq

[1] ق

[1] قسم المحاصيل الحقلية، كلية زراعة، جامعة كركوك، كركوك، العراق.

[2] قسم النباتات الطبية والصناعية، كلية زراعة– الحويجة، جامعة كركوك، كركوك، العراق

• تاريخ استلام البحث 30/03/2023 وتاريخ قبوله 19/04/2023

المستخلص

أجريت هذه الدراسة في موسم الزراعي 2021–2022 في محطة البحوث والتجارب الزراعية (منطقة الصيادة) العائدة لكلية الزراعة في جامعة كركوك، باستخدام تصميم القطاعات العشوائية الكاملة (R.C.B.D) وبثلاث مكررات تضمت كل قطاع عشرون وحدات تجريبية هي بعدد التراكيب الوراثية من الحنطة الخشنة هي (Bejah–6/SLA،DW38، Halio، Mikki، Guayacan، Amedakul s، Fadda98، Icarasha 2، 5 Sham،Lahnaucan Sardar ، بغداد، DW10، اكساد5، سيميتو،Crezo، كورفيلا،واحة العراق، سورة كول، ام ربيع) حيث أظهرت النتائج وجود فروق معنوية بين التراكيب الوراثية عند مستوى الاحتمال 5% لعدد الافرع ومرحلة الاستطالة ، ووجود فروق معنوية بين التراكيب الوراثية عند مستوى الاحتمال 5% لصفات المدروسة ، حيث تفوق التركيب الوراثي Sardar لصفة (عدد الاشطاء الكلية، عدد الاشطاء الفعالة، عدد الايام لعدد التفرعات، 50%الطرد السنابل) بأعلى المتوسط اذ بلغ متوسطهم (583.20فرع،526.37فرع ،103.00يوم، 16.73فرع، 116.66يوم) واعلى متوسط لعدد الافرع في مرحلة (Z21و Z23و Z24و Z25 و Z26و Z27و Z28و Z29)حيث بلغ متوسطهم (1.20، 7.10، 8.46، 9.90، 12.43، 14.36، 15.60، 16.73) وتفوق التركيبين الوراثين Mikki و Crezo لصفة مساحة ورقة العلم بأعلى المتوسط اذ بلغ متوسطهم (42.35، 42.18)على التوالي بينما التركيب ام ربيع بأعلى متوسط لارتفاع النبات حيث بلغ متوسطها 83.82 والتركيب الوراثي كورفيلا بأعلى متوسط لمحتوى الكلوروفيل لورقة العلم حيث بلغ قمته 47.28 والتركيب الوراثي Lahnaucan يعطي اعلى متوسط لعدد الافرع في مرحلة (Z22 و Z23و Z24و

Z25)حيث بلغ متوسطهم (4.20، 7.40، 8.46، 9.60) والتركيب الوراثي Fadda98 اعطى اعلى متوسط لعدد الافرع في مرحلة (Z24 وZ25) حيث بلغ متوسط هم (7.83 ، 9.70) والتركيب الوراثي–Bejah 6/SLAيعطي اعلى متوسط لعدد التفرع في مرحلة (Z29) حيث بلغ متوسطه (16.00) وتفوق التركيب الوراثي سورة كول في مرحلة الاستطالة (لعقد الاول والعقد الثاني والعقد الثالث والعقد الرابع والعقد الخامس) اعلى متوسط في عدد ايام حيث بلغ (80.00 و86.66 و92.66 و99.33 و99.33) والتركيب الوراثيFadda98 في (عقد الرابع والخامس) اعلى متوسط في عدد ايام حيث بلغ (99.33)، احتاجت النباتات للدخول في المرحلة التفريع الى الحرارة المتراكمة قدرها 379.0 م^0 بينما دخلت نباتات جميع التراكيب الوراثية الى مرحلة اقصى عدد من الفروع تطلب التجميع الحراري 707.0 م^0، وتطلب التجميع الحراري لاكتمال المرحلة الاستطالة 635.5 م^0.

كلمات مفتاحية: التجميع الحراري، الحنطة الخشنة، التفريع والاستطالة.