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Estimation genetic parameter, genotypic and phonotypic correlation, path and cluster analysis of quantitative traits for Bread Wheat genotypes in Erbil under rain- fed condition

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ABSTRACT

This study was conducted in two seasons (2020-2021) and (2021-2022). First year (45) single plants and (45) samples (variety) with three replications were studied which they collected from (45) bread wheat field farmers under rain-fed condition. In the second year (12) varieties planted in Randomized Complete Block Design (R.C.B.D.) by three replications in Directorate of Agriculture Research-Erbil. First year result showed that most lines had higher yield and yield components than the standard varieties, and (L42) had outperformed than other lines. Second year results showed variety (Hewlir 4) had outperformed than all other varieties in most of the traits, it obtained high yield and thousand grain weight by (16.9 g and 30.9 g) respectively. There was high phenotypic and genotypic correlation between yield/plant and thousand grain weight, seed/spike, grain per plant, and harvest index. High heritability (98 and 97) and high expected genetic advance (57 and 39) found in yield/plant and thousand grain weight respectively.

تقدير المعالم الوراثية والارتباط الوراثي وتحليل العنقودي والمسار للصفات الكمية لتراكيب وراثية من حنطة الخبز تحت ظروف الزراعة الجافة في اربيل

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الخلاصة

أجريت هذه الدراسة خلال الموسمين الزراعيين الشتويين (٢٠٢١) و (٢٠٢٢). في السنة الأولى تم دراسة (٤٥) نبته مفردة و (٤٥) عينة (صنف) مع ٣ مكررات تم جمعها من (٤٥) مزارعا في حقول قمح الخبز تحت ظروف الزراعة الجافة. في السنة الثانية تم زراعة (١٢) صنف وفق تصميم القطاعات العشوائية الكاملة في مديرية البحوث الزراعية-اربيل. أظهرت نتائج السنة الأولى أن معظم الخطوط تفوق في معظم الصفات على الاصناف القياسية وأن (٤٢L) تفوقت على باقي الخطوط. في السنة

الثانية أظهرت النتائج أن الصنف Hewlir (٤) قد تفوق على بقية الأصناف في وزن الف حبة حاصل النبات الفردي بمقدار (٣٠.٩ غم ١٦,٩ غم نبات) على التوالي. كان هناك ارتباط عالي مظهري بين حاصل النبات الفردي وصفات وزن الف حبة وعدد البذور في السنبله ودليل الحصاد والحاصل البايولوجي. وكانت نسبة التوريث عالية وبنسبة (٩٨% و ٩٧%) والتحسين الوراثي (٥٧% و ٣٩%). في وزن الف حبة وحاصل النبات الفردي على التوالي.

الكلمات المفتاحية: انتاجية حنطة الناعمة، درجة التوريث، الارتباط، تحليل المسار، تحليل العنقودي

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is the common wheat is largely produced by the farmers in most countries. Grain yield is the most valuable features in economic aspect for bread wheat (Delzer et al., 1995). World warming and climate change are mostly affecting the agriculture sector, wheat production is highly affected by these two problems. Water shortage is a vital problem that reasons for abiotic stress and is irritant for plant breeders. Consequently, plant breeders in the proper fields are investigating reliable screening principles for drought tolerance in wheat cultivars (Abdolshahi et al., 2015). Crop production is reduced and affected by many factors such as drought, high and low temperatures, salinity and floods (Lawlor & Cornic, 2002). Drought is a complicated environmental concern for most cereals. Bread wheat is the important crop which its production affected highly by the drought. The loss production of bread wheat by the water deficiency is become huge dilemma in many countries. Drought has become the most crucial environmental stress in agriculture for most regions in the world; hence, breeders mostly relied on the optimum yield variety under deficient water situation (Cattivelli et al., 2008). Most studies prefer the characteristic higher production of genotypes under water limitation in cereals and the selection is relying on the morphological and physiological features to evaluate the resistance to the drought (Dhanda et al., 2004).

Bread wheat varieties are differing to adaptation or tolerance to the drought. As a result, selecting varieties which tolerant to the drought is desirable and suitable to avoid reduction of bread wheat yield. Genotypes with highly resistance to drought has ability to persist the activity of metabolic in the tissue while there is lacking of water potential (Kopecká et al., 2023). During the water stress given to plant at all stages of the plant growth affects the total grain yield but it has taken place in the critical stages of the growth which ultimately decreased grain yield sharply (Subhani et al., 2015). During propagative stage, the crop yield decreased by the 70-80% due to draught stress stated (Sallam et al., 2019).

Therefore, now a day it has essential to improve the new enhanced yield performance genotypes, adaptable to the sever climate condition such as drought stress (Mahmood et al., 2019). The first and main target of wheat breeders is high wheat production under drought condition. Grain yield is the best trait that breeders highly aimed to obtain for on selecting optimum and suitable genotypes under drought condition (Atlin et al., 2009). The requirement of varieties which adapt to the drought condition and having optimum yield is essential to the regions of north of Iraq. This study aims to find the optimum and adaptable variety to drought condition.

MATERIALS AND METHODS

Approximately seventy-five locations were visited in the first year for the provinces (Erbil, Sulimani and Dohuk) for the (2020–2021) season. In the year of selection, the condition of the most field was drought especially the south of Erbil, some farmers lost the yield because of the low rainfall. The seventy-five locations contained high number of the fields which included bread wheat (*Triticum aestivum* L.). In these locations (45) superior plants were selected as well as (45) random samples collected (each sample three replication with sample area 0.5 m²) in the same field which single plants were selected. For nominating the genotypes, it followed name of the place and the filed and the variety which genotypes come from and for distinguish among them and the follow is the symbol of the genotypes which used for the next two seasons of the study: The samples that taken from the field were ordered as (V1 to V45) and same order was putted for plants (single plant) (L1 to L45) (table1). In the second year (12) variety (table 2) were planted by Randomized Complete Block Design (R.C.B.D.) with three replications in Directorate of Agriculture Research

Erbil in season (2021-2022). Traits measured and accounted (number of spikes per plant, number of grains per spike, grain plant yield, thousand grain yield (TKW), biological yield (BY) and harvest index (HI%). OPSTAT software (Sheoran et al., 1998) used to analyze path analysis and genetic and phenotypic correlation .

Table (1): Origin of samples (variety) single plant (line) location

#	Origin name (samples)	Symbol in this study		Location/Province
		Variety	Lines	
1	Hewlir 2	V1	L1	Jizhnikan/Erbil
2	Hewlir 2	V2	L2	Rania/Erbil
3	Hewlir 4	V3	L3	Jizhnikan/Erbil
4	Hewlir 4	V4	L4	Harir/Erbil
5	Wfia	V5	L5	Rania/Erbil
6	Hewlir 2	V6	L6	Bnaw/Erbil
7	Hewlir 2	V7	L7	Kany Qrzhala/Erbil
8	Wfia	V8	L8	Mortka/Erbil
9	Panda	V9	L9	Bistana/Erbil
10	Jihan	V10	L10	JK.Qrzhala/Erbil
11	Slimany2	V11	L11	Rania/Sulimania
12	Jihan	V12	L12	Jihan/MlaQara/Erbil
13	Adana	V13	L13	Adna/Sattor/Erbil
14	Jihan	V14	L14	Jihan/Bnbirz/Erbil
15	Hewlir 2	V15	L15	Kany Qrzhala/Erbil
16	Adana	V16	L16	Smailawa/Erbil
17	Jihan	V17	L17	Tobzawa/Erbil
18	Hewlir 4	V18	L18	Qalatga/Erbil
19	Hewlir 2	V19	L19	Srdsht/Erbil
20	Wfia	V20	L20	Rania/Sulimania
21	Aras	V21	L21	Palany/Erbil
22	Jihan	V22	L22	Grdarasha/Erbil
23	Adana	V23	L23	Ismawa/Dhok
24	Wfia	V24	L24	Bnbirz/Erbil
25	Wfia	V25	L25	Qalatga/Erbil
26	Jihan	V26	L26	Shixshirwan/Erbil
27	Adana	V27	L27	Shixshirwan/Erbil
28	Hewlir 4	V28	L28	Sibiran/Erbil
29	Rzgary	V29	L29	Reshkin/Erbil
30	Hewlir 2	V30	L30	Reshkin/Erbil
31	Hewlir 2	V31	L31	Gomagro/Erbil
32	Adana	V32	L32	Awina/Erbil
33	Hewlir 4	V33	L33	Jzhnikan/Erbil
34	Hewlir 2	V34	L34	Hamzakor/Erbil
35	Hewlir 4	V35	L35	Koya/Erbil
36	Adana	V36	L36	Bhrka/Erbil
37	Hewlir 4	V37	L37	Karzor/Erbil
38	Tmoz 2	V38	L38	Smil/Dhok
39	Hewlir 4	V39	L39	Awina/Erbil
40	Hewlir 2	V40	L40	Grdjotyar/Erbil
41	Hewlir 2	V41	L41	Yarmja/Erbil
42	Hewlir 4	V42	L42	Yarmja/Erbil
43	Hewlir 4	V43	L43	Jmka/Erbil
44	Hewlir 8	V44	L44	Bhrka/Erbil
45	Hewlir 6	V45	L45	Grdjotyar/Erbil

We classified (45) varieties by the two methods: first; variety character, it is the method which is vital to identify the variety and differentiate it from other variety inside the species according to the (UPOV), this relies on the morphological features or color symbol such as (grain color, grain size and shape, glume and lemma color, plant height). The varieties were also compared to the varieties in Directorate of Agriculture Erbil by our experience and with discussion with the agronomist specialist in this directorate. In addition, we did cluster analysis to classify the varieties (figure 1). Secondly; variety replication, it is essential which replicates the same variety replicate in the same variety (Celestina et al., 2023). From these two methods we identified that (45) varieties of farmer's field were (12) varieties of bread wheat (Table 2).

Table (2): groups of origin (12) with included there (45) variety

12 variety	45 variety
Adana	(V13, V16, V27, V32, V36)
Hewlir 2	(V1, V2, V6, V7, V15, V19, V30, V31, V34, V40, V41)
Jihan	(V10, V12, V14, V17, V22, V26)
Wafia	(V5, V8, V20, V24, V25)
Hewlir 4	(V3, V4, V18, V28, V33, V35, V37, V39, V42, V43)
Aras	V21
Sulimany2	V11
Tamoz 2	V38
Panda	V9
Rzgary	V29
Hewlir 8	V44
Hewlir 6	V45

RESULT AND DISCUSSION

1. Single plants (Lines) farmers' field (2020-2021):

In the (Table 3), it shows the (45 single plant) with (5) standard variety of farmers' field (2020-2021). In yield plant trait, this table shows closely (38) % single plants were higher than the highest standard variety and the highest single plant was (L42) by (22.4)g. For trait Thousand Kernel Weight (TKW), closely (62) % single plants were had higher TKW than the highest standard variety, while (L42) had highest single plant for TKW by (37.7) g. In addition, (31) % of the single plants were had higher seed/spike and highest single plant was (L42) by (66.4 seed/spike). In regarding to the Harvest Index percentage (HI)%, (26) % of the single plants were had higher HI% than the highest standard variety and the highest single plant was (L42) by (35) %. For Biological yield (BY) trait, (97) % of the single plants were obtained higher than the highest standard variety, and the highest single plant was (L35) by (52.5) g. Moreover, (9) % single plants were had higher spike/plant than highest standard variety and the highest single plant was (L22) with (12 spike/plant). Finally, (22) % of single plants were had higher seed/spike than the highest standard variety and the highest single plant was (L28) with (667 grain per plant). Similar results were obtained by (Tadesse et al., 2022). These results indicate that the selection for these genotypes will be an establishment for selecting optimum plants with high yield and yield components. These results also showed the selection is essential for improving varieties .

Table (3): five standard varieties and (45) plants Augmented design in (2020-2021)

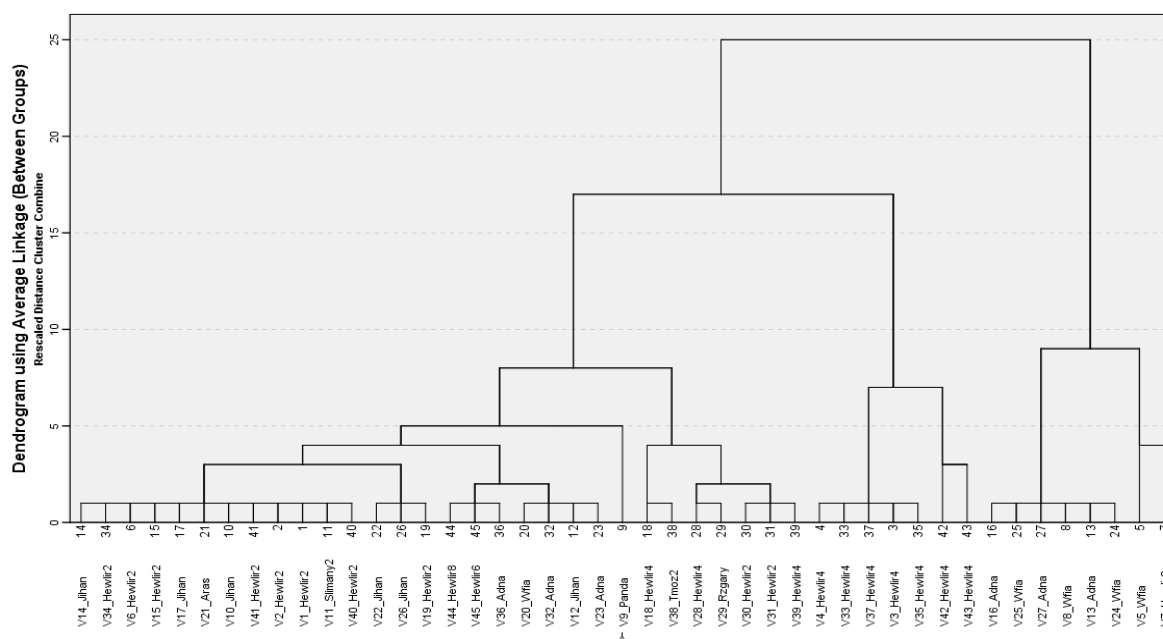
G	Y/p g	G	TKW g	G	seed/ spike	G	HI%	G	BY g	G	spike/ plant	G	seed/ plant
L42	22.4	L42	37.5	L42	66.4	L42	35.0	L35	52.5	L22	12	L28	667
L35	21.5	L3	36.7	L35	63.8	L33	33.2	L10	50.7	L23	11	L22	660
L18	21	L33	36.5	L33	63.0	L3	33.0	L28	50	L25	11	L35	638
L33	20.7	L4	35.5	L30	61.9	L43	32.8	L12	49	L28	11	L30	619
L28	20	L43	34.1	L18	61.8	L30	32.7	L4	48.5	V2	10.6	L18	618
L30	20	L18	34	L41	60.7	L39	32.5	L18	48	V24	10.6	L41	607
L43	19.4	L35	33.7	L28	60.6	L18	32.4	L15	47.4	V38	10.6	L42	597
L3	19.3	L37	33	L37	60.6	L40	32.1	L7	47.2	L10	10	L17	593
L37	18	L30	32.3	L15	60.3	L37	31.3	L17	47	L12	10	L39	592
L39	18	L39	30.4	L17	59.3	L41	31.1	L2	47	L13	10	L40	590
L4	18	L28	30	L39	59.2	L35	30.9	L33	45.7	L16	10	V38	578
L40	17.7	L40	30	L40	59.0	L28	30.6	L42	45.4	L17	10	V2	572
L41	17	L7	29.5	L34	58.7	V38	30.0	L30	45.2	L18	10	L43	569
L29	16.4	L1	29	L3	58.4	V2	29.8	L23	45	L19	10	L33	567
L17	16	L2	29	V17	57.78	L31	29.5	L38	45	L2	10	L29	566
L2	16	L29	29	L43	56.9	L29	29.3	L29	44.4	L21	10	L38	564
L38	15	L31	28	L29	56.6	L4	29.2	L11	44	L27	10	L2	552
V38	14.3	L41	28	L38	56.4	L19	28.8	L37	44	L29	10	L37	545
L19	14.3	L17	27	L4	56.3	L25	28.7	L43	43.8	L30	10	L6	543
L21	14	L19	27	L31	55.6	L26	28.6	L22	43.3	L35	10	L15	542
L22	14	L20	27	L2	55.2	V17	28.0	L3	43.3	L38	10	L10	539
L31	14	L21	26.7	L26	55.1	L17	27.7	L21	42	L39	10	V17	539
L34	13.2	L38	26.6	L22	55.0	L2	27.7	L41	42	L40	10	L19	530
V2	13.2	L25	26	L11	54.6	L21	27.6	L34	41.8	L41	10	L34	528
L1	13	L5	26	L14	54.5	L44	27.5	L40	41.7	L43	10	L3	526
L10	13	L24	25	V38	54.3	L38	27.4	L39	41.6	L44	10	L21	524
L15	12.8	L34	25	L6	54.3	L1	27.1	L27	41	L6	10	L9	524
V17	12.4	L11	24.4	L10	53.9	L22	27.0	L9	41	L8	10	L44	517
L12	12.2	V38	24.30	V2	53.6	V11	26.6	L1	40.3	L9	10	L12	517
L11	12	L10	24.1	L19	53.0	L34	26.7	L19	40.3	V11	9.6	V11	509
L26	11.4	L12	23.6	V11	52.80	L32	26.1	L5	40	V17	9.3	L4	507
L6	11.4	L15	23.6	L21	52.4	L6	26.1	L13	39	L1	9	L23	505
L25	11.3	V17	23.17	L9	52.4	L45	26.0	L8	39	L11	9	L31	500
L23	11	V2	23.0	L44	51.7	L36	25.0	L14	38.8	L14	9	L26	496
L9	11	L26	23	L12	51.7	L24	24.9	L31	38.3	L15	9	L11	492
V11	10.9	L27	23	L7	51.3	L14	24.4	L6	38	L24	9	L14	491
L7	10.6	L32	22	L20	51.3	L11	24.1	L20	37.7	L26	9	L8	467
L14	10.5	L13	21.9	L32	50.5	L9	24.1	L24	37.4	L3	9	V24	458
L44	10.5	L23	21.8	L45	50.0	L15	23.8	L16	37.3	L31	9	L32	455
L24	10.4	V11	21.4	L1	49.8	L20	23.7	L32	34	L32	9	L1	448
L32	10	L14	21.4	L36	48.3	L8	23.5	L26	33.4	L33	9	L36	435
L5	10	L8	21.4	L8	46.7	V24	23.2	L25	33.1	L34	9	L25	435
L8	10	L22	21.2	L24	46.2	L5	23.1	L36	33	L36	9	L24	416
L20	9.7	L6	21	L23	45.9	L10	22.8	L44	33	L37	9	L13	411
L13	9	L9	21	V24	42.9	L12	22.5	V17	31.9	L4	9	L16	400
L36	9	L36	20.7	L5	42.7	L23	22.4	V2	30.9	L42	9	L45	400
L16	8	L44	20.3	L13	41.1	L13	22.0	V38	30.6	L5	9	L5	385
L27	8	L16	20	L16	40.0	L16	21.1	V11	30.0	L45	8	L7	359
L45	8	L45	20	L25	39.5	L7	21.1	L45	28.5	L20	7	L20	359
V24	7.6	V24	16.7	L27	34.8	L27	19.6	V24	25.2	L7	7	L27	348

Yield/plant(Y/P) (g), One thousand kernel weight(TKW)(g), Harvest Index%(HI%), Biological yield(BY)(g), Genotypes(G) (45 lines(L) with 5 standard varieties in **Bold**

2. Cluster analysis:

Clusters will classify genotypes according to the relationship and variation in the groups of clusters or in one cluster (Carbonera & Abel, 2014). Hierarchical cluster type of cluster used and Ward's method with Squared Euclidean Distance was used Dendrogram used for plot B-plot to show the genotypes linkage. The cluster used to measure the relationship and distance of the

genotypes. The cluster contained four main traits (Yield/plant, TKW, seed/spike and seed/plant). In (figure 1) the cluster analysis provided the linkage of the (45) varieties. There in this cluster most varieties are had linkage together. The cluster had three main group and divided in to nearly (12) groups, the first group which starts from (14 to 40) included most of the (Hewir 2) and it mostly contains all Jihan variety. In addition, other Jihan variety are very similar included in the nearest subgroups. However, there was some varieties located in different cluster it is belong to difference of the environmental condition as these varieties obtained from different environment condition. From subgroups (18 to 43) it is included all (Hewlir 4), however with some different in subgroups while all of the subgroups are very close to each other. Most of Adana variety were located at subgroups from (16 to 24) in the third group. In addition, Wafia variety mostly located in the third group at subgroups linked closely. Thus, these results confirmed our result that these genotypes were (12) varieties, however some variation due to the environment condition for different location of collection.



3. Varieties field trial (2021-2022):

This study found that all (45) varieties were in origin are (12) varieties. Analysis of variance was used in SPSS software (IBM CORP, 2019) to identify the significant difference among (12) varieties for the traits in this study. In the (table 5) it shows that all traits (yield/plant, one thousand kernel weight (TKW), spike/plant, seed/plant, seed/spike, harvest index (HI %) and Biological yield (BY) were significantly difference at the level of the (0.01). This result indicated that genotypes were difference in production and it is optimum result for breeding improvement for low rainfall condition. This study agreed with (Lonbani & Arzani, 2011).

Table (4): Mean square of 12 varieties in season (2021-2022)

Source of Variation	D.f	Yield/plant g	TKW g	seed/plant	spike/plant	seed/spike	HI%	BY g
Replicates	2	0.06	0.8	405	0.5	8.1	10.1	14.3
Variety	11	26.8 **	51.5 **	19474 **	1.22 **	117.9 **	59.58 **	135.8 **
Error	22	0.173	0.49	527	0.3381	15.55	4.83	3

For identifying which pairs of means are significantly difference, Duncan Multiple Range Test (DMTR) was used. In the (table 6) variety (Hewlir 4) had outperformed than all other varieties in traits Yield/plant and TKW by (16.9 g and 30.9 g) respectively. In addition, had outperformed than other varieties in the trait (HI and B.Y) by (31.6 % and 36.6 g), while Tamo2 and Rzgary were

produced same result with (Hewir 4) in both traits respectively. Moreover, variety Rzgary had highest seed/plant and spike/plant than all other varieties by (650 seed/plant, 10.3 spike/plant and 62.9 grain per spike) respectively. This result agreed with (Zareian et al., 2013).

Table (5): Means variation for 12 varieties in (2021-2022)

Variety	Yield/ Plant ⁻¹ g	TKW g	BY g	HI%	seed plant ⁻¹	seed spike ⁻¹	spike/ plant
Adana	7.1 f	19.3 e	22.4 d	24.2 c	371 ef	43.3 c	8.5 bc
Aras	12.8 b	23.3 c	31.2 ab	29.1 ab	552 b	59.1 ab	9.3 b
Hewlir2	11.8 c	23.2 c	30.7 b	27.8 ab	511 c	58.5 ab	8.7 bc
Hewlir 4	16.9 a	30.9 a	36.6 a	31.6 a	548 b	62.8 a	8.7 bc
Hewlir 6	7.1 f	17.0 fg	28.0 bc	20.2 d	419 e	52.4 b	8.0 c
Hewlir 8	8.2 e	17.9 f	32.0 ab	20.3 d	458 d	57.3 ab	8.0 c
Jihan	10.6 d	21.3 d	27.2 bc	28.1 ab	502 c	58.6 ab	8.5 bc
Panda	8.1 e	16.0 g	23.2 d	25.9 b	509 c	58.7 ab	8.6 bc
Rzgary	13.0 b	20.1 e	28.9 bc	31.1 a	650 a	62.9 a	10.3 a
Sulimany2	10.9 d	21.4 d	26.7 c	28.9 ab	510 c	58.8 ab	8.6 bc
Tmuz 2	13.0 b	25.4 b	36.2 a	26.5 b	515 bc	59.4 ab	8.6 bc
Wafia	8.6 e	24.6 b	26.0 cd	24.6 c	351 f	43.4 c	8.0 c

same letters in column are not significantly difference

4. Genotyping and Phenotyping Correlation

Genotypic and phenotypic correlation was measured for the (12) varieties for traits. In (Table 6) genotypic and phenotypic is shown. In genotypic correlation there was high significant correlation between plant yield and (thousand grain weight, No. grains per plant, seed/spike, (HI)% and BY) by (0.81, 0.74, 0.76, 0.76, 0.86) respectively, while it had moderate correlation with spike per plant by (0.62). In addition, TKW had moderate correlation with (HI)% and (BY) with (0.70 and 0.62) respectively. In contrast, TKW was not correlated grain per plant, spike per plant and seed/spike. Moreover, grain per plant was highly correlated with (No. of grains per plant, seed/spike and BY) by (0.95, 0.96 and 0.76) respectively, while it was not correlated with (HI %). Spike per plant was highly correlated with grain per spike and B.Y with (0.84 and 0.83) respectively, while it had no correlation with HI%. Furthermore, grain per spike was moderately correlated with (HI% and BY) by (0.62 and 0.66) respectively. Finally, there was no correlation between HI% and BY. These results were agreed with (Arya et al., 2017). In phenotypic correlation (Table6), there was high correlation between plant yield with TKW, number of grains per plant, (HI)% and B.Y with degree of correlation (0.80, 0.73, 0.71 and 0.82) respectively. It had moderate correlation with spike per plant and grain per spike with (0.46 and 0.63) respectively. TKW was moderately correlated with (HI% BY) by (0.63 and 0.59) respectively. On other hand, it had not correlation with grain per plant, number of spike per plant and grain per spike .

Likewise, grain per plant was highly correlated with grain per spike by (0.83) and with (B.Y) by (0.71), and it correlated moderately with number of spike per plant and (HI)% by (0.67 and 0.42) respectively. In addition, number of spike per plant was only correlated moderately with BY and it had no correlation with number of grains per spike and (HI)%. Finally, number of grain per spike was moderately correlated with (HI (%) and B.Y) by (0.54 and 0.48) respectively and HI (%) was not correlated with (B.Y). These results indicated there was low environment effect on most of the traits however some traits were affected by environment. That is agreed with (Baye et al., 2020). This finding agree with results of (Abdulhamed et al., 2021), which they recommended that harvest index and TKW are important to improving bread wheat yield as they had positive correlation to the yield.

Table (6): Genotypic (upper) and Phenotypic (lower) correlation of 12 varieties (2021-2022)

Trait	Plant yield (g)	TKW (g)	Grain per plant	No. of spikes of plant	No. of grains per spike	(HI)%	B.Y (g)
Plant yield (g)	1	0.81 **	0.74 **	0.62 *	0.76 **	0.76 **	0.86 **
TKW(g)	0.80 **	1	0.22 NS	0.13 NS	0.26 NS	0.70 *	0.62 *
Grain per plant	0.73 **	0.18 NS	1	0.95 **	0.96 **	0.44 NS	0.76 **
No. of spikes of plant	0.46 *	0.09 NS	0.67 *	1	0.84 **	0.14 NS	0.83 **
No. of grains per spike	0.63 *	0.18 NS	0.83 **	0.15 NS	1	0.62 *	0.66 *
(HI)%	0.71 **	0.63 *	0.42 *	0.04 NS	0.54 **	1	0.34 NS
B.Y (g)	0.82 **	0.59 *	0.71 **	0.62 *	0.48 **	0.20 NS	1

NS: non-significant, significant ** 0.01, * 0.05

For analyzing the regression (multiple line regression) SPSS software (IBM COR, 2019) was used to analyses the regression. Stepwise method was used and yield as dependent variable and other traits as independent variable. Results demonstrated in the (Table 8). There was high correlation between yield and other yield components, and all independent variables (B.Y, Harvest index, spike / plant number of grains per plant, number of grains per spike, TKW) were entered to regression. In addition, R square was very high (0.996) and it is indicated that most traits involved in regression were had significant effect on e yield (Table 7).

Table (7): Regression result of independent and dependent variables

Variables Entered/Removed a				Change Statistics					
Model	Variables Entered	Variables Removed	Method	R	R Square	Adjusted R Square	F cal.	df1	df2
1	B.Y, Harvest index, spike/plant, Number of grains per spike, TKW, Number of grains per plant	None	Enter	0.998a	0.996	0.995	1192	6	29

a. Dependent Variable: Yield/plant (g) b. All requested variables entered a. Predictors: (Constant), BY, Harvest index, spike/plant, Number of grains per spike, TKW, Number of grains per plant b. Dependent Variable: Yield/plant (g)

In (Table 8) which represented the output of the Regression ANOVA, the result indicated that all of the independent variable were had significant effect on the dependent variable (predictor variables) had statically significant relationship with yield/plant at level significant level (0.01). Thus, all traits in this study were had significant relationship with the yield /plant, this is an important point to establish breeding program according to these to improve yield/plant.

Table (8): Mean square of regression for the traits of the 12 variety

Model	Sources	d.f	Sum of Squares	Mean Square	F cal.	Sig.
1	Regression	6	298	49.66 **	1191.8	.000
	Residual	29	1.20	.042		
	Total	35	299.2			

** Significant 0.01

Path direct and indirect phenotypic are represented for the correlation of path coefficient for the traits in (Table 9). The residual was very low 0.0034, it indicated that error was very low. For direct path effect, table shows high significant correlation between plant yield with biological yield and

harvest index (0.419 and 0.349) respectively. However, number of grains per spike, TKW and number of spikes per plant were had high correlation with plant yield directly B.Y (0.305 0.286 and 0.226) respectively, while number of grains per plant had negative correlated coefficient with plant yield.

In indirect effect path coefficient, TKW had significant indirect effect on plant yield through BY and HI by (0.249 and 0.229) respectively. In addition, TKW had low indirect effect on plant yield through number of grains per spike and number of spikes per plant, and with low negative effect by seed/plant. Seed/plant was high indirect effect on plant yield through B.Y, number of grains per spike, number of spikes per plant and by (0.299, 0.254, 0.153 and 0.147) respectively, while it had no effect on yield through TKW. In addition, number of grains per plant had high indirect effect on yield/plant through biological yield only with (0.262), while it had not any indirect effect on yield through other traits. Number of grains per spike had high indirect path effect on plant yield through (B.Y and HI %) with result (0.204 and 0.189) respectively. (Saini et al., 2024) suggested that biological yield is highly correlated to yield/plant in bread wheat. Finally, total of indirect and direct path effect on yield/plant was high significant for (B.Y) and (TKW) by (0.825 and 0.801) respectively and it was high (0.731, 0.717 and 0.639) for number of grains per plant, HI% and number of grains per spike respectively and low for number of spikes per plant by (0.461). This results are similar to finding of (Anwar et al., 2009), who found TKW had positive correlation to improve plant yield in bread wheat. (Shamuyarira et al., 2022) suggested that biological yield and seed/plant had positive correlation with plant yield

Table (9): Phenotypic Direct (bold) and indirect path coefficient analysis

Trait	TKW(g)	No. grains per plant	spike/ plant	No. grains per spike	HI %	B.Y (g)	Yield per plant (g)
TKW(g)	0.286	-0.033	0.022	0.056	0.221*	0.24*	0.80**
No. grains per plant	0.054	-0.176	0.153*	0.254*	0.147*	0.29*	0.73*
spike/plant	0.028	-0.119	0.226	0.048	0.015	0.26*	0.46
No. grains per spike	0.052	-0.146	0.035	0.305	0.189*	0.204*	0.63*
Harvest index %	0.181*	-0.074	0.010	0.165*	0.349	0.08	0.71*
Biological yield (g)	0.170*	-0.126	0.142*	0.149*	0.072	0.419	0.82**

Thousand grain weight (TKW), Harvest index (HI %) Biological weigh (BY). Residual is 0.00384

In the table (10) it shows genotypic direct and indirect path analysis. Thousand grain weight had high positive path direct by (0.91) and indirect by (0.82) effect on the grain yield per plant. Number of grains per spike also had positive direct and in direct path effect on the grain yield per plant by (0.70 and 0.73) respectively. However Biological yield, Harvest index and number of grains per plant had high positive path effect on grain yield indirectly, but they had no effect on the grain yield directly and the residual was (0.00363). From phenotypic and genotypic path analysis it was indicated that most of the traits were influenced mostly by genetic and environment had low influence.

Table (10): Genotypic Direct (bold) and indirect path coefficient analysis

Trait	TKW(g)	No. grains per plant	spike/plant	No. grains per spike	HI %	B.Y (g)	Yield per plant (g)
TKW(g)	0.91	-0.04	0.04	0.15	-0.12	-0.13	0.82**
No. grains per plant	0.18	-0.22	0.32	0.67	-0.15	-0.08	0.72**
spike/plant	0.12	-0.21	0.33	0.58	-0.17	-0.03	0.63*
No. grains per spike	0.20	-0.21	0.27	0.70	-0.12	-0.11	0.73**
Harvest index %	0.56	-0.17	0.28	0.44	-0.20	-0.06	0.77**
Biological yield (g)	0.64	-0.10	0.05	0.42	-0.07	-0.18	0.85**

Thousand grain weight (TKW), Harvest index (HI %) Biological weigh (BY). Residual is 0.00363

The most important features in plant breeding are heritability and expected genetic advance of mean in plant genotypes. Heritability is ranged from spike plant by (47%) to plant yield by (98%) In addition, high heritability and high genetic advance of mean were obtained by plant yield, TKW, BY and seed/plant with percentage of (98, 97, 94 and 92) and (57, 39, 36, 27) respectively (table11). However, seed/ spike was obtained (69%) heritability and (18 %) of expected genetic advance. In the table (11) there it demonstrated that for all traits the genotypic variance was higher than environmental variance, except spike/plant which may affected by the environment. These results indicated that most traits were correlated with genotypes rather than environment, and it is an essential objective for improving yield production in plant breeding. These traits are powerful for introducing them n plant breeding program to accelerate the yield production in bread wheat.

Table (11): Genetic parameters of 12 varieties in season (2021-2022)

Genetic Parameters	Yield per plant (g)	TKW (g)	BY (g)	No. grains per plant	spike/plant	No. grains per spike	HI%
Environmental Variance	0.17	0.49	3.00	527.30	0.34	15.55	4.83
Genotypic Variance	8.89	17.02	44.29	6315.52	0.29	34.14	18.25
Phenotypic Variance	9.06	17.51	47.29	6842.82	0.63	49.69	23.08
Environmental Coefficient of Variance	3.88	3.21	4.71	4.66	6.69	6.95	7.54
Genotypic Coefficient of Variance	27.79	18.99	18.10	16.11	6.24	10.30	14.64
Phenotypic Coefficient of Variance	28.06	19.26	18.71	16.77	9.15	12.43	16.47
h ²	98	97	94	92	47	69	79
GA	6.08	8.38	13.27	157.27	0.76	9.98	7.82
GA%	57	39	36	32	9	18	27

Heritability in broad sense (h²), Genetic advance (GA), Expected genetic advance of mean (GA %), Thousand grain weight (TKW), Biological yield (B.Y), and Harvest index (HI %)

CONCLUSIONS

Results above it showed that single plants were had higher result than standard varieties in plant yield and other yield components. In addition, this study found that (Hewlir 4) was outperformed than all other varieties in plant yield most of yield component traits. The study found that in both genotypic and phenotypic correlation traits there was very high correlation between yield with TKW and B.Y. Similarly, Yield/ plant and TKW had higher heritability and expected genetic

advance than other traits. This study suggested that the superior genotypes could be entered in program of breeding to improve yield of bread wheat in drought regions.

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