Performance of Newly Improved Bread Wheat (*Triticum aestivum* L.) Genotypes in Multi-Environments of Iraqi Kurdistan Region

Mohammed A. Hussain[1], Fathi A. Omer[1]* and Abed A. Hassan Al-Doski[2]

[1] Department of Field Crops, College of Agricultural Engineering Sciences, University of Duhok, Kurdistan Region, Iraq; dr.mohammedali1953@uod.ac; fathiemenky@uod.ac

[2] Department of Agricultural Extension and Rural Development, College of Agricultural Engineering Sciences, University of Duhok, Kurdistan Region, Iraq; abid.ali@uod.ac

* Correspondence: fathiemenky@uod.ac

Abstract

This study was carried out to study fifteen new genotypes of bread wheat in multi-environments, the seed of these genotypes were sown at three different locations, the first at the field of the College of Agricultural Engineering Sciences, University of Duhok, the second location at the Zenawa and the third location at the Zakho, the date of planting was in the end of November under rainfall conditions. The planting was in three lines for each genotype, with 3m and 0.25m between lines. In each location, the experiment includes fifteen genotypes using a Randomized Complete Block Design with three replications, the data recorded on plant height, flag leaf area, spike length, number of seeds per spike, seed weight in spike, 1000-seed weight, and grain yield. The results showed that the combined analysis across three locations, the mean square due to locations exhibited a significant effect of plant height (**684.91), lead area (**192.42), heading dates (**2011.82), spike weight (**0.18), number of seeds per spike (**39.42), 1000-seed weight (**41.60), and final grain yield (**43.25). Also, the bread wheat genotypes gave a significant effect for all traits, indicating high variation among genotypes. Regarding to interaction between genotypes and locations, the result exhibited a significant effect on all traits. The genotypes 2, 5, and 12 gave the highest yield and the most yield components, genotypes 1, 2, 3, 13, 14, and 15 were moderate in their stability, while genotypes 7, 8, and 9 were highly responsive to environmental changes.

Keywords: Bread wheat, stability, genotypes, yield.

Introduction

Wheat is one of the most important crops and is a stable food for many countries of the world, including Iraq. The seed of bread wheat is still a main source of food for more than 35% of the world’s population [14]. To meet the growing demand of our population, wheat production and productivity must be increased [12]. Wheat breeders are required to renew the varieties that have good stability for yield and other agronomic traits, as planting the same varieties decreases the productivity over time. Environmental conditions, including biotic and abiotic factors are unstable from one agricultural season to another, as well as across various locations, and thus affect the stability performance of bread wheat genotypes [3]. Information about phenotypic stability is useful for the selection of genotypes in a

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breeding program. Plant breeders encounter genotype x environment interaction (G x E) when testing different genotypes across several environments [9]. Wheat grain yield and its components with other traits depend in terms of their performance on the nature of the genotype, environmental conditions, and the interaction of genotype with environment [8].

The evaluation of promising genotypes across various environments when applied breeding programs, the interaction of genotypes x environment leads to selecting superior genotypes, understanding the interaction of these factors and how they affect grain yield is crucial for maintaining high yield [15] emphasized the role of G x E interaction in stability analysis of wheat and defined the genotypes was stable if has high mean yield related with low fluctuation under differ environments. These are different methods (parametric and non-parametric) used to measure stability by modeling the G x E interaction. Baker indicated that the result of instability among genotypes from one environment to another maximizes as a result of the method of expression of different environments or the difference in the responses of the same group of genes to different environments. The stability of grain yield across genotypes can be characterized by a linear response to environmental advantages and the extent of deviation from that response [13]. According to the method proposed by [7], the stability of yield and yield components from other traits can be described by the pooled variance analysis using the regression coefficient. Different parametric stability models are variable, such as the environment variance (Si^2), coefficient of variance (CV), and superiority index (Pi), Wicks eco-valence (W^2i), regression and approach (bi), and deviation from regression (S^2di). [10] recommended that the S^2di, W^2i, σ^2 and CV should be used concurrently to estimate the stability effect. Hence, this study was suggested to estimate the grain yield stability of 15 bread wheat genotypes in the Kurdistan region, Iraq, using some stability parametric measurements.

Materials and Methods

Fifteen genotypes of bread wheat (*Triticum aestivium* L.) were adopted in the current study (Table 1). The seeds of these genotypes were sown at three locations, the first at the field of the College of Agricultural Engineering Sciences, University of Duhok (Duhok), the second location at Zenawa (located 85km east of Duhok), and the third location was Zakho (located 75km west of Duhok), the date of planting was on November 25 under rainfed conditions. Data in Table 2 show the amounts of rainfall (mm) and their distribution through the growing season in the three locations. The field soil was prepared by plowing with a moldboard plow twice and perpendicularly, then smoothing, levelling, and planning, operations were carried out for each location.

The planting was in three lines for each genotype with 3m length and 0.25m between lines. Compound fertilizer (NPK, 20:20:20) was added at the rate of 120kg per hectare during land preparation before planting, and urea fertilizer (N% 46) at the rate of 160kg per hectare in two periods, the first in the tillering stage and the second before flowering. In each location, the experiment includes 15 treatments using a Randomized Complete Block Design with three replications. Weed control was carried out with the Topic pesticide for narrow-leaved and Granstar for broad-leaved at 3-4 leaves-stage for both types of weeds with the scientifically recommended dosages for each pesticide. Data were recorded on plant height(cm), flag leaf area (cm^2), spike length(cm), number of seeds per spike, seed weight in spike (g), 1000-seed weight, and grain yield (ton per hectare), accordingly, each in their optimal stage. A combined analysis of variance for genotype data across location was performed according to the method of experimental design, as well as an analysis of variance of genotypes across environment (fifteen genotypes and three environments). Differences among the means of genotypes and the three environments were compared by Duncan's Multiple Range Test method [2]. The phenotypic variance components and broad-sense heritability (HBs) were estimated in the manner indicated by [4] from the equation:

$$\mathrm{Hbs} = \emptyset\mathrm{g}/\emptyset\mathrm{pH} =$$

$$\emptyset\mathrm{g}/(\emptyset\mathrm{g} + \emptyset\mathrm{gL}/\mathrm{L} + \emptyset\mathrm{gd}/\mathrm{d} + \emptyset\mathrm{gLd}/\mathrm{Ld} + \emptyset\mathrm{e}/\mathrm{Ldr}$$

Where $\emptyset g$ total genetic variance, $\emptyset pH$ phenotypic variance, $\emptyset gL$ variance of genotypes with location, $\emptyset gd$ variance genotypes with planting interaction, $\emptyset gLd$ variance of genotypes with locational planting, $\emptyset e$ environmental variance, L number of location, d number of dates and r number od replications, as well as, the expected genetic advance in the next generation as percentage of the trait mean was estimated. To test the fifteen genotypes at different environments adopted in the study, the linear regression model proposed by [5] was used, namely:

$$yij = M + bilj + \sigma ij + eij$$

where yij refer to the mean genotype (i) in the environment (j) and bi is the regression coefficient of genotype (i) at the specific environmental index, which means the response of the genotype to environmental change, Ij is the environmental index, which is defined as the deviation of the mean of the all genotypes in a specific environment from the general mean, σij the deviation from the regression for genotype (i) at σijal j and eij the mean expected error.

Table 1. Cross and source of bread wheat used in this study

Source	Cross	Entry No.
ISBW17S-TR-0598-0TR-0TR-7MR-0MR	QAFZAH-19/VEE7/KAUZ/3/KEKEBA/5/SERI.1B//KAUZ/HEVO/3/AMAD/4/KAUZ/GY S//KAUZ	1
ISBW17S-TR-0125-0TR-0TR-4MR-0MR	UTIQUE 98/FLAG-1//SR 22/CO 1213/7/SERI.1B//KAUZ/HEVO/3/AMAD/4/PYN/BAU//MILAN/5/OPATA/RAY ON//KAUZ/6/SR 50+SR 45# 1/8/TERBOL/9/DEBEIRA//MILAN/PASTOR/4/URES/BOW//OPATA/3/HD22	2
ISBW17-TR-0019-0TR-0TR-7MR-0MR	KHIDER/5/NEJMAH-6/PAVON SR 24+ SR 26+SR	3

	31/4/ATTILA/TNMU//TNMU/3/SR 33+SR 45 #36	
ISBW17-TR-0068-0TR-0TR -5MR-0MR	ACHTAR 5/SERI. 1B*2/3/KAUZ*2/BOW/KAUZ/4/TEVEE'S/BOBWHITE #1	4
ISBW14T-205-0SD-010KU-3KUL-0KUL	QAFEDU	5
ISBW17-TR-1051-0TR-0TR -7MR-0MR	MILAN/KAUZ//PRINIA/3/BAV92/4/BAVIS/6/PREMIO/5/CROC_1/AE.SQUA RROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2	6
ISBWS18-TR-0057-0TR-0TR-8TR-0TR	QAFZAH- 18//P1.861/RDWG/4/HUIRIVIS #1*2/MURGA/3/TACUPETO F2001/BRAMBLING*2//KACHU	7
ISBWS18-TR-0919-0TR-0TR-5TR-0TR	ALTAR 84/AE. SQUARROSA (JBANGOR)//ESDA/3/HEILO/5/CNO79//PF70354/MUS/3/PASTOR/4/BABAX/7/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI/5/PAVON SR 24+ SR 31+SR 50/6/05W90045 U.S.A.-08CJ/PAVON SR 24+ SR 26+SR 31/8/PBW343/ETBW 4921//QAMAR-6/9/KACHU #1/YUNMAI 47//KACHU/5/SAUAL/3/C80.1/3*BATAVIA//2*WBLL2/4/SITE/MO//PASTOR/ 3/TILHI/6/KACHU #1/KIRITATI//KACHU	8
ISBW17-MR-18-0KUL-8MR-0MR	ATTILA*2/PBW65//PFAU/MILAN/3/HUBARA-3*2/SHUHA-4	9
ISBWS18-TR-0058-0TR-0TR-5TR-0TR	QAFZAH-18//P1.861/RDWG/3/BECARD/AKURI//WAXBI	10
ISBW17-TR-0020-0TR-0TR -3MR-0MR	KHIDER/4/P1.861/RDWG//ESWYT99#18/ARRIHANE/3/PFAU/MILAN	11
ISBWS18-TR-0188-0TR-0TR-6TR-OTR	KAUZ//ALTAR 84/AOS 3/KAUZ/3/ATENA-1/4/FLAG-7/5/KFA/2*KACHU/3/KINGBIRD #1//INQALAB	12

	91*2/TUKURU/4/KFA/2 KACHU	
ISBW17-TR-0028-0TR-0TR -1MR-0MR	DANDA/4/P1.861/RDWG//ESWYT99#18/ARRIHANE/3/PFAU/MILAN	13
ISBW17-TR-1043-0TR-0TR -5MR-0MR	PFAU/MILAN/3/BABAX/LR42//BABAX*2/4/NIINI #1/5/DANDA	14
Cihan-3 variety	Local check	15

Table 2. Rainfall data for Duhok, Zakho, and Zinawa districts from November 2023 to June 2024.

Zinawa (mm)	Zakho (mm)	Duhok (mm)	Month
56	75	80	November 2023
51	90	95	December 2023
56	110	165	January 2024
65	85	100	February 2024
75	126	120	March 2024
24	32	40	April 2024
25	29	55	May 2024
2	1	3	June 2024
354	548	658	Total

* Rainfall data were recorded at the meteorological station at each location.

Results and Discussion

The results listed in Table 3 show the combined analysis across the three locations. Mean square due to locations or environments exhibited a significant effect for PH, LA, SL, HD, SSW, NSS, 1000-SW, and TGY/ha; also, the bread wheat genotypes gave a significant effect on all eight studied traits. From the results in the same table, high variations among genotypes were also indicated.

Regarding the interaction between genotypes and locations, the results demonstrated that seven traits (PH, LA, SL, HD, NSS, 1000-SW, and TGY), except SSW, gave a significant difference at 5% probability. This means that the genotypes of bread wheat behaved differently according to the three locations. Also, it is noted from Table 2 that the total amount of rainfall varied between locations and from one month to another, especially in the last months of 2024. [16] reported that highly significant differences among bread wheat genotypes were observed for the most studied traits when studying different genotypes of wheat across different locations.

Table 3. Combine Variance Analysis of genotypes planted across three locations.

Traits								df	Source
TGY t/ha	1000SW (gm)	N.S.S	SSW (gm)	H.D	SL (cm)	L.A (cm^2)	PH (cm)		
**43.25	**41.60	**39.42	**0.18	**2011.82	**31.20	**192.42	**684.91	2	Locations
*0.28	3.62	1.93	0.01	2.30	0.53	0.79	1.94	6	Rep. Loc.
**18.80	**60.25	**474.51	**1.03	***52.53	**8.54	*129.75	**558.60	14	Genotypes (G)
**0.66	**24.60	**33.84	*0.16	**1.48	**2.50	**45.05	**103.80	28	L x G
0.09	2.27	0.73	0.01	0.70	0.38	0.51	1.47	84	Error
								134	Total

Where: (*) (**) significant at 5% and 1% probability, G; Genotypes; Loc.; Locations; PH- plant height; L.A- leaf area (cm^2); SL- spike length (cm); H.D- heading dates; SSW-seed per spike weight; N.SS- number of seeds per spike; 1000-SW- 1000 seed weight (g) and GTY- total grain yield (t/ha).

The reflection of the analysis of variance results is noted on the comparison between the means of genotypes as an average for the three locations (Table 4) and the mean of the three locations as an average of genotypes (Table 5). For plant height, the G6 recorded the longest plant height (96.0 cm), followed by G13 and G11 with values 94.11 and 91.33cm respectively, while the shortest genotypes were found in G4 (70.44 cm), indicating that high variation between genotypes used in this experiment . For leaf area, 23% was increased when comparing G5 with the local variety G15, this reflected in the yield and some components. The results in the same table indicated that the G2 recorded the longest spike length (12.0 cm), while the shortest spike length was found in the local variety (8.55 cm), with an increase of 24% when comparing G5 and G15. As for days to maturity, the shortest day to maturity was recorded for the G5, which gave the minimum days to maturity (195.44 days) while the longest value for this trait was obtained by G9, with a value of 203.22 days, and early percent maturity reaching 3%. Regarding spike weight, the G2 gave the maximum value 2.38g, followed by G6 with a value 2.17g, while the lowest value was found in G8 with a value 1.30g. For the number of seeds per spike, genotype G2 gave the highest value (58.44 seeds per spike) for this trait, while genotype G8 had the lowest value (34.44), increasing by 21% in comparison with the local variety. From the results in the same table, the genotype G12 recorded the maximum value of 1000-grain weight (43.0g), while the minimum value (34.33g) was recorded by genotype G11, but when compared with the local variety, the genotype 12 gave an increase of 10%. The results in Table 4, also evident that genotype 6 produced the highest grain yield per hectare (11.56 t.ha^{-1}) followed by genotypes 2 and 5 with values 11.36 and 11.26 t.ha^{-1} respectively. The genotypes increased over the general mean by 21%. From the results from the same table, the genotypes 6, 2, and 5 surpassed the others in this study.

Table 5 exhibited the studied traits across three locations; the Duhok location was surpassed in all studied traits (plant height, leaf area (cm^2), spike length (cm), spike weight (g), number of seeds per spike, 1000-seed weight, and total grain yield (t.ha^{-1}) except days to maturity. This may be due to the fact that the amount of rainfall in the Duhok location was more than in others, in addition to the amount of rainfall in May in the Duhok location being more than Zakho and Zinawa locations (Table 2).

Table 4. Mean of genotypes for studied traits.

Traits								Genotypes
Yield (t/ha)	1000-grain weight (g)	No. of seed spike	Spike weight (g)	Maturity days	Spike length (cm)	Lead area (cm^2)	Plant height (cm)	
7.49 f	41.22 bc	51.55 de	2.15 bc	197.66 f	9.66 hi	39.85 ed	79.22 i	G1
11.36 a	41.0 bc	58.44 a	2.38 a	201.55 c	12.0 a	46.91 b	89.66 d	G2
9.35 c	40.11 cd	53.66 c	2.15 bc	198.55 e	9.55 hi	39.23 ef	85.44 f	G3
7.56 f	39.11 def	55.22 b	2.04 c	202.11 bc	8.88 jk	39.10 ef	70.44 m	G4
11.28 a	41.66 ab	51.55 de	2.15 bc	195.44 g	11.22 bc	48.47 a	81.55 h	G5
11.56 a	42.0 ab	51.11 ef	2.17 b	201.44 c	10.77 cd	38.92 f	96.0 a	G6

7.76 f	39.33 de	50.55 f	2.08 bc	197.77 ef	10.55 de	40.01 d	75.88 j	G7
9.33 c	37.66 fg	34.44 j	1.30 f	202.22 bc	10.11 e-h	37.45 h	87.22 e	G8
8.13 e	37.77 efg	56.0 b	2.19 bc	203.22 a	9.44 ij	34.18 i	83.55 g	G9
9.44 c	38.77 def	41.11 i	1.73 d	201.88 bc	9.88 e-h	39.63 edf	73.11 L	G10
8.52 d	34.33 h	49.0 g	1.59 e	202.55 ab	9.77 ghi	38.18 g	91.33 c	G11
10.66 b	43.0 a	48.88 g	2.12 bc	197.55 f	11.77 ab	45.42 c	89.33 d	G12
7.68 f	36.88 g	33.77 j	1.24 f	199.88 d	10.33 e-g	39.80 ed	94.11 b	G13
8.44 d	34.33 h	50.44 f	1.73 d	202.11 bc	10.44 edf	39.51 edf	86.77 e	G14
8.66 d	38.77 def	45.88 h	1.78 d	202.55 ab	8.55 k	37.28 h	74.44 k	G15

*The mean values followed by the same letter for each trait are not significantly different from each other.

Table 5. Mean of studied traits across three locations.

Traits								Locations
Yield t.ha^{-1}	1000-grain weight (g)	No. of seeds per spike	Spike weight (g)	Maturity days	Spike length (cm)	Lead area (cm^2)	Plant height (cm)	
10.13 a	39.86 a	49.82 a	1.97 a	194.2 c	10.86 a	42.64 a	97.33 a	Location 1 (Duhok)
9.15 b	38.00 c	47.97 b	1.84 b	199.4 b	9.26 c	39.26 b	81.17 b	Location 2 (Zakho)
8.17 c	39.33 a	48.62 b	1.93 a	207.5 a	10.46 b	38.88 b	73.11 c	Location 3 (Zinawa)

The mean values followed by the same letter for each trait are not significantly different from each other.

Table 6 shows the combined analysis of variance of the data for eight traits of fifteen bread wheat genotypes planted in the three locations. The results indicated that the mean squares of genotypes and locations were significant for all studied traits except PH, SL, TGY/ha, and significant for HD in the case of genotypes. Also, the mean square for interaction of genotypes with locations exhibited non-significant for all studied traits except HD, that indicated the same in the behavior for the all genotypes according to the different locations in which they grow; the locations linear for all studied traits except SL and TGY/ha, while the interaction of location and genotypes exhibited linear but non-significant for studied traits except HD and NSS. These results agree with those of [1] but differ from what some researchers have found, such as [8,15].

Table 6. Results of the combined analysis of genotypes planted for three locations.

Traits								df	Source
TGY t/ha	1000SW (gm)	N SS	SW (gm)	HD	SL (cm)	L.A (cm^2)	PH (cm)		
1.34	7.14	**73.93	*0.14	4.84	1.30	*18.10	77.89	14	Genotypes
1.04	**38.41	**307.42	**0.79	*24.49	0.01	**82.46	144.03	2	Environment (Locations)
**2.15	4.72	18.02	0.04	*4.83	0.81	6.90	43.51	28	Geno. x En.
2.08	6.97	37.31	0.09	6.14	0.76	11.94	50.21	30	En + Geno. x En.
2.08	**76.82	**614.84	**1.59	**48.98	0.03	**164.93	*288.05	1	En. Linear
1.22	5.14	**28.40	0.04	*8.13	0.78	5.44	27.37	14	Env x gen line
2.88	4.02	7.13	0.04	1.42	0.79	7.81	55.68	15	Pooled deviation
0.41	8.70	11.20	0.05	1.02	1.09	12.01	31.67	84	Pooled error

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

Table 7 shows the interaction effects between the three locations and fifteen genotypes. Regarding plant height (PH), the L2 × G13 combination recorded the maximum value of 110.88 cm, whereas genotype G10 exhibited the minimum value., 65.66cm, across locations . Also, the results in the same table, the G5 had the highest value, 57.43cm^2 at location one, and G10 gave the lowest value, 33.33cm^2 at location three. For SL, the G5 had the maximum value of 12.66cm at location one, where the G4 had the minimum value of 7.0cm at location two. Regarding M.D, the G5 was the earliest among genotypes used in this study and gave 188.66 days at location one, while the G15 had the latest for this trait with a value of 210.33 days at location three. This means that the G5 is earlier by 10% compared to the G15. For S.W., the G9 recorded the maximum value of 2.53g, and G13 recorded with value of 1.10g at location two. ForN.SS, the G9 gave 60.33 at location one, whereas the G13 had a minimum value of 32.66 at location two. From these results, G9 appears to be superior in two traits for yield components. Regarding 1000-SW, the G12 gave the highest value, 46.33g at location two, and the G14 gave the lowest value, 33.33g at location two. Finally, for TGY/ha, the G12 recorded the maximum value 12.78t/ha, followed by G6 with value 12.63 t/ha at location one, while the lowest value 6.60t/ha was obtained by G7 at location three. From the results in Table 7, G5, G9, and G12 were superior among the genotypes used in this study.

Table 7. Effect of interaction (genotypes x locations) on mean traits bread wheat planting in the three locations.

Traits								combination	Locations
Y (t/ha)	1000SW (gm)	N.SS	S.W (gm)	M.D	SL (cm)	L.A (cm^2)	PH (cm)		
7.99 mno	43.00 cde	54.33 c	2.36 a-d	191.00 p	9.33 h-i	38.90 k-n	87.00 i	L_1G_1	L1
12.16 b	41.66 c-i	61.00 a	2.53 a	195.66 mno	12.00 ab	50.06 b	109.33 ab	L_1G_2	
11.01 cde	41.33 d-j	57.33 b	2.40 abc	191.66 p	10.66 cde	39.03 j-n	101.66 ed	L_1G_3	
8.51 klm	38.33 k-p	57.00 b	1.85 ghi	191.66 mno	10.00 d-g	47.30 c	86.66 j	L_1G_4	
12.78 a	42.33 c-j	53.33 cde	2.27 b-e	188.66 q	12.66 a	57.43 a	95.33 f	L_1G_5	
12.63 ab	40.66 e-k	47.00 kl	1.92 fg	195.33 no	10.66 cde	38.10 m-o	104.66 c	L_1G_6	
8.88 jk	43.33 b-e	56.33 b	2.46 ab	192.33 p	12.66 a	46.70 cd	90.66 hi	L_1G_7	
10.33 fg	39.33 h-m	33.66 s	1.34 m	196.33 lmn	10.66 cde	39.03 j-n	101.00 e	L_1G_8	

8.61 kl	42.00 c-h	60.33 a	2.53 a	197.33 kl	10.00 d-g	32.23 s	91.33 gh	L_1G_9	
10.33 fg	40.66 e-j	40.66 p	1.64 jkl	195.66 mno	11.00 bcd	45.90 de	82.66 lm	L_1G_{10}	
9.67 hi	33.66 st	52.66 def	1.76 g-k	195.66 mno	10.00 d-g	36.23 pqr	107.66 b	L_1G_{11}	
11.22 cd	39.66 g-l	42.00 op	1.67 i-l	192.33 p	12.00 ab	47.26 c	103.00 cde	L_1G_{12}	
8.86 jk	30.00 i-n	33.00 s	1.29 m	194.66 o	10.66 cde	41.40 gh	110.66 a	L_1G_{13}	
9.22 ij	34.00 rst	51.66 fgh	1.75 g-k	195.66 mno	12.00 ab	42.20 g	103.33 cd	L_1G_{14}	
9.74 hi	39.00 i-n	46.66 kl	1.82 g-j	196.33 lmn	8.66 hi	37.86 no	85.00 jk	L_1G_{15}	
7.80 nop	36.33 n-s	51.33 fgh	1.86 ghi	196.33 lmn	8.33 i	35.00 rs	78.33 n	L_2G_1	L2
11.53 c	38.66 j-o	57.66 b	2.30 cde	200.66 j	11.33 bc	45.00 e	84.00 kl	L_2G_2	
9.40 ij	35.33 q-t	52.33 efg	1.83 g-j	195.00 klm	8.66 hi	38.00 m-o	80.66 m	L_2G_3	
7.53 op	39.00 i-n	54.00 cd	2.10 ef	201.00 j	7.00 j	35.33 rs	59.00 u	L_2G_4	
11.56 c	46.00 ab	50.66 h	2.36 a-d	194.66 o	10.33 c-f	42.33 g	77.33 no	L_2G_5	
11.53 c	41.33 d-j	52.33 efg	2.15 e	201.00 j	9.00 ghi	43.66 e	91.00 hi	L_2G_6	
7.80 nop	36.66 m-r	44.33 mn	1.88 gh	197.00 klm	8.33 i	37.33 op	72.00 rs	L_2G_7	
9.50 hi	36.00 o-t	33.66 s	1.21 mn	201.66 ij	10.00 d-g	37.33 op	85.66 jk	L_2G_8	
7.23 pq	37.66 l-q	57.33 b	2.16 de	203.00 hi	8.66 hi	35.66 rs	93.33 g	L_2G_9	
9.56 hi	39.66 j-l	38.66 q	1.54 l	201.00 j	9.66 e-h	39.66 i-k	71.00 s	L_2G_{10}	
8.66 kl	33.66 st	48.66 j	1.63 jkl	202.00 ij	8.66 hi	38.33 l-o	91.33 gh	L_2G_{11}	
10.76 def	43.00 cde	53.66 cde	2.30 b-e	196.33 lmn	10.66 cde	42.66 fg	89.00 i	L_2G_{12}	
7.53 op	33.66 st	32.66 s	1.10 n	198.33 k	10.00 d-g	40.33 hij	81.33 m	L_2G_{13}	
8.40 klm	33.33 t	49.00 ij	1.63 jkl	201.00 j	10.00 d-g	39.33 j-m	90.66 hi	L_2G_{14}	
8.46 klm	39.66 j-l	43.33 no	1.73 g-l	201.00 j	8.33 i	39.00 j-n	73.00 qrs	L_2G_{15}	
6.70 qr	44.33 abc	50.33 hi	2.23 cde	205.66 g	11.33 bc	45.66 de	72.33 rs	L_3G_1	
10.40 fg	42.66 e-f	56.66 b	2.40 abc	208.33 cde	12.66 a	45.66 de	75.66 op	L_3G_2	
7.66 nop	43.66 a-d	51.00 gh	2.23 cde	207.00 def	9.33 f-i	40.66 hi	74.00 pqr	L_3G_3	

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6.63 r	40.00 f-l	54.66 c	2.18 de	209.66 abc	9.66 e-h	34.66 s	65.66 t	L_3G_4	L3
9.50 hi	36.66 m-r	50.66 h	1.83 g-j	203.00 hi	10.66 cde	45.66 de	72.00 rs	L_3G_5	
10.53 efg	44.00 a-d	54.00 cd	2.43 abc	208.00 def	12.66 a	35.00 rs	92.33 gh	L_3G_6	
6.60 r	38.00 k-q	51.00 gh	1.92 fg	204.00 h	10.66 cde	36.00 qrs	65.00 t	L_3G_7	
8.16 lmn	37.66 l-q	36.00 r	1.35 m	208.66 bcd	9.66 e-h	36.00 qrs	75.00 pq	L_3G_8	
8.56 klm	33.66 st	50.33 hi	1.69 h-l	209.33 a-d	9.66 e-h	34.66 s	66.00 t	L_3G_9	
8.43 klm	36.00 o-t	44.00 n	1.59 kl	209.00 a-d	9.00 ghi	33.33 t	65.66 t	L_3G_{10}	
7.23 pq	35.66 p-t	45.66 lm	1.80 g-k	210.00 ab	10.66 cde	40.00 ijk	75.00 pq	L_3G_{11}	
10.00 gh	46.33 a	51.00 gh	2.40 abc	204.00 h	12.66 a	46.33 cd	76.00 op	L_3G_{12}	
6.66 r	38.00 k-q	35.66 r	1.34 m	206.66 fg	10.33 c-f	37.66 no	90.33 hi	L_3G_{13}	
7.70 nop	35.66 p-t	50.66 h	1..82 g-j	209.66 abc	9.33 f-i	37.00 opq	66.33 t	L_3G_{14}	
7.76 nop	37.66 l-q	47.66 jk	1.79 g-k	210.33 a	8.66 hi	35.00 rs	65.33 t	L_3G_{15}	

Table 8 shows thevarainance of components and some genetic parameters .The results, observed that the variance of genotypes was higher than the variance of environments for all studied traits, is means that all traits are under genetic control. For the heritability the results in the same table indicate that the heritability was high for PH, HD, SSW, NSS, and TGY/ha (63%, 85%, 64%, 81% and 87%) respectively, and this means that these traits are more sensitive to appropriate environment conditions as compared with other traits, indicating that there is stress during the reproduction and maturity stages causing a decrease in their inheritance. Also, for the expected genetic advance values as percent of the mean were high for SS, NSS, and TGY t/ha (29.12, 27.68, and 30.40) respectively, and moderate for PH, LA, and SL, and low for HD and 1000SW g. These results were in agreement with findings of [6, 16,17].

Table 8. Variance components, heritability, genetic advance, and coefficient of genetic and phenotypic parameters.

Traits								Parameters
TGY (t/ha)	1000SW (gm)	N SS	SSW (gm)	HD	SL (cm)	L.A (cm^2)	PH (cm)	
2.07	6.44	52.64	0.11	5.75	0.90	14.33	61.90	Vg
0.73	2.36	18.64	0.04	2.06	0.33	5.097	21.94	SEg
0.19	7.44	11.03	0.05	0.25	0.70	14.84	34.10	Veg
0.058	2.12	2.91	0.01	0.13	0.21	3.87	8.93	Seg
0.09	2.27	0.73	0.01	0.70	0.38	0.51	1.47	Ve
0.01	0.34	0.11	0.002	0.11	0.05	0.07	0.22	SeE
2.36	16.15	64.41	0.17	6.71	1.99	29.72	97.49	VP
0.87	0.39	0.81	0.64	0.85	0.45	0.48	0.63	Heritability
2.78	3.30	13.51	0.55	4.57	1.32	5.42	12.91	GA
30.40	8.45	27.68	29.12	2.28	12.95	13.47	15.39	GA%
15.75	6.49	14.86	17.59	1.19	9.33	9.41	9.38	Gcv
16.80	10.28	16.44	21.90	1.29	13.85	13.53	11.77	Pcv

[5] suggested that both components, linear (regression coefficient Bi) and non-linear (deviation from regression S^2di), are important in predicting the stability of genotypes. When the regression coefficient is close to one and is associated with a value of deviation from regression equal to zero, this indicate that the genotype has a good response and stable for the wide range of environmental changes, and if the regression coefficient is greater than one, the genotype is described by highest sensitivity to environmental changes, and it adapts in high-proactivity (good environment, but when the regression coefficient is less than one, this is an indication that the genotype characterized by high resistance to environmental changes (higher than moderate stability) and this increases the determination of adaptation to low-yielding environments. For obtained results, it is indicated that the PH trait that genotype 1, 2, 4, 5, 6, 7, 8, 9, 13, 14 and 15 had non-significant regression coefficients from unity (Bi=1), among which the genotypes, where the value of the S^2di and Bi were both non-significant for genotypes 7, 8, 9, 13, 14 and 15 for PH, indicating that the genotypes are

highly responsive to environmental changes (genetically stable). The values of the S^2di were non-significant, and Bi were significant and positive, the 3, 10, 11, and 12 indicating that the genotypes respond to a good environment. When the values of S^2di are significant, the genotypes 1, 2, 3, 4, 5, and 6 indicate that the genotypes respond to good environments. For LA, the value of Bi and S^2di was non-significant for the 1, 2, 3, 7, 8, 9, 10 genotypes and were highly responsive for this trait, while 4, 5, 6, 11, 12, 13, 14, and 15 genotypes a good for environmental changes. Regarding SL, the G4, G6, and G14, the values S^2di and Bi are non-significant; these genotypes were highly responsive for this trait, while G13 and G15 were stable for a good environmental change. The values of S^2di and Bi were non-significant for the G10 and G11 are highly responsive to environmental changes, while the value of Bi was positive and significant, and S^2di was non-significant for the G2, 3, 7, 8, 9, 13, 14, and 15; these genotypes showed a good response to environmental changes. The values of Bi were negative, and the S^2di was non-significant for genotypes 4 and 5; hence, these genotypes responded to poor environmental changes. For SW, the values of Bi were positive and significant, and S^2di was non-significant for the G1, 2, 3, 5, 7, 8, 9, 11, 12, 13, 14, and 15; these genotypes responded to a good environmental change. For N. SS, the genotypes 4, 5, 6, 7, 8, 9, 13, 14 and 15 were a good response for a good environment changes due to Bi was positive and significant and S^2di non-significant, while the G10, 11 and 12 where the values of these genotypes were non-significant indicating that these genotypes were highly response to environment changes for this trait. For 1000 SW, the values of Bi were positive and non-significant, indicating that the genotypes 1, 2, 3, 7, 8, 9, 10, 11, 12, 14, and 15 were a good response to environmental changes, while genotype 4 was a poor response to environmental changes. Finally, for TGY (t/ha), the G1, 2, 3, 14, and 15 were moderate in their stability because the Bi was non-significant and S^2di was significant, also the genotypes 7, 8, and 9, then Bi and S^2di were non-significant. These genotypes are highly responsive to environmental changes.

Table 9. Stability parameters for the studied traits.

MD		SL (cm)		L.A (cm^2)		PH (cm)		Genotypes
S^2di	Bi	S^2di	Bi	S^2di	Bi	S^2di	Bi	
4.040**	1.578*	0.142	-17.143	-2.187	0.362	79.941**	1.614	G1
0.886	2.345*	0.277	-11.786	-3.926	0.226	111.139**	1.274	G2
0.138	1.694*	-0.366	-15.00	-2.706	0.079	90.363**	1.755*	G3
-0.073	-1.936*	0.023	7.500	0.405	1.374*	105.773**	0.521	G4
-0.118	-0.877*	0.277	26.786*	-1.343	1.507*	92.730**	0.604	G5
2.175*	-1.468*	-0.080	12.857	1.150	1.398*	103.845**	0.463	G6

0.993	1.009*	-0.358	-5.357	-2.586	0.405	-10.027	1.455	G7
1.677	1.793*	-0.294	-16.071	-3.314	0.336	-9.891	1.349	G8
1.643	0.954*	0.023	-7.500	-0.599	0.303	-9.174	1.584	G9
0.875*	0.320	0.595	-13.929	1.007	1.085	37.343	2.328*	G10
0.115*	0.132	0.428	-8.571	4.682	0.932*	14.937	2.409*	G11
-0.227	0.485	0.595	-13.929	3.157	0.939*	30.201	2.516*	G12
1.373	3.090*	2.809**	32.143*	24.452*	2.295*	16.946	-0.977	G13
1.856	2.847*	0.976	9.643	25.044*	1.847*	15.095	-1.095	G14
0.773	3.034*	1.420*	35.357*	13.962	1.911*	7.645	-0.801	G15
	0.660		18.595		0.843		1.703	SE (Bi)

Y ta/ha		1000SW		N.SS		SW		Genotypes
S^2di	Bi	S^2di	Bi	S^2di	Bi	S^2di	Bi	
7.389**	3.247	11.098	1.902*	-0.898	0.287	0.046	0.712*	G1
8.207**	1666	8.134	2.211*	-3.546	0.372	0.041	0.777*	G2
9.011**	1.495	6.354	2.417*	-0.571	0.161	0.042	0.822*	G3
7.084**	-2.073	6.632	-1.168*	-3.425	1.166*	-0.011	0.455	G4
2.182**	-3.469	-1.394	0.095	-3.726	0.769*	-0.011	0.672*	G5
2.998**	-4.148	2.985	-0.642	-2.807	0.938*	-0.015	0.521	G6
-0.127	2.952	-2.382	1.141*	-1.066	2.517*	0.013	2.265*	G7
-0.137	3.573	-1.945	0.722*	-1.820	2.500*	0.019	2.112*	G8
-0.136	4.376	-2.701	1.143*	-2.519	2.441*	0.002	2.143*	G9
-0.085	-1.335	-1.153	1.051*	8.699	0.364	0.070	-0.135	G10
-0.010	-1.251	-2.785	1.773*	6.004	0.271	0.020	0.819*	G11
0.243	-1.330	-2.332	1.672*	16.462	0.338	0.036	0.875*	G12
1.699**	4.482	-2.212	0.411	12.770	0.996*	0.034	0.860*	G13

1.532**	3.662	-1.915	1.139*	18.524*	0.920*	0.034	1.024*	G14
1.342**	3.153	0.375	1.133*	8.960	0.962*	0.047	1.139*	G15
	4.556		0.886		0.417		0.638	SE (Bi)

Conclusion

Our study on fifteen new wheat genotypes in Duhok, Zakho, and Zinawa showed that the best performers were G6, G2, and G5, which produced the highest yields and are strongly recommended for farmers. G12 also showed very good grain weight and yield. For farmers in areas with less rain or uncertain conditions, stable genotypes such as G1, G2, G3, G13, G14, and G15 are safer choices. On the other hand, G7, G8, and G9 depend a lot on weather and may not do well in dry years; thus, they should only be used carefully under supplementary irrigation. In Duhok, where rainfall is higher, farmers can use the high-yielding types (G6, G2, G12), while in Zakho and Zinawa it is better to plant the stable types. For dry areas, early-maturing wheat such as G5 is especially useful to avoid late-season drought. Farmers are advised to first test these promising wheat genotypes in small plots on their own land before planting them widely.

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