

Path coefficient analysis and estimation of some genetic parameters in F₂ durum wheat

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ABSTRACT

Six characters of F₂ populations derived from $\Delta \times \Delta$ intervarietal half diallel cross of durum wheat (*Triticum durum* Desf.) were studied using RCBD design with three replications. Genotypic and phenotypic variances were significant for all studied characters. Phenotypic and genotypic correlations were positive and highly significant between grain yield and each of No. of spikes per plant and biological yield. The phenotypic and genotypic path analysis showed that the No. of spikes per plant and biological yield had the highest direct effects on grain yield, and these two characters exhibited intermediate broad sense heritability (0.9 and 0.90) and expected genetic advance as percent of the character mean (31.07 and 29.00) respectively. Great importance of these two characters mentioned predicting grain yield with determination coefficient (0.37 and 0.38) and contributed percent of both (4.41%) among yield.

INTRODUCTION

Wheat grain yield is a complex character, it is the product of the contributions made by its components, it can not be wholly used as a criterion for selection because its low heritability and wide fluctuations as a result of its interaction with the environment. Grafus (1961) indicated that selection of one grain yield components instead of the yield depend mainly on the correlation between yield and its components. Estimation of direct and indirect effects were quite important, (Wright, 1921). Such principles had been used by (Yousif and Kasim, 1998; Budak, 2000; Ahmed, 2003; AL-Hamdany and Yousif 2006 and Ayoob, 2006). Heritability used to indicate the relative degree to which a character is transmitted from parents to offspring, such estimation is of great importance because it indicates the breeding program to be used for the improvement of a character. Evaluation of heritability and genetic advance for grain yield and its components were studied in wheat (Rashid, 1989 and Yousif and Kasim, 1999), (AL-Saffar, 2001) in F₂ generation in barley. (AL-Rawi and Ahmad 1984) in upland cotton. AL-Hamdany *et al.* (2009) revealed that No. of spikes/plant and 100-grain weight showed higher determination coefficient and contributing percent in F₂ generation in durum wheat.

Using F₂ diallel cross generation considered of great useful to estimate the genetic parameters which control the studied characters, then to improve the yield through, due to the segregation in the genetical material as well as to F₂ grain availability in self pollinated crops (Hanafi and Gallis, 1999; Esmail, 2002; AL-saffar, 2001; Aghwan, 2000 and Yousif, 2008).

This study was conducted to estimate the genotypic-phenotypic correlations, path coefficient analysis, heritability, genetic advance as percent of the character mean, for some quantitative characters of durum wheat.

MATERIALS AND METHODES

The genetic materials used in this study were $\Delta \times \Delta$ F₂ populations derived from $\Delta \times \Delta$ diallel cross of durum wheat. These varieties were: leeds, Waha, Um-Rabi, Azeghar, Um-Rabi, Brashua, Cyprus and Korfila. Al-Hamdany (2000) indicated the variety sources, the experimental design and hybridization to obtain F₂. Parents and F₁ were sown in November 2007 using RCBD design with three replications at the Fields of Agric. and Forestry college, Mosul University. Each plot consisted of two lines of each entries 3m Long, 30cm apart, at plant to plant distance of 10cm between plants. The following characters were measured for 10 randomly chosen plants of each plot: no. of spikes per

plant (X_1), no. of grains per spike (X_2), 100-grain weight in gm (X_3), harvest index as percent (X_4), biological yield in gm (X_5) and grain yield in gm (Y).

(SAS) and Microsoft office Excel 2003, were used to:

- 1- Construct Analysis of variance of studied characters according to the experimental design method used (AL-Rawi and Khalaf Allah, 2000).
- 2- Genotypic (VG), phenotypic (VP), Environmental Variances (VE) and broad sense heritability ($h^2_{b.s}$) as outlined by Singh and Chaudhary (2007). $h^2 < 0.2$ low, $0.2-0.6$ moderate and > 0.6 high (Ali, 1999).
- 3- Genotypic (rG) and phenotypic (rp) correlations according to Walter (1970).
- 4- Path coefficient analysis by (Wright, 1921), Fig 1.
- 5- The expected genetic advance (GA) over direct selection for yield of second filial generation (Allard, 1960), where $GA = k h^2_{b.s} \sigma_p$, $k =$ selection differential = 2.76 for 5% selection and $\sigma_p =$ phenotypic standard deviation in F_2 .
- 6- Expected genetic advance as a percent of each character to general mean in F_2 (GA%) from the equation $GA\% = (GA / \text{character mean}) \times 100$. Agarwal and Ahmad (1982) reported that $GA\% < 10\%$ Low, $10-30\%$ moderate, $> 30\%$ high.

Estimated values of geno-phenotypic and environmental variances presented in Table (1), were significant for all studied characters at 1% or 5% of probability level.

Falconer, (1981) indicated that genetic correlation takes place either by linkage of genes or by pleiotropy or both of them. Table (2) showed Phenotypic-genotypic correlation coefficients, which were positive and significant for grain yield, with each of biological yield, harvest index, no. of grains per spike and no. of spikes per plant.

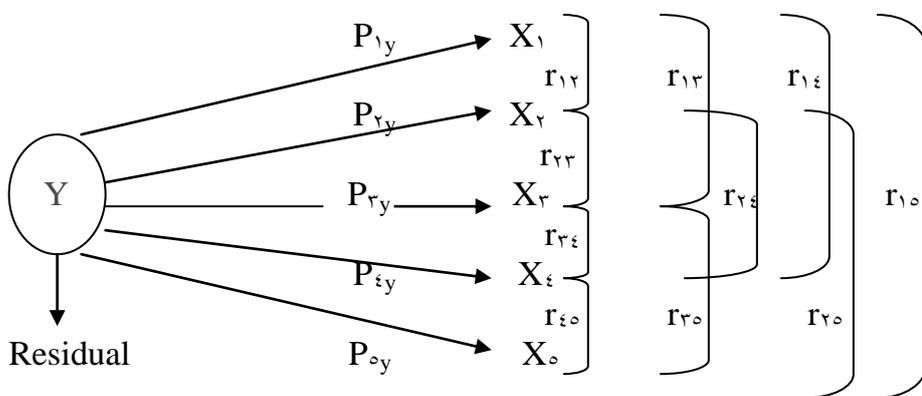


Fig 1. Path coefficient diagram of factors affecting grain yield in durum wheat.

Table (1). Genotypic- environmental and phenotypic variances for studied characters in F_2 .

Variance	Characters					
	no. spikes per plant	no. grains per spike	100-grain weight(gm)	harvest index%	biological yield(gm)	grain yield(gm)
VG	28,276*	41,438**	0,102*	2,190*	72,60**	10,037*
	± 10,107	± 10,92	± 0,037	± 0,718	± 26,369	± 3,603
VE	27,390*	01,170*	0,109	1,488	74,163*	10,344*

	± ٧,١٩٤	± ٣١,٤٣٧	± ٠,٠٢٨	± ٠,٣٩٠	± ١٩,٤٧٦	± ٢,٧١٠
VP	٥٥,٦٧١*	٩٢,٦٠٨*	٠,٢١١*	٣,٦٨٤*	١٤٦,٧٦٥*	٢٠,٣٨١*
	± ١٥,١٥١	± ٢٥,٢٠٤	± ٠,٠٥٧	± ١,٠٠٢	± ٣٩,٩٤٤	± ٥,٥٤١

(**) and (*) Significant at ١% and ٥% respectively

The relationships between each of no. of spikes per plant and biological yield, no. of grains per spike and harvest index were positively highly significant, in such case any increasing in one character lead to increasing in an other, a negative significant correlation coefficient shown between each of pairs: no. of grains per spike and ١٠٠-grains weight, harvest index and biological yield, so any increasing in a character will lead to a decreasing in another. The correlation between either yield and any of it's components or between any pairs considered of a good magnitude to the breeder, therefore the selection depend on any character in early generations will give a chance to have a high product progenies. Positive and negative correlations were determined by numerous researchers such as (Rashid, ١٩٨٩; Ferreira *et al.*, ١٩٩٧; Yousif and Kasim ٢٠٠٠ and Al-Hamdany and Yousif, ٢٠٠٦). The phenotypic correlation direct effect were positive for all characters on yield, Table(٣,) but high for biological yield and no. of spikes per plant (٠,٨٤٠٨ and ٠,٥٤٣) respectively. The genotypic direct effect were positive and high for no. of spikes per plant and biological yield,(٠,٥٧٧ and ٠,٨٧٠) moderate for

Table(٢). Phenotypic and genotypic correlations among yield and its components in F_٧.

Characters	Correlation Coefficient	Characters				
		biological yield(gm)	harvest index%	١٠٠-grain weight(g m)	no. grains per spike	no. spike per plant
Grain yield(gm)	rp	٠,٧٧٠**	٠,٤٢٠٩**	٠,٠٩٥٥	٠,٥٦٦٤**	٠,٦٥٧٤**
	rG	٠,٦٠١**	٠,٥٩٩١**	٠,١٠٢١	٠,٦٢٣١*	٠,٥١٠**
no. spikes per plant	rp	٠,٧٧٩١**	-٠,٠٧٠٢	٠,٠٢٦٩	٠,٠٢٣٧	
	rG	٠,٨١١٠**	-٠,٠٩٩١	٠,٠٣٦٦	٠,٠٣٣٢	
no. grains per spike	rp	٠,١٧٦٧	٠,٦٢٢٠**	-٠,٣٦٩٥**		
	rG	٠,١٩٩٢	٠,٧٤٠٠**	-٠,٤٢٠١**		
١٠٠-grain weight(gm)	rp	٠,٠١٢٢	٠,١٦٣٨			
	rG	٠,٣٢١	٠,١٨٢٨			
harvest index%	rp	-٠,٢١٤٠*				
	rG	-٠,٢٣٣٠*				

(**) and (*) Significant at ١% and ٥% respectively.

Table(٣): Path coefficient analysis between grain yield and it's component in F_٧

Characters		no. spikes per plant	no. grains per spike	١٠٠-grain weight(g m)	harvest index%	biological yield(gm)	grain yield(g m)
no. spikes per plant	pheno.	(٠,٥٤٣١)	٠,٠٠٢١	٠,٠٠٠٨	-٠,٠٣٨٢	٠,٦٥٥١	١,١٦٢٩
	geno.	(٠,٥٧٧٠)	٠,٠٠٣٢	٠,١٠٠٠	-٠,٠٢١١	٠,٦٧٧٠	١,٣٣٦١
no. grains per spike	pheno.	٠,٠٠٠٩	(٠,٠٨٩٧)	-٠,٠١٠٥	٠,٣٣٧٨	٠,١٤٨٦	٠,٥٦٦٤
	geno.	٠,١١٠٠	(-٠,٣٠١)	-٠,٠٠١١	٠,٣٦٦١	٠,١٥٣٢	٠,٣٢٧٢
١٠٠-grain weight(g)	pheno.	٠,٠٠١٠	-٠,٠٣٣١	(٠,٠٢٨٤)	٠,٠٨٩٠	٠,٠١٠٣	٠,٠٩٥٥
	geno.	٠,٠١٣٣	-٠,٠٢٢٠	(٠,٢١١٠)	٠,٠٩٢٢	٠,٠١٣٣	٠,٣٠٧٨

m)							
harvest index%	pheno.	-0.026	0.008	0.046	(0.376)	0.1799	0.2703
	geno.	-0.012	0.066	0.061	(0.261)	0.1140	0.2021
biological yield(gm)	pheno.	0.293	0.108	0.003	-0.1162	(0.8408)	0.7700
	geno.	0.231	0.161	0.291	-0.1022	(0.8702)	0.8363
Residual effect (pheno.)			0.8326			0.0321	
				Residual effect (geno.)			

100-grains weight, and low for harvest index on grain yield. Other wise no. of spikes per plant through harvest index, no. of grains per spike through 100-grains weight and biological yield through harvest index have negative geno-phenotypic indirect effects, that is due to the negative correlation between such pairs of characters. A residual effects related to the errors among samples or to other characters not dependent (i.e out of this study) which still have an effects on yield, similar results were reported by Ahmed (2003) and AL-Hamdany and Yousif (2006).

Table(4) showed that no. of spikes per plant, harvest index and biological yield have a higher heritabilities (09,6, 00,8 and 49,0) respectively, these characters have been governed by genes effects, while the remaining characters showed an intermediate ranges due to close values of their genetic environmental variance (as in table 1).

Table (4) Some genetic parameters of yield and it's components in F₂ half diallel cross.

Characters	\bar{X}	$h^2_{b.s}$	GA	GA%
no. of Spikes/plant	7,084	0,096	2,306	31,072
no. of Grain/Spike	13,889	0,447	8,870	20,246
100-grain weight (gm.)	4,198	0,483	0,407	10,892
Harvest index (%)	34,083	0,008	7,807	22,900
Biological-yield (gm.)	41,837	0,490	12,340	29,008
Grain-yield (gm.)	13,889	0,492	4,080	32,970

The expected genetic advance with respect to the characters mean used as a criterion of selections, so that it was called by (Falconer, 1981) a response to selection. Table 4. showed also a significant amount of genetic advance was expected in no. spikes plant 31,1%, biological yield 29.0, harvest index 22,9 and no. of grains per spike 20,2%. While a small amount of genetic advance was expected for 100-grains weight 10,9%, such agreed with Rashid (1989), Kasim *et al.*, (1992), Ali (1990), Yousif and Kasim (1999), Ahmed (2003), Ayoob (2006) and Al-Hamdany (2007) in wheat Al-saffar (2001) and Yousif *et al* (2003) in barely. Table 5. revealed that the biological yield and no. of spikes per plant have determination coefficient (0,68 and 29,49) respectively from the yield variance, the contributed effects of both was (0,47%).

Table (5): Components (direct and joint effect) in percentage of grain yield variation.

Source of Variation	determination coefficient	contributing percent
Direct effect of no. of spikes plant	0,294906	13,700
Direct effect of no. grains spike	0,008040	0,374
Direct effect of 100-grain weight(gm)	0,008000	0,037
Direct effect of harvest index %	0,001414	0,066
Direct effect of biological yield(gm)	0,706883	32,839
$X^1.X^2$	0,000160	0,007

X ¹ .X ³	٠,٠٠٠٠٥٨	٠,٠٠٣
X ¹ .X ^٤	-٠,٠٠٢٨٧١	٠,١٣٣
X ¹ .X ^٥	-٠,١٦٠٨١٨	٧,٤٧١
X ^٢ .X ^٣	-٠,٠٠١٨٨٠	٠,٠١٨٧
X ^٢ .X ^٤	٠,٠٦٠٥٧٥	٢,٨١٤
X ^٢ .X ^٥	٠,٠٢٦٦٤٣	١,٢٣٨
X ^٣ .X ^٤	٠,٠٠٥٠٤٨	٠,٢٣٥
X ^٣ .X ^٥	٠,٠٠٠٥٨٥	٠,٠٢٧
X ^٤ .X ^٥	٠,٠٤٩٢٧٠	٢,٢٨٩
Residual effect	٠,٨٣٢٥٨٦	٣٨,٦٧٩
Total	١	١٠٠

From the above results we could concluded that biological yield and no. of spikes per plant were recommended as a criterion for selection in the second filial generation for improving grain yield potential of durum wheat.

تحليل معامل المسار وبعض المعلمات الوراثية في الجيل الثاني للحنطة الخشنة

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الخلاصة

تمت دراسة ستة صفات لثمانية وعشرين عائلة في الجيل الثاني استحصلت من التهجين التبادلي النصفى لثمانية أصناف في الحنطة الخشنة. زرعت الأصناف وهجنها التبادلية بتصميم القطاعات العشوائية الكاملة بثلاثة مكررات. تم تقدير التباينات الوراثية والمظهرية والبيئية والتوريث والتحسين الوراثي المتوقع واعتمد تحليل المسار لتجزئة الارتباطات بين الحاصل ومكوناته إلى تأثيرات مباشرة وغير مباشرة وتقدير الأهمية النسبية لمساهمة كل صفة. كان التباين المظهري والوراثي موجباً ومعنوياً لجميع الصفات المدروسة. ارتبط حاصل الحبوب بمعنوية عالية مع كل من عدد السنابل بالنبات وعدد الحبوب بالسنبله ودليل الحصاد والحاصل البيولوجي، وكان لصفتي عدد السنابل بالنبات والحاصل البيولوجي تأثيراً مباشراً عالياً على الحاصل. كما أظهرت هاتان الصفتان قيماً متوسطة للتوريث بالمعنى الواسع (٥٠,٩٦, ٤٠,٩٥) على التوالي، وقيماً متوسطة (٣١,٠٧ و ٢٧,٥٠) للتحسين الوراثي المتوقع كنسبة مئوية من تباين الصفة. كانت قيمة معامل التحديد لهاتين الصفتين (١٣,٧٠ و ٣٢,٨٤) من تباين الحاصل على التوالي، في حين بلغ التأثير المشترك (٧,٤٧١%) لكليهما على الحاصل.

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