

GENETIC VARIABILITY AND CORRELATIONS ON YIELD AND ITS COMPONENTS IN CERTAIN GENOTYPES OF DURUM WHEAT

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ABSTRACT

Twenty genotypes of durum wheat, which includes, eight varieties, seven crosses and other seven reciprocal crosses with local variety Waha were grown in RCBD design with three replications. Genetic variability, heritability, genetic advance, correlations and multiple regression equations were estimated for grain yield per plant, number of active tillers per plant, number of spikelet per spike, grain yield per spike, number of spikes per plant, number of grains per spike, 100-grain weight and biological yield. Significant differences between genotypes were observed for all studied characters. Number of active tillers per plant, number of grains per spike and biological yield had the maximum phenotypic and genotypic coefficient of variability and greatest genetic advance expressed as percentage of their means. Broad sense heritability estimates ranged from 54.28% for 100-grain weight to 99.73% for number of grains per spike. Grain yield per plant had higher positive correlations with number of active tillers per plant, grain yield per spike, number of spikes per plant and 100-grain weight, and lower correlations with the remainder characters. Partial correlations also exhibited the true association of grain yield per plant with number of active tillers per plant, grain yield per spike, number of spikes per plant and 100-grain weight. Stepwise regression analysis showed the higher importance of grain yield per spike and number of spikes per plant in predicting grain yield per plant with determination coefficient = 98.54% and Malu value, $C_{(p)} = 7.283$. The results revealed the importance of these two characters for improvement of grain yield per plant.

INTRODUCTION

Durum wheat (*Triticum turgidum* var. *durum*) covers approximately 20 million hectares world wide, which represent less than 10% of the total wheat areas. More than half of its hectareage lies in the Mediterranean region, where it may account for more than 50% of the land area under wheat, annual production is estimated around 30-35 million tons, one fourth of which in the European Union, followed by Southwest Asia and America, and production fluctuations are mainly due to climatic conditions, especially erratic rainfalls, which heavily affect the per hectare crop yield (Bozzini, 1988). The main use of durum wheat grain is for pasta making, including couscous and purgul, although in the Mediterranean countries a large part of the harvest is devoted to bread preparation (Quaglia, 1988).

For any planned breeding programs to improve grain yield potentials of this crop, it is necessary to obtain adequate information on the magnitude and type of genetic variability and their corresponding heritability. This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability for example, is used to indicate the relative degree to which a character is transmitted from parents to offspring. The magnitude of such estimates also suggests the extent to which improvement is possible through

selection. Briggs and Knowles (1967) put forward the view that if environmental variability is negligible compared to genetic variability, selection will be effective in improving the character if

such character with high genotypic variability and also easily measurable happened to be highly correlated with yield.

Now efforts are underway to develop better durum wheat genotypes. Such breeding efforts need critical evaluation of existing genetic variability, heritability, genetic advance and interrelationship between grain yield per plant and other traits of its components as studied by numerous researchers. For example, Austin (1994) believes that selection for lower stem, larger number of spikes per surface unit and larger number of grains per spike have made a major contribution to the wheat grain yield increase. Bahadur and Lodhi (1995) established that the indirect selection for grain yield through a larger number of grains per spike might increase wheat grain yield, while Calderini *et al.* (1995) established that the latest high yield cultivars had an increased grain weight in relation to older cultivars, and Okuyama *et al.* (2004) reported moderate correlation of number of spike m^2 and number of grains per spike with grain yield. Mc Neil *et al.* (1978) claims that the selection for 1000 grain weight and number of grains per plant or spike, was more successful in increasing grain yield of wheat than the selection for one component.

Present investigation was planned to measure extent of genetic variability, heritability and interrelationship of various traits to devise suitable selection criteria for further yield improvement.

MATERIALS AND METHODS

Twenty two genotypes of durum wheat: eight varieties, (1) Leeds, (2) Waha, (3) UmRabie5, (4) Azeghar1, (5) UmRabie3, (6) Brashua, (7) Cyprus1, (8) Korfilla, seven crosses with local variety Waha, (9) Leeds x Waha, (10) Waha x UmRabie5, (11) Waha x Azeghar1, (12) Waha x UmRabie3, (13) Waha x Brashua, (14) Waha x Cyprus1, (15) Waha x Korfilla, and seven reciprocal crosses with local variety Waha, (16) Waha x Leeds, (17) UmRabie5 x Waha, (18) Azeghar1 x Waha, (19) UmRabie3 x Waha, (20) Brashua x Waha, (21) Cyprus1 x Waha and (22) Korfilla x Waha, were sown using randomized complete block design with three replications at the research farm of field crops department, center of Mosul University in mid December 2006. Each plot was consist of one (2 meter long) line spaced 25 cm between them, and the grains dibbled at a distance of 5 cm. Observations were recorded for the following seven characters on five random plant from mid each plot: (1) Grain yield per plant in gram (GY), (2) Number of active tillers per plant (NT), (3) Number of spikelets per spike (NSS), (4) Grain yield per spike in gram (GYS), (5) Number of spikes per plant (NSP), (6) Number of grains per spike (NGS), (7) 100-grain weight in gram (HGW) and (8) Biological yield in gram (BY).

The analysis of variance and the estimation of simple and partial correlations among grain yield per plant and other traits were made according to the methods described by Gomez and Gomez (1983) and Al-Rawi (1987) respectively, as well as the following estimators were calculated:

- a- Genotypic variance (σ^2_G), Environmental variance (σ^2_E) and Phenotypic variance (σ^2_P) as follows: $\sigma^2_E = MSe$; $\sigma^2_G = (MSg - Mse)/r$; $\sigma^2_P = \sigma^2_G + \sigma^2_E$. Where, MSe, MSg and r, error mean square, genotypic mean square and replications respectively.
- b- Phenotypic and genotypic coefficient of variability (PCV and GCV) as follows:
 $PCV = [(Phenotypic\ variance)^{1/2} / \text{mean value of the trait}] \times 100$
 $GCV = [(Genotypic\ variance)^{1/2} / \text{mean value of the trait}] \times 100$
- c- Broad sense heritability [$h^2_{(bs)}$] = (Genotypic variance / Phenotypic variance) x 100
- d- Expected genetic advance (GA) as percent of the mean (y) from the equation:

$GA = K \times (\text{Phenotypic variance})^{1/2} \times h^2_{(bs)}$; Where K is selection intensity at 5% level (=2.06)

GA as % of mean = (GA / mean value of the trait) x 100

- e- Stepwise regression procedure used to select superior regression equations which reflect the relation among plant yield and its components.

All statistical procedures done with the help of Statistical Analysis System (SAS) and Microsoft Office Excel 2003.

RESULTS AND DISCUSSION

The analysis of variance results are given in Table 1 that revealed highly significant differences among genotypes for all studied characters, which indicated that the population was amenable to selection for all the eight characters studied. The orthogonal contrast test showed significant differences among parents mean and all hybrids mean for NSS, NSP and NGS, among parents mean and hybrids mean (with out reciprocals) and among parents mean and reciprocal hybrids mean for NSS, GYS, NGS

Table 1. Analysis of variance for grain yield per plant and its components.

Source	df	Mean Square							
		GY	NT	NSS	GYS	NSP	NGS	HGW	BY
Reps.	2	0.036	0.082	0.051	0.005	0.046	0.037	0.017	38.2
Genotypes	21	2.697**	1.49**	10.21**	0.163**	1.068**	69.02**	0.26**	98.3**
1-8 vs 9-22	(1)	0.345	0.144	71.58**	0.016	0.204*	43.19**	0.169	18.38
1-8 vs 9-15	(1)	0.055	0.204	29.21**	0.045*	0.289*	28.86**	0.322*	22.16
1-8 vs 16-22	(1)	0.064	0.232	30.42**	0.049*	0.305*	29.67**	0.331*	31.22
9-15 vs 16-22	(1)	0.167	0.077	6.33**	0.077**	0.137	32.07**	0.137	68.15*
Error	42	0.115	0.098	0.457	0.009	0.052	0.061	0.057	10.83

(*) Significant at P = 0.05; (**) Significant at P = 0.01.

and HGW, and among hybrids mean and reciprocal hybrids mean for NSS, GYS, NGS and BY. Ajmal *et al.* (2000), Baloch *et al.* (2001), Mahmood and Chowdhary (2002), Al-Hamdany (2006) and Alniami (2006) reported significant differences between durum wheat genotypes for several traits from their studies. The means of genotypes for studied characters with the results of DMRT test are presented in Table 2. Six genotypes, "19", "1", "7", "5(i)", "3(i)", "5(ii)", "4" and "9" recorded the highest values for GY (14.25), NT (6.97), NSS (20.77), GYS (2.08), NSP (7.00), NGS (55.73), HGW (5.90) and BY (51.77) respectively. Lowest values for the corresponding characters were recorded by genotypes: "6(i)", "13", "21(i)", "9", "6(ii)", "21(ii)", "1" and "6(iii)" respectively. Genotype "3" (UmRabie5) possessed the highest values for five characters (GY, NT, NSP, HGW and BY), while the genotype "6" had the lowest values for GY, NT, NSS, NSP and BY).

The highest phenotypic coefficient of variability (Table 3) existed for BY (14.457), followed by NT (12.619). Moderate phenotypic coefficient of variability were exhibited by NSS, NGS, GYS and NSP. Comparatively low variability was shown by GY (7.604) and HGW (6.514). Though the variability of GY as such was low, it was high for its components such as BY and NT. High genotypic coefficient of variability were shown by BY (12.345), NT (11.466) and NGS (11.600). Moderate to low values were shown by the remainder characters. The genotypic coefficient of variability followed

Table 2. Plot means for grain yield per plant and its components for durum wheat genotypes.

Genotype	Traits							
	GY	NT	NSS	GYS	NSP	NGS	HGW	BY
1	13.31def	6.97a	18.33b	2.00hi	6.67ab	40.27g	4.73f	49.80ab
2	12.25hij	5.57fg	18.43b	2.23efg	5.50f	43.60d	5.13ef	38.73efg
3	14.0abc	6.93a	16.87cde	2.00hi	7.00a	36.17kl	5.83abc	51.57a
4	14.0abc	5.70efg	15.43f-i	2.50bcd	5.60ef	42.27e	5.90a	44.67b-e
5	14.0abc	5.20g	19.87a	2.80a	5.00g	55.73a	5.10ef	34.07gh
6	11.20 l	4.67h	14.87hij	2.40cde	4.67g	43.50d	5.40cde	31.87h
7	12.60ghi	6.03c-f	20.77a	2.07ghi	6.10cd	38.27i	5.50a-e	45.37bcd
8	11.79jkl	5.97c-f	20.20a	2.03hi	5.80def	39.37h	5.23e	48.30abc
9	12.73fgh	6.83a	17.10cd	1.93i	6.60b	36.40k	5.57a-e	51.77a
10	13.56b-e	5.80ef	17.67bc	2.30ef	5.90c-f	45.33b	5.17ef	49.77ab
11	14.1abc	6.13c-f	16.87cde	2.30ef	6.10cd	40.57fg	5.53a-e	42.43c-f
12	14.15ab	5.83def	16.20d-g	2.53bc	5.60ef	44.57c	5.87ab	39.77d-g
13	11.48kl	4.60h	15.67e-h	2.27ef	5.07g	45.30b	5.30de	38.77efg
14	12.74fgh	6.50abc	15.43f-i	2.03hi	6.27bc	36.03kl	5.73a-d	43.10c-f
15	12.05ijk	6.40a-d	16.43c-f	1.97i	6.13cd	37.33j	5.50a-e	45.57a-d
16	13.09efg	6.77ab	16.10d-h	2.00hi	6.57b	36.10kl	5.43b-e	51.67a
17	13.4cde	5.77efg	16.53c-f	2.30ef	5.83c-f	45.03b	5.10ef	49.53a
18	13.72a-d	5.97c-f	15.87d-h	2.30ef	5.97cde	40.77f	5.43b-e	42.33c-f
19	14.25a	5.73efg	15.10g-j	2.60b	5.50f	44.30c	5.73a-d	39.87d-g
20	11.59kl	4.63h	14.20ij	2.33def	4.97g	45.23b	5.13ef	37.33fgh
21	12.74fgh	6.47abc	14.00j	2.07ghi	6.17cd	35.83 l	5.57a-e	41.67def
22	13.08efg	6.23b-e	15.87d-h	2.17fgh	6.03cd	37.20j	5.37de	44.43b-e
Mean	12.99	5.941	16.72	2.233	5.87	41.33	5.42	43.74

- Values for each trait having the same letter are not significantly different.

Table 3. Mean, Range, PCV, GCV, heritability and genetic advance as percent of the mean for grain

Yield per plant and its components.

Traits	Estimates					
	Mean \pm SD	Range	PCV	GCV	$h^2_{(bs)}$	GA%
GY	12.99 \pm 0.95	11.201 \pm 14.250	7.604	7.142	88.21	13.818
NT	5.941 \pm 0.705	4.600 \pm 6.970	12.619	11.466	82.56	21.461
NSS	2.233 \pm 0.233	14.000 \pm 20.770	11.517	10.784	87.68	20.801
GYS	5.87 \pm 0.597	1.930 \pm 2.800	10.999	10.146	85.08	19.279
NSP	5.367 \pm 0.625	4.670 \pm 7.000	10.648	9.914	86.69	19.015
NGS	41.33 \pm 4.796	35.830 \pm 55.730	11.616	11.600	99.73	23.865
HGW	5.420 \pm 0.295	4.730 \pm 5.900	6.514	4.799	54.28	7.284
BY	43.74 \pm 5.723	31.870 \pm 51.770	14.457	12.345	72.92	21.715

the trend of phenotypic coefficient of variability. Thus the genotype-environment interactions were apparently non-significant. Very high estimates of heritability (which is an index of

transmissibility of a character) were observed for all characters under study except HGW (it was moderate and equal 54.28). NGS showed the highest heritability estimate of 99.73% , followed by GY (88.21%), NSS (87.68%), NSP (86.69%), GYS (85.08%), NT (82.56%) and BY (72.92%). At 5% level of selection, the highest moderate genetic advance of 23.865 expressed as percentage of mean was expected for NGS. The GY, NT, NSS, GYS, NSP and BY had similarly moderate expected genetic advance of 13.818%, 21.461%, 20.801%, 19.279%, 19.015% and 21.715%, respectively. Relatively low genetic advance was expected for HGW (7.284%). The three characters NT, NSS and NGS, which had high PCV and GCV, exhibited the same trend of high heritability estimates. Evidently, the same three characters showed the maximum expected genetic advance expressed as percentage of their means, therefore, with this trend of extremely high relation between PCV, GCV, heritability and genetic advance, it is easy to guess that the genetic advance in the next generation even only on the basis of estimates of PCV. In such populations mass-selection technique of improvement will prove most successful. Similar trend as that far for these three characters was not observed for remaining characters. BY, which had moderately higher GCV had relatively lower heritability. GY, which had lowest GCV (7.142), had proportionately high heritability (88.21%). For these characters the expected genetic advance was not in direct proportion with the GCV. Therefore GCV is always not a true estimate of heritable variation. Thus, heritability must be considered while selection is made. The characters which had low estimates of GCV necessarily did not show similarly low values of heritability. These findings lead to the conclusion that genetic advance under selection will depend upon both GCV and heritability. Singh and Bains (1968) also made similar conclusion and advocated that the expected genetic advance is the product of (i) the selection differential measured in terms of the phenotypic standard deviation, (ii) the GCV, and (iii) the square-root of heritability ratio. The estimates of heritability (54.28% to 99.73%) were rather high. This may partly be explained by failure of deducing the environment-genotype interaction in the present study. These estimates also presumed that all the genetic effects were additive.

Simple correlation coefficients for GY per plant and its components are presented in Table 4. GY showed significant positive correlation with NT, SY and NSP, and non-significant positive correlation with other characters. NT showed highly significant correlation, positive with NSP and BY, and negative with GYS and NGS. NSS was negatively significantly correlated with HGW and non significantly, positive or negative with other characters. SY showed highly significant correlation, positive with NGS and negative with NSP and BY, and positive non-significant correlation with HGW. NSP was negatively strongly associated with NGS, and positively strongly associated with BY, while NGS showed negative significant correlation with HGW and BY. The significant positive relationship of GY with NT, GYS and NSP suggests that improvement in NT, GYS or NSP is likely to bring some improvement in GY. These three characters which along with many other characters, are the components of GY, each of them may not be safely taken as the only character to be considered for bringing about an improvement in the later. Correlation among the components of GY has an important bearing on this point. For instance BY which has strong positive association with NT was non-significantly associated with GY. The partial correlation coefficient between GY and BY became positive and highly significant if the effect of GYS was eliminated, and negative non-significant if the effect of NT was eliminated (Table 5). It was shown that the partial correlation between GY and NT or GYS remained positive and significant for the most cases irrespective of holding any character

Table 4. Simple correlation among grain yield per plant and its components.

Traits	NT (2)	NSS (3)	GYS (4)	NSP (5)	NGS (6)	HGW (7)	BY (8)
GY (1)	0.3952*	0.0640	0.3731*	0.3499*	0.1399	0.3268	0.2463
NT (2)		0.1562	- 0.6618**	0.9653**	- 0.7246**	0.2096	0.7748**
NSS (3)			- 0.0897	0.1516	0.1778	- 0.3723*	0.2435
GYS (4)				- 0.7348**	0.8596**	0.0455	- 0.6708**
NSP (5)					- 0.7506**	0.1834	0.8499**
NGS (6)						- 0.3708*	- 0.5803**
HGW (7)							0.0099

(*) Significant at $P = 0.05$; (**) Significant at $P = 0.01$.

Constant, and between GY and NSP remained significant positive irrespective of holding NSS, GYS and NGS, non-significant positive irrespective of holding HGW and BY constant and non-significant negative irrespective of holding NT constant. GYS and NSP were the most important characters which if held constant gave higher positive significant correlations ($r_{15.4} = 0.9917$ and $r_{14.5} = 0.9918$). The low correlation of GY with NSS ($r = 0.0640$) remained in the same trend through the elimination of any other characters, that is an indication of unimportant of this characters for predicting high grain yield. The same indication could be suggested for the relation of GY with NGS, HGW or BY. The partial correlation among the components of GY shown in table 6. The simple phenotypic correlation of NT with NSP, GYS with NGS and NSP with BY positive and very strong ($r = 0.9653$, 0.8596 and 0.8499 respectively), the elimination of the effect of GY and any other characters still increased this associations. The same thing was true for most cases found in Table 6, unless some correlations that changed through the Elimination of some variables, for instance, the non-significant positive correlation of NT with NSS that transformed to significant negative through elimination of BY effect ($r_{23.8} = - 0.503$), and the positive highly significant correlation of NT with BY which became negative non-significant through elimination of NSP. All seven components of grain yield per plant were considered for constructing superior regression equations could be used for predicting high GY, by working out stepwise regression procedure. Table 7 introduced six regression equations as a result of stepwise regression program that used in this analysis with values of computed F from analysis of variance for each regression equation, determination coefficient (R^2) and Malu values (C_P). The equations 3, 4, 5 and 6 had significant F, high determination coefficients (98.63%, 98.54%,

Table 5. Partial correlation among grain yield per plant (1) and its components.

Particulars	Coefficient of correlation when holding the following characters constant:						
	NT (2)	NSS (3)	GYS (4)	NSP (5)	NGS (6)	HGW (7)	BY (8)
1 and 2	----	0.3908*	0.9232**	0.2348	0.7277**	0.3535*	0.3335
1 and 3	0.0025	----	0.1055	0.0118	0.0402	0.2117	0.0043
1 and 4	0.9216**	0.3812*	----	0.9918**	0.4997*	0.3794*	0.7489**
1 and 5	- 0.1317	0.3449*	0.9917**	----	0.6953**	0.3121	0.2752
1 and 6	0.6733**	0.1309	- 0.3814	0.6503**	----	0.2974	0.3583*
1 and 7	0.2716	0.3786*	0.3343	0.2852	0.4118*	----	0.5951**
1 and 8	- 0.1032	0.2384	0.7217**	- 0.1035	0.4061*	0.2572	----

(*) Significant at P = 0.05; (**) Significant at P = 0.01.

Table 6. Partial correlation among components of grain yield per plant.

Particulars	Coefficient of correlation when holding the following characters constant:							
	GY (1)	NT (2)	NSS (3)	GYS (4)	NSP (5)	NGS (6)	HGW(7)	BY (8)
2 and 3	0.143	----	----	0.129	0.038	0.420*	0.258	-0.503**
2 and 4	-0.949**	----	-0.659**	----	0.268	-0.111	-0.687**	-0.303
2 and 5	0.961**	----	0.965**	0.942**	----	0.925**	0.964**	0.921**
2 and 6	-0.857**	----	-0.774**	-0.407	-0.001	----	-0.712**	-0.534**
2 and 7	0.093	----	0.292	0.320	0.127	0.747**	----	0.319
2 and 8	0.761**	----	0.769**	0.595**	-0.331	0.613**	0.790**	----
3 and 4	-0.123	0.019	----	----	0.032	-0.482**	-0.079	0.102
3 and 5	0.138	0.003	----	0.127	----	0.438*	0.241	-0.108
3 and 6	0.171	0.428*	----	0.501*	0.447*	----	0.046	0.404*
3 and 7	-0.417*	-0.419*	----	-0.370	-0.412*	-0.335	----	-0.386*
3 and 8	0.236	0.196	----	0.248	0.220	0.433*	0.266	----
4 and 5	-0.996**	-0.490*	-0.733**	----	----	-0.265	-0.757**	-0.421*
4 and 7	-0.087	0.251	0.013	----	0.270	0.768**	----	0.070
4 and 8	-0.848**	-0.334	-0.672**	----	-0.129	-0.413*	-0.672**	----
5 and 6	-0.862**	-0.284	-0.799**	-0.343	----	----	-0.748**	-0.599**
5 and 7	0.078	-0.074	0.261	0.320	----	-0.155	----	0.332
5 and 8	0.841**	0.618**	0.848**	0.709**	----	0.769**	0.919**	----
6 and 7	-0.445*	-0.325	-0.334	-0.803**	-0.359*	----	----	-0.448*
6 and 8	-0.641**	-0.043	-0.653**	-0.009	0.166	----	-0.621**	----
7 and 8	-0.077	-0.247	0.112	0.055	-0.282	-0.271	----	----

(*) Significant at P = 0.05; (**) Significant at P = 0.01.

98.71%, 98.88%) and lower $C_{(P)}$ values (7.87, 7.283, 6.67, 5.876) respectively, and from these results, equation 4 could be chosen as a superior one for prediction or selection of high GY per plant, that is due to its consistency of lower number of variables (GYS and NSP), which together accounted for 98.54% of the total variability for GY per plant in the population. It is revealed that a compromise between GYS and NSP brought about by assigning their partial regression coefficients will lead to maximum improvement in GY per plant.

Table 7. Superior regression equations among grain yield per plant and its components

Sq	Regression equations	Cal. F	R ²	C _(p)
1	$GY = 9.831 + 0.532 NT$	3.70 ^{ns}	15.62	1331.6
2	$GY = - 6.416 + 1.537 NT + 4.599 GYS$	65.22**	87.29	187.3
3	$GY = - 12.419 - 0.159 NT + 5.628 GYS + 2.349 NSP$	432.8**	98.63	7.87
4	$GY = - 12.107 + 5.579 GYS + 2.155 NSP$	643.1**	98.54	7.283
5	$GY = - 11.729 + 5.808 GYS + 2.119 NSP - 0.017 NGS$	458.3**	98.71	6.67
6	$GY = - 12.078 - 0.232NT + 5.945GYS + 2.395NSP - 0.021NGS$	376.1**	98.88	5.873

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بعض التراكيب الوراثية من الحنطة الخشنة

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المستخلص

تضمنت الدراسة اثنان وعشرون تركيباً وراثياً من الحنطة الخشنة، وهي ثمانية اصناف وسبعة هجن وسبعة هجن عكسية مع الصنف واحة المعتمد في العراق. زرعت التراكيب الوراثية باستخدام تصميم القطاعات العشوائية الكاملة بثلاثة قطاعات. تم تقدير التغيرات الوراثية ونسبة التوريث والتحسين الوراثي المتوقع لصفات حاصل الحبوب بالنبات وعدد الاشطاء الفعالة بالنبات وعدد السنبيلات بالسنبلة وحاصل حبوب السنبلة وعدد السنايل بالنبات وعدد الحبوب بالسنبلة ووزن 100 حبة والحاصل البايولوجي، ثم قدرت قيم معاملات الارتباط البسيط والجزئي بين حاصل الحبوب ومكوناته ووفقت معادلات انحدار متعدد للتنبؤ بالحاصل العالي. اظهرت النتائج وجود اختلافات معنوية عالية بين التراكيب الوراثية للصفات جميعها. تميزت صفات عدد الاشطاء بالنبات وعدد الحبوب بالسنبلة والحاصل البايولوجي بقيم عالية لمعامل الاختلاف المظهري والوراثي والتحسين الوراثي المتوقع كنسبة مئوية من المتوسط. تراوحت نسبة التوريث بالمعنى الواسع بين 54.28% لوزن 100 حبة و 99.73% لعدد الحبوب بالسنبلة. كان ارتباط حاصل الحبوب بالنبات موجباً ومعنوياً مع عدد الاشطاء بالنبات وحاصل السنبلة وعدد السنايل بالنبات ووزن 100 حبة وضعيفاً مع بقية الصفات. اظهر الارتباط الجزئي العلاقة الحقيقية لحاصل الحبوب مع كل من عدد الاشطاء بالنبات وحاصل حبوب السنبلة وعدد السنايل بالنبات ووزن 100 حبة. تبين من تحليل الانحدار المتدرج ان لصفتي حاصل حبوب السنبلة وعدد السنايل بالنبات الاهمية الاكبر في التنبؤ لحاصل الحبوب العالي بالنبات بمعامل تحديد = 98.54% وقيمة مالو $C(P)$ تساوي 7.283. وأشارت النتائج الى اهمية هاتين الصفتين في تحسين حاصل الحبوب بالنبات.