HERITABILITY, VARIABILITY, GENETIC CORRELATION AND PATH ANALYSIS FOR QUANTITATIVE TRAITS IN DURUM AND BREAD WHEAT UNDER DRY FARMING CONDITIONS

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ABSTRACT

Two field experiments were carried out during the 2009-2010 growing season at the station of Directorate of Agricultural Researches/Erbil under dry farming conditions. The first experiment included 25 strains of durum wheat, and the second included 20 strains of bread wheat. Growth trait, yield and its components were studied, and then data are entered in the statistical genetic analysis, as well as the path coefficient analysis. The results showed high genetic variation, heritability and genetic advance for plant height, number of spikes, 1000 grain weight, biological yield and grain yield in durum wheat. While it was high in all traits in bread wheat. The grain yield was correlated genetically positive and significantly with 1000 grain weight, biological yield and harvest index in durum wheat, while showed genetically positive and significant correlation with all traits in bread wheat. The path coefficient analysis revealed that harvest index and biological yield had the maximum positive direct effects on grain yield in durum wheat reached 0.966 and 0.242, respectively. While the harvest index had the maximum positive direct effect (1.417) on grain yield in bread wheat, which was used as a criterion for the selection of superior genotypes in each group.

INTRODUCTION

The grain yield is a complex traits which is influenced by many factors, would be plant breeders interested to know the nature of the relationship and the kind between these traits, especially under dry farming conditions, where the water is the main limiting factor in many areas of wheat production around the world due to uneven rainfall distribution during the growing season, so it is important that characterized cultivars cultivated in these areas in the superior performance of grain yield and its components under the limited and non-limited of moisture conditions (Okuyama *et al.,* 2004). Grain yield is the result of many developmental and physiological events that occur during the life cycle of the plant, and grain yield is determined by three main components; the number of spikes/plant, number of grain/spike and weight of grains (Poehlman, 1987). Hochman (1982) and McMaster *et al.* (1984) referred that the influence of each one of these components on the product of grain depends on the stage of growth that occurs due to water deficit. At elongation stage, the inadequate availability of water or rain affect on the components of grain yield by increasing the number of spikes/plant, grains/spike, and weight of grains/plant, while leading to increased weight of grains during the grain filling stage (McMaster *et al.,*1984). Simane *et al.* (1993) reported high correlation between the number of grains/spike and grain yield along the span of

water stress.The wheat plants are more sensitive to water stress between the two phases (booting stage) and (grain filling) as compared to all other periods (Fisher *et al.,* 1977 and Hochman, 1982). On the other hand, avoiding of wheat plants to water stress during the tillering and elongation stages is more important than the flowering and grain filling stages (Thompson and Chase, 1992).

The breeding program for higher yield depends on the estimation of genetic variability, heritability, genetic advance and the correlations between yield and its components, but it is not sufficient to understand the importance of each one of these components in determining the grain yield (Dewey and Lu, 1959). Path analysis is a standarized partial regression coefficient that measures the direct influence of one variable upon another, it also provides a means of partitioning both direct and indirect effects and effectively measuring the relative importance of causal factors, which, helps to build an effectively selection program. Using this method (Kumar and Hunshal, 1998) observed that the harvest index, biomass yield, spikes/plant and grains/spike had most important direct effects on the grain yield. Under the water deficit conditions, but a long period of grain filling Simane *et al.*(1998) found high correlation between drought tolerance and spikes/m^2 and grains/spike. Yagdi (2009) found that the 1000 grain weight have high direct effect on grain yield. This research aims to estimates heritability, genetic variation and genetic correlation between different quantitative traits in a number of strains selected from durum and bread wheat, and then to identify the most important traits of a direct effect on the grain yield to be adopted as a criterion for selection.

MATEREALS AND METHODES

Two field experiments were carried out separated during the season 2009-2010 at the research station of the Directorate of Agricultural Research in the area of Ainkawa in Erbil/Kurdistan region of Iraq under the circumstances amounted to rain (315 mm) with good distribution depend on meteorological in the search site. The first experiment included 25 advanced strains of durum wheat (*Triticum durum* Desf.), and second included 20 advanced strains of bread wheat (*Triticum aestivum* L.) (Table, 1) was originally selected (on the basis of phenotypic characteristics and grain yield in the nursery of the observations had been planted during the season 2008-2009) of 57 and 67 advanced strain of two types, respectively. Each experiment was carried out according to randomized complete block design with three replicates and each experimental unit included a one row of each one of genotype. The grains were dibbled in rows (using 120 kg/ha seeding rate) keeping between row distances at 20 cm. Single row of 2.5 m length served as an experimental unit. Conducted service operations of soil and crop, and when plants reached the flowering stage, were recorded the flag leaf area of mother shoot according to formula (leaf length × width × 0.95) (Thomas, 1975), and at maturity data were recorded for plant height (cm), then harvested plants of each line as a whole to calculate biomass yield (t/ha), grain yield (t/ha), harvest index, spike Genetic statistical analysis for all the traits studied were computed, then the estimates of genetic variation, heritability and coefficints of genetic correlation between traits were done by the components of expected mean squares from

Table (1): Pedigree of durum and bread wheat strains used in the study.

No.	I g	crop	pop type	Selection
Durum wheat				
No.	I g	crop	pop type	Selection
1	114239	ICDW	UM	ICD86-0471-ABL-0TR-8AP-0TR-20AP-0TR
2	114251	ICDW	UM	ICD85-1340-ABL-6AP-0TR
3	114262	ICDW	UM	ICD85-0641-ABL-6AP-0TR-2AP-0TR-4AP-0TR
4	114293	ICDW	UM	ICD84-0322-7AP-TR-20AP-0TR
5	114300	ICDW	UM	ICD83-0050-4AP-14AP-TR-3AP-0TR
6	114322	ICDW	UM	ICD78-0064-19AP-4AP-1AP-1AP-1AP-0SH
7	114326	ICDW	UM	ICD-BM-ABL-413-0AP
8	114347	ICDW	UM	CD 523-3Y-1Y-2M-0Y
9	114385	ICDW	UM	12938-5L-1AP-1AP-4AP-0AP
10	129068	ICDW	UM	ICD86-0041-ABL-13AP-0TR-7AP-0TR
11	129076	ICDW	UM	ICD88-1233-ABL-8AP-0AP-6AP-0AP
12	139248	ICDW	CV	ICD78-0030-2AP-2AP-3AP-2AP-0AP
13	139250	ICDW	CV	CD 20632-2AP-3AP-0AP
14	139251	ICDW	CV	CD 39513-12AP-3AP-0AP
15	139252	ICDW	CV	ICD79-0852-13AP-3AP-2AP-0AP
16	139253	ICDW	CV	ICD79-1463-1AP-2AP-2AP-1AP-0SH
17	139255	ICDW	CV	ICD85-0642-ABL-28AP-0TR-2AP-0TR
18	139256	ICDW	CV	ICD89-0263-AL-4AP-0AP-6AP-0AP
19	139258	ICDW	CV	ICD91-0083-AB-1AP-0AP-5AP-0AP
20	139259	ICDW	CV	ICD91-0811-AB-3AP-0AP-2AP-0AP
21	139262	ICDW	CV	ICD89-0278-AL-1AP-0AP-6AP-0AP
22	139263	ICDW	CV	ICD91-1251-AB-8AP-0AP-12AP-0AP
23	139264	ICDW	CV	ICD91-1251-AB-11AP-0AP-1AP-0AP
24	139265	ICDW	CV	ICD92-0150-CABL-7AP-0AP-7AP-0TR
25	simeto	check		

No.	I g	crop	pop type	Or I	province
Bread wheat					
No.	I g	crop	pop type	Or I	province
1	41587	ICBW	LA	PAK	Baluchistan
2	41668	ICBW	LA	PAK	Baluchistan
3	41675	ICBW	LA	PAK	Baluchistan
4	41680	ICBW	LA	PAK	Baluchistan
5	41762	ICBW	LA	PAK	Baluchistan
6	41772	ICBW	LA	PAK	Baluchistan
7	41946	ICBW	CV	MAR	Ten sift
8	43244	ICBW	LA	PAK	Baluchistan
9	43252	ICBW	LA	PAK	Baluchistan
10	43257	ICBW	LA	PAK	Baluchistan
11	44266	ICBW	LA	TUN	Safaqis [Sfax]
12	94857	ICBW	LA	TUN	Safaqis [Sfax]
13	94867	ICBW	LA	TUN	Safaqis [Sfax]
14	115798	ICBW	LA	JOR	Az Zarqa
15	122110	ICBW	LA	IRN	Tehran
16	138362	ICBW	LA	TKM	Ashkhabad
17	138388	ICBW	LA	SYR	Damascus
18	138841	ICBW	LA	IRN	Khorasan
19	138888	ICBW	LA	AFG	Samangan
20	cham-6	check			

* LA= Landrace; I g=ICARDA genetic code number; UM= un release material; CV= Current Variety;
   Source = ICARDA

length (cm) and the components of grain yield [number of spikes/m^2, number of grains/spike and 1000 grain weight (g)].

analysis of variance and covariance between traits were estimated as the below:

S.O.V.	(EMS)xx	(EMCP)xy	(EMS)yy
Genotypes	$\sigma^2 E_x + r\sigma^2 G_x$	$\sigma E_x E_y + r\sigma G_x G_y$	$\sigma^2 E_y + r\sigma^2 G_y$
Error	$\sigma^2 E_x$	$\sigma E_x E_y$	$\sigma^2 E y$

Genotypic ($\sigma^2 G$), Phenotypic($\sigma^2 P$) and environment variance ($\sigma^2 E$) were estimated according to the following formula (Walter, 1975), using the Excel program.

$$\sigma^2 G = \frac{MSG - MSE}{r} \qquad \sigma^2 E = MSE \qquad \sigma^2 P = \sigma^2 G + \sigma^2 E$$

Variance of $\sigma^2 G$ and $\sigma^2 E$ was estimated by applying the following two equations (Kempthorne, 1969):

$$V(\sigma^2 G) = \frac{2}{r^2}\left[\frac{(MSG)^2}{(K+2)} + \frac{(MSE)^2}{(K+2)}\right] \qquad V(\sigma^2 E) = \frac{2(MSE)^2}{K+2}$$

While the variance of $\sigma^2 P$ has been estimated by applying the following formula (Mather and Jinks, 1982):

$$V(\sigma^2 P) = \frac{2(\sigma^2 P)^2}{N}$$

Where r is the number of replicates; N is the sum of degrees of freedom for genotypes, and the experimental error; $\sigma G_x G_y$ is the genetic covariance between x and y traits.

Taking the square root of the variations above we then get the standard error (SE) for each variance for the test of significant of each one of these variances using statistical t-test. Genetic coefficient of variation ($GCV\%$) and genetic correlation (rG) were estimated by the following equations:

$$GCV\% = \frac{\sqrt{\sigma^2 G}}{\overline{X}} \qquad rG = \frac{\sigma G_x G_y}{\sqrt{\sigma^2 G_x . \sigma^2 G_y}}$$

Heritability in the broad sense estimated by using the equation: $H^2_{B.S.} = \frac{\sigma^2 G}{\sigma^2 P}$, and Expected genetic advance by formula: $EGA = H^2_{B.S.} k\sigma P$, as well as the expected genetic advance for the mean were calculated by the equation: $EGA\% = \frac{GA}{\overline{X}}.100$, where K is the degrees of freedom for each source of variation; and σP is the phenotypic standard deviation, and i is constant (k= 1.76), at 10% selection intensity.

Path coefficient analysis was performed as described by (Dewey and Lu, 1959). Grain yield was kept as resultant variable and other traits as causal ones.

Estimation of the path coefficients (direct effects) for the independent variables in the depend variable (grain yield) using the genetic correlation matrix, and a linear equation is represented:

$Yi = p_1 y X_1 + p_2 y X_2 + ... + e$, and then the normal equation is:

$R[\underline{p}] = [\underline{r}]$

$\therefore \lfloor p \rfloor = [R]^{-1} \lfloor r \rfloor$, where: $\lfloor p \rfloor$ = vector of path coefficients; $[R]^{-1}$ = matrix inverse of genetic correlation coefficients between the independent variables (causal). $\lfloor r \rfloor$ = vector of genetic correlation coefficients between the independent variables and the dependent variable.

RESULTS AND DISCUSSION

1: Durum wheat.

a - The performance of genotypes and phenotypic differences: Table (2) shows the means of 25 genotypes of durum wheat, which differed in all the studied traits, according to analysis of variance and F values (Table, 3). Genotype 1 was superior in spike length (7 cm), 1000 grain weight (51.7 grams), grain yield (6.49 t/ha) and harvest index (0.51). The genotypes 7 shows superiority in plant height (108.7 cm); 25 in the flag leaf area (47.33 cm^2); 6 in the number of spikes/m^2 (348 spikes); 19 and 21 in biomass yield (13.44 t/ha). The results shows existence of a wide range of genetic variation between the genotypes in most of the traits as reflected through the values of genetic variability, which reached the high significant in plant height, number of spikes/m^2, 1000 grain weight, biomass yield and grain yield, which were (91.9, 1395.6, 21.0, 1.67 and 0.98 respectively) and this was reflected high-contrast positive and that higher values of heritability of these traits, which were high, reached 82.53% for plant height and 74% of the 1000 grain weight and medium to the number of spikes/m^2, biomass yield and grain yield, which means little affected by the environment in time which decreased the heritability of the other traits which was very affected by the environment as is evident in the high variability of environmental values of these traits more than the traits which gave high and medium heritability values. The high values of genetic variation in these traits led to an increase in the values of phenotypic variation and heritability, which led eventually to the lifting of the values of expected genetic advance, amounted to 18.0 cm for plant height, 49.5 spike/m^2, 5.18 g of the 1000 grain weight, 1.62 t/ha for biomass yield and 1.31 t/ha for grain yield (Table, 3).

b – Genetic correlation and path coefficient analysis: Data presented in Table (4) are the values of genetic correlation coefficients between traits and it notes the existence of a negative correlation or weak between plant height and other traits. Flag leaf area showed high positive genetic correlation and significantly with spike length, number of spikes/m^2 and the number of grains/spike, but weak or negative with other traits. Spike length show significantly negative genetic correlation with the number of spikes/m^2, and weak or negative with other traits. The genetic correlation between the number of spikes/m^2 and the biomass yield is positive and significant, while weak or negative with the other traits. The number of grains/spike shows genetically positive correlation but not significant with harvest index, grain yield, biomass yield and 1000 grain weight, while the genetic correlation between 1000 grain weight and harvest index, grain yield and biomass yield is positive and significant, as well as among grain yield, biomass yield and harvest index. It is noted here also appears positive genetic correlation between grain yield and its components and the same ingredients except for the negative and weak genetic correlation between the numbers of spikes / m^2 and 1000 grain weight,

Table (2) Mean of the studied traits in durum wheat genotypes.

Genotypes	PH (cm)	FLA (cm^2)	SL (cm)	SN/m^2	G/S	1000 GW (g)	BY (t/ha)	GY (t/ha)	HI (%)
1	82.3	43.33	7	225	36.33	51.7	12.78	6.49	0.51
2	92.7	33.33	7	251.33	35	42.1	11.58	4.02	0.35
3	100	33	467	343	34.67	38.17	13.19	6.35	0.48
4	98.7	33.67	6.67	230	27	37.3	8.03	1.93	0.27
5	100	24.67	6.67	292	27.67	45.77	11.92	5.44	0.45
6	77	29.33	6.67	348	36.33	36.76	11.58	2.82	0.24
7	108.7	39	6.67	188.67	39.33	32.8	8.39	2.76	0.31
8	81.3	34.33	6	230.33	35.33	45.23	12.25	5.52	0.46
9	85.3	33	7	251	36	44.9	11.28	4.86	0.44
10	77.67	43.33	6	249	36.67	47.37	12.08	3.76	0.31
11	90.67	38.67	7	270.33	36.33	40.67	12.08	5.51	0.46
12	86.67	41.33	6.67	282.33	32.33	40.17	11.72	5.19	0.44
13	86.67	38	7	253.67	35	34.37	10.94	3.63	0.33
14	86.33	40	7	217.67	40.33	45.57	10.56	4.27	0.42
15	77	43	6.67	285	27.33	42.43	11.94	5.18	0.43
16	80	33	6.33	270.33	29	39.50	11.69	4.78	0.41
17	104.67	41.33	6.33	192.67	29.33	32.17	7.50	2.40	0.32
18	87.33	36	6	283.33	33	38.43	11.69	4.33	0.37
19	88.67	35.67	6.33	307.33	36.33	40.50	13.44	4.90	0.37
20	82	33.33	6.33	235.67	31.67	38.13	10.06	3.08	0.31
21	91.67	31	6.67	298.33	33	43.17	13.44	5.11	0.39
22	96.33	32.67	6	344.67	32.33	40.8	12.94	3.76	0.29
23	94.33	37.67	6	296.33	32.67	41.13	12.53	4.39	0.35
24	65.67	39.33	6.67	333.67	37	32.06	13.39	2.92	0.23
25	80	47.33	7	234.33	39.33	40.03	12.44	3.92	0.32
LSD (5%)	**7.20**	**11.80**	**1.00**	**72.63**	**4.35**	**2.73**	**2.72**	**1.93**	**0.15**

PH= Plant height; FLA= Flag leaf area; SL= Spike length; SN/m^2; G/S= Number of grains/spike; 1000 GW= 1000 grain weight; By= Biomass yield; GY= Grain yield; HI= Harvest index.

that is in agree with (Sinha *et al.,* 1984, Ali, 1995, Ozkan *et al.,* 1997, Nofouzi *et al.,* 2008 and Talebi *et al.,* 2011). These results in terms of the positive genetic correlation between grain yield and many traits that have direct relevance to its components like biomass yield and harvest index an important indicator of the reliability of the selection for high grain yield on any of these traits. It has been followed up on these positive results of the path coefficient analysis which the results had described in Table (5), as a result of the high and positive genetic correlation between harvest index and grain yield (0.977) is higher positive direct effect of harvest index on grain yield (0.966), followed by the positive direct effect of the biomass yield (0.242) resulting from the high positive correlation between them (0.776). These positive correlations led to show the positive indirect effect for each of these two traits through the other on grain yield (0.542 and 0.136)

respectively, while the result of positive genetic correlation between 1000 grain weight and grain yield (0.849) have a negative direct effect of 1000 grain weight on grain yield (-0.116), but showed the highest positive indirect effect through harvest index, and this underlines the lack of necessity for the status of the positive genetic correlation with grain yield direct effect positively upon this supports the findings of the many researchers (Garcia del Moral *et al .,* 2003 and Bhutta *et al.,* 2005). While the other traits showed negative or weak direct and indirect effects. These results emphasize the importance of determining the biomass yield and harvest index to develop grain yield of durum wheat, which can be used as a guide to the selection. These results are consistent with Ali (1995, Kumar and Hunshal (1998), Ali (2006) and Gashaw *et al.* (2007). Accordingly, we select superior genotypes in both traits in addition to the grain yield, namely, (1, 3, 5, 8 and 11) to continue to be evaluated within the program of the selection.

Table (3): Phenotypic variation and genetic parameters for studied traits in durum wheat.

Genetic Parameters	PH (cm)	FLA (cm^2)	SL (cm)	SN/m^2	G/S	1000 GW(g)	BY (t/ha)	GY (t/ha)	HI (%)
$\overline{X}$	88.1	36.25	6.49	268.6	33.97	40.45	11.58	4.29	0.37
F. value	15.2*	1.75*	2.29*	3.1*	1.96*	9.85*	2.79	3.11*	2.37*
$\sigma^2 G$	91.9*	7.8	0.16	1395.6*	6.91	21.0*	1.67*	0.98*	0.003
$\sigma^2 E$	19.4*	52.3*	0.37*	1978.1*	21.5*	7.11*	2.80*	1.40*	0.008*
$\sigma^2 P$	111.3*	60.0*	0.52*	3373.8*	28.5*	28.1*	4.46*	2.39*	0.01*
GCV%	10.9	7.68	6.11	13.9	7.74	11.32	11.14	23.11	15.85
$H^2_{B.S.}$	82.6	12.94	30.11	41.4	24.30	74.67	37.32	41.27	31.28
EGA	18.0	2.07	0.45	49.5	2.67	5.18	1.62	1.31	0.068
EGA%	20.4	5.70	6.93	18.4	7.86	12.81	13.99	30.54	18.38

* = Significant at 5% probability level.

Table (4): Coefficients of genetic correlation between studied traits in durum wheat.

	HI (%)	GY (t/ha)	BY (t/ha)	1000 GW (g)	G/S	SN/m^2	SL (cm)	FLA (cm^2)
PH (cm)	0.147	-0.077	-0.582*	-0.217	-0.333	-0.311	0.281	-0.312
FLA (cm^2)	-0.203	-0.241	-0.356	0.056	0.684*	0.752*	0.443*	
SL (cm)	-0.094	-0.253	-0.309	0.165	0.232	-0.618*		
SN/m^2	-0.032	0.222	0.634*	-0.094	-0.312			
G/S	0.127	0.164	0.335	0.106				
1000 GW (g)	0.845*	0.849*	0.566*					
BY (t/ha)	0.561*	0.776*						
GY (t/ha)	0.977*							

* = Significant at 5% probability level.

Table (5): Direct and indirect influences of studied traits on grain yield in durum wheat.

	PH (cm)	FLA (cm^2)	SL (cm)	SN/m^2	G/S	1000 GW (g)	BY (t/ha)	HI (%)	rG with GY
PH (cm)	**_-0.085_**	-0.011	-0.016	0.002	0.007	0.025	-0.141	0.142	**-0.077**
FLA (cm^2)	0.027	**_0.034_**	-0.025	-0.004	0.015	-0.006	-0.086	-0.196	**-0.241**
SL (cm)	-0.024	0.015	**_-0.057_**	0.003	-0.005	-0.019	-0.075	-0.091	**-0.253**
SN/m^2	0.026	0.026	0.035	**_-0.005_**	0.007	0.011	0.153	-0.031	**0.222**
G/S	0.028	-0.023	-0.013	0.002	**_-0.022_**	-0.012	0.081	0.123	**0.164**
1000GW(g)	0.018	0.002	-0.009	0.0005	-0.002	**_-0.116_**	0.137	0.816	**0.849***
BY (t/ha)	0.049	-0.012	0.018	-0.003	0.007	-0.066	**_0.242_**	0.542	**0.776***
HI (%)	-0.012	-0.007	-0.005	0.0002	-0.003	-0.098	0.136	**_0.966_**	**0.977***

* = Significant at 5% probability level.

2. Bread wheat.

a - The performance of genotypes and phenotypic differences: Twenty genotypes of bread wheat different in all traits, as is evident from the values of F given in the Table (7). (Table 6) Shows means of these genotypes in the studied traits. Genotypes 12 shows superiority in plant height (109.67 cm), grain yield (4.46 t / ha) and harvest index (0.44); 2 give higher flag leaf area (44.33 cm^2) with the observation that there are many genotypes with low values in this trait, especially genotypes 1 and 2 due to sensitive to rust disease that has spread time account status. And the superiority of genotype 11 in spike length and 1000 grain weight, giving (10.33 cm) (45.13 g), respectively, while the genotype 10 gave the highest number of spikes / m^2 (345 spike), and genotype 7 in the number of grains / spike (32.33). The wide range of variation among genotypes find vary high genetically significant for all these traits (Table, 6), which is required to build effectively selection program due to these traits gave high heritability ranged between 64.42% for the spike length to 88.25% for harvest index, which led to an increase values of expected genetic advance in these traits, amounted to (25.69, 22.44, 1.38, 117.83, 13.71, 11.31, 4.17, 2.61 and 0.19) to the plant height, flag leaf area, spike length, number of spikes / m^2, number of grains / spike, 1000 grain weight, biomass yield, grain yield and harvest index, respectively. These results are supported with other researchers who created a high genetic variance and genetic advance in many of the traits of the bread wheat genotypes included studies of them (Ozkan *et al.,* 1997, Ahmed *et al.,* 2003 and Zaeifizadeh *et al.,* 2011).

b – Genetic correlation and path coefficient analysis: Values of genetic correlation coefficients between traits presented in Table (8) that was positive and significant between all traits except between plant height and number of grains / spike and between spike length and number of spikes / m^2, although these positive results make it easier for plant breeders to build the effective selection, but these correlations alone is not sufficient and the guarantor to achieve that, therefore, has been introduced in the path coefficient analysis which provides an effective way of finding out direct and indirect sources of correlations by using genotypic into direct

and indirect effects to identify statistically the most important traits of a direct effect and this is was actually from the data presented in Table (9), where it is

Table (6) Mean of the studied traits in bread wheat genotypes.

Genotypes	PH (cm)	FLA (cm^2)	SL (cm)	SN/m^2	G/S	1000 GW(g)	BY (t/ha)	GY (t/ha)	HI (%)
1	95	3	8	187	8.33	27.73	4.41	0.58	0.13
2	51.33	0	7.67	44	5.67	15.33	2.87	0.27	0.09
3	97.67	4.67	8.33	200	11	30.4	3.80	0.70	0.19
4	94	26.33	7	328	12.67	36.3	6.38	1.68	0.26
5	84.67	26.67	8.33	131.33	14.67	36.03	4.36	0.88	0.20
6	99.33	7.67	8.33	268.33	12.67	30.4	5.5	1.43	0.27
7	79.33	26.67	9.33	271	32.33	26.17	8.97	3.31	0.37
8	102.33	13.67	7.67	321.67	11.67	34.83	6.01	1.5	0.25
9	98.33	27	8.33	299	15.33	37.07	7.14	2.12	0.30
10	99.33	5.67	9	345	12.33	29.17	6.19	1.34	0.22
11	102.33	33.67	10.33	268.33	24.67	45.13	9.37	4.16	0.44
12	109.67	27.33	9.67	305	23	43.03	10.24	4.46	0.44
13	109	30.33	10	280.33	25.67	41.7	9.64	4.14	0.43
14	109	36.67	9.33	341	20.67	33.1	9.13	3.02	0.33
15	109.33	44.33	9.33	329.33	23	34.9	10.2	2.9	0.29
16	91.33	28.33	10	265	19	33.33	7.37	1.96	0.27
17	107.33	32	10	299.67	24	41.37	9.24	4.03	0.44
18	104	33.33	9.33	255.33	14	33.13	6.75	2.11	0.31
19	85.33	28	8.67	281	17.33	30.67	7.44	1.27	0.18
20	81.67	35	8.67	325	32	30.63	9.61	3.71	0.39
LSD (5%)	*9.74*	*10.61*	*1.02*	*80.71*	*5.06*	*6.08*	*1.54*	*0.61*	*0.07*

PH= Plant height; FLA= Flag leaf area; SL= Spike length; SN/m^2; G/S= Number of grains/spike; 1000 GW= 1000 grain weight; By= Biomass yield; GY= Grain yield; HI= Harvest index.

noted that the higher positive genetic correlation between harvest index and grain yield created a positive direct effect for the harvest index on grain yield, but all its indirect effects via other traits were negative or weak, as it did not show any trait a positive direct effect among the other traits that are relevant to the positive correlation with the grain yield except flag leaf area (0.352) with the negative or weak direct effects of other, and this confirms as we went in the past is no need to be positive genetic between any trait and grain yield have a positive direct effect on the grain yield, as is evident in many of the traits that were have a positive genetic correlation with grain yield in bread wheat, but it had the negative direct effects. On the other hand it was showed that all traits had a high positive indirect effects via harvest index only, while all other effects were negative or weak. This shows clearly the maximum relative importance of the harvest index in determining high grain yield in bread wheat and confirms this, too, that the genotypes superior in harvest index were superior in the grain yield as well (Table, 7), which is can be used as an selection index between genotypes, This is created by Sharma (1993),

Table (7): Phenotypic variation and genetic parameters for studied traits in bread wheat.

Genetic parameters	PH (cm)	FLA (cm^2)	SL (cm)	SN/m^2	G/S	1000 GW(g)	BY (t/ha)	GY (t/ha)	HI (%)
$\overline{X}$	95.5	23.52	8.87	267.27	18	33.52	7.23	2.28	0.29
F. value	16.6*	11.78*	6.43*	7.01*	17.36*	9.75*	17.35*	38.55*	23.52*
$\sigma^2 G$	185.4*	151.7*	0.71*	4901.9*	52.43*	40.51*	4.86*	1.74*	0.010*
$\sigma^2 E$	35.58*	42.22*	0.39*	2443.0*	9.61*	13.88*	0.89*	0.14*	0.002*
$\sigma^2 P$	221.0*	193.9*	1.09*	7344.9*	62.05*	54.39*	5.75*	1.88*	0.012*
GCV%	14.26	52.38	9.47	26.20	4023	18.99	30.48	57.95	35.20
$H^2{}_{B.S.}$	83.90	78.23	64.42	66.74	84.50	74.48	84.50	92.60	88.25
EGA	25.69	22.44	1.38	117.83	13.71	11.31	4.17	2.61	0.19
EGA%	26.90	95.43	15.66	44.09	76.18	33.76	57.73	114.87	68.11

* = Significant at 5% probability level.

Table (8): Coefficients of genetic correlation between studied traits in bread wheat.

	HI (%)	GY (t/ha)	BY (t/ha)	1000 GW (g)	G/S	SN/m^2	SL (cm)	FLA (cm^2)
PH (cm)	0.556*	0.501*	0.554*	0.845*	0.221	0.773*	0.546*	0.447*
FLA (cm^2)	0.715*	0.761*	0.899*	0.640*	0.785*	0.575*	0.629*	
SL (cm)	0.798*	0.801*	0.758*	0.632*	0.688*	0.334		
SN/m^2	0.598*	0.564*	0.739*	0.551*	0.535*			
G/S	0.877*	0.902*	0.913*	0.467*				
1000 W(g)	0.760*	0.705*	0.668*					
BY (t/ha)	0.921*	0.948*						
GY (t/ha)	0.988*							

* = Significant at 5% probability level.

Table (9): Direct and indirect influences of studied traits on grain yield in bread wheat.

	PH (cm)	FLA (cm^2)	SL (cm)	SN/m^2	G/S	1000 GW (g)	BY (t/ha)	HI (%)	rG with GY
PH (cm)	***0.152***	0.157	0.039	0.065	-0.096	-0.232	-0.068	0.788	**0.501***
FLA (cm^2)	-0.068	***0.352***	0.045	0.048	-0.343	-0.175	-0.111	1.013	**0.761***
SL (cm)	-0.083	0.221	***0.071***	0.028	-0.301	-0.173	-0.093	1.131	**0.801***
SN/m^2	-0.117	0.202	0.024	***0.084***	-0.234	-0.151	-0.091	0.847	**0.564***
G/S	-0.024	0.276	0.049	0.045	***-0.437***	-0.128	-0.112	1.243	**0.902***
1000GW(g)	-0.128	0.225	0.045	0.046	0.204	***-0.274***	-0.082	1.077	**0.705***
BY (t/ha)	-0.084	0.316	0.054	0.062	-0.399	-0.183	***-0.123***	1.305	**0.948***
HI (%)	-0.085	0.252	0.057	0.051	-0.383	-0.208	-0.113	***1.417***	**0.988***

• = Significant at 5% probability level.

Ali (1995) and Khayatnezhad *et al.* (2010). Accordingly, we can select genotypes (7, 11, 12, 13 and 17) to continue to be evaluated in the program of the forthcoming selection. It is necessary to note that plant breeders looking usually for the traits

with a direct effect, but it is important to have these traits with a positive genetic correlation with grain yield to ensure the achievement of genetic improvement in the grain yield when relied upon as a criterion for selection, or it has to be depend on hybridization program, in addition to the need of these traits highly inherited in two sets of durum and bread wheat contained in this study.

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التوريث والتباين والارتباط الوراثي وتحليل المسارللصفات الكمية
في الحنطة الخشنة والخبز تحت ظروف الزراعة الجافة

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الخلاصة

نفذت تجربتين حقليتين خلال الموسم ٢٠٠٩-٢٠١٠ في محطة مديرية البحوث الزراعية / أربيل تحت ظروف الزراعة الجافة . تضمنت الأولى ٢٥ سلالة من الحنطة الخشنة، والثانية ٢٠ سلالة من الحنطة الناعمة. درست بعض صفات الحاصل وم كوناته، ثم أدخلت البيانات في التحليل الاحصائي الوراثي وكذلك تحليل معامل المسار . أظهرت النتائج وجود تباين وراثي وقوة توريث وتحسين وراثي عالي لارتفاع النبات وعدد السنابل ووزن ١٠٠٠ حبة والحاصل البيولوجي وحاصل الحبوب في الحنطة الخشنة، في حين كانت عالية لجميع ا لصفات في الحنطة الناعمة . أظهر حاصل الحبوب ارتباطاً وراثياً موجباً ومعنوياً مع وزن ١٠٠٠ حبة والحاصل البيولوجي ودليل الحصاد في الحنطة الخشنة فيما أظهر ارتباطاً وراثياً موجباً ومعنوياً مع جميع الصفات في الحنطة الناعمة . بينت نتائج تحليل معامل المسار اظهار دليل الحصاد والحاصل البيولوجي أعلى تأثير مباشر موجب على حاصل الحبوب في الحنطة الخشنة بلغ ٠,٩٦٦ و٠,٢٤٢ على التوالي، بينما كان لدليل الحصاد أعلى تأثير مباشر موجب على حاصل الحبوب في الحنطة الناعمة بلغ ١,٤١٧ واللذين استخدما كمعيار لانتخاب التراكيب الوراثية المتفوقة في كل مجموعة.

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