

Effect Genetic correlation of growth characteristics and yield of barley under different seeding rates

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Received:	Abstract
Aug. 27, 2022	to This study was carried out in the field of the College of Agricul-
	tural Engineering Sciences - University of Baghdad - Jadriya in the
	win-ter season 2019-2020 in order to study the genetic correlations of
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Oct. 28, 2022	with the effect of three seed rates (130, 160 and 190 kg ha_1). The
	experiment was applied using the split plot design and with three rep-
	lications according to the randomized complete block design. The
Published:	main plots included three seeding rates, while the Sub-plots in-cluded
Dec. 5, 2022	four varieties. The results showed that the genetic correlation was
Dec. 5, 2022	positive and highly significant between the traits of the number of
	spikes and the trait of the number of grains in the spike with the grain
	yield and for all seeding rates, so that plant breeders can rely on them
	as a selective evidence for high yield in barley
	Kaywords: Genetic correlation barley seeding rates

Keywords: Genetic correlation, barley, seeding rates.

Introduction

Knowing the relationship between genotypes is one of the important foundations in genetics and plant breeding, so plant breeders show interest in the distinct genetic structures of some desirable traits, and plant breeders need to estimate genetic variations in the various studied traits [1]. The genetic link arises from the genetic linkage and the multiple action of the gene pleiotropy, or from the relationships of evolutionary origin between the components of the crop due to the indirect influence of the genetic act. There are also negative correlations between the components of the yield [2]. Associated traits as selective guides in the process of breeding and improvement, as estimating the correlations between pairs of traits is important in evaluating breeding programs and choosing a more efficient breeding program. The genetic correlation is the correlation of the genotype values of two traits and depends on the similarity between relatives, and it is calculated from the components of the common variance of the two traits when analyzing the covariance. Fathi et al. [3] concluded that the genetic correlation was significant and negative for this trait with the grain yield and the weight of 1000 grains in the barley crop. Al-Fahdawi [4] found in a study of the field characteristics of the barley crop a positive significant correlation between the grain yield and the area of the flag leaf, and AL-Hamadany et



al. 5 found positive and significant correlations for the attribute of the area of the flag leaf with the grain yield. Jalal [6] concluded that the genetic correlations for the number of straws were significant and positive with the grain yield (Anwar et al. [7], Yani and Rashidi [8]) found a positive correlation between the number of days to physiological maturity and the grain yield. Heumez [9] get a significant finding in the characteristics of the number of spikes m-2 plant, the number of spike grains and grain yield m-2 in barley, as the results of [10] indicated that the genetic and phenotypic correlation of the number of days to physiological maturity with the grain yield was significant and positive at the seeding rate of 200 kg ha-1, and this trait also showed a correlation significantly positive with flag leaf area at the genetic level across seed rates 120, 160 and 200 kg ha-1. Hassan [10] mentioned when studying 21 genotypes of the wheat crop found that the genetic correlation of the growth rate of the crop with the grain yield was positive and highly significant for the seed rate of 120 kg ha-1 and the seed rate of 200 kg ha-1, as well as the correlations of this trait with the two traits. Dry matter yield at flowering and biological yield at seeding rates 120, 160 and 200 kg ha-1 is highly positive, genetically and environmentally positive, with the exception of genetic correlation with biological yield at seed rate of 160 kg ha-1, which was positive insignificant. On the contrary, this trait showed a significant negative genetic correlation with plant height only across different seed rates, and [10] mentioned that the genetic correlations for biological yield trait were positive and highly significant with grain yield and across three seed rates (120, 160 and 200) kg ha-1 and it was also mentioned that the genetic correlations for the trait of grain yield were positive and highly significant across seed rates (120, 160 and 200) kg ha-1, as Pakniyat et al. [11] found that the genetic correlations for number of spikes were positive and highly significant with grain yield. significant correlation for number of grains in spike with the height of the plant, number of tillers m-2, number of spikes m-2, and the weight of 1000 grains [12]. Yetsedaw et al. [13] found that the trait of spike length was positively and weakly correlated with barley grain yield.

Materials and Methods

The aim of this study is to know the genetic correlation of growth characteristics of barley cultivars by the effect of seed rates. A field experiment of the crop was carried out in the field of the Department of Field Crops - College of Agricultural Sciences - University of Baghdad in Jadiriyah for the winter season for the year 2019-2020. The experiment was applied by split plot design and in three replications according to the RCBD. The main plots included three seeding rates of 130-160-190 kg ha⁻¹. As for the sub-plots, four cultivars Iba 99, Iba 265, Bohuth 244, and Amal. 100 kg ha⁻¹ triple superphosphate was added, (20% P). While urea fertilizer was used with 200 kg ha⁻¹ (46% N) was divided into two treatments, the first was

applied two weeks after sowing and the second at the beginning of the flowering stage. The seeds were manually sown within the lines, the distance between one line and another was 20 cm, with a depth not exceeding 5 cm. The field was also weeded. At flowering, the aphid was controlled with Sumsdin. Field characteristics: days to



50% flowering, plant height (cm), flag leaf area (cm²), number of days from planting to physiological maturity (day), crop growth rate (gm. Plant day⁻¹), spike length (cm), number of spikes m⁻², number of grains spike⁻¹, weight of 1000 grain (gm), dry weight (gm), biological yield (kg ha⁻¹), grain yield (kg ha⁻¹). The genetic correlation analyzes were performed as reported by [14] using the statistical program SPAR 2.0. The following formula was used to calculate genetic correlation.

$$\mathbf{r}_{\mathrm{Gxy}} = \frac{cov\overline{Gxy}}{\sqrt{\partial^2 GX \cdot \partial^2 GY}}$$

Results and Discussion Genetic correlation

Tables (1 to 6) show the genetic correlations for all possible pairs among thirteen traits. The most important results of these correlations are as follow:

Number of days from planting to 50% flowering

Tables (1, 3 and 5) indicate that the characteristic of the number of days from planting up to 50% of flowering was genetically negative and highly correlated with grain yield in all three seed rates except for the genetic link, which was positive and highly significant in the third seed rate (190 kg ha⁻¹). These results in agreement with [15, 16 and 17] and the correlation of this trait with plant height was genetically negatively significant in seed rates 130 kg ha⁻¹ and 160 kg ha⁻¹, while the genetic correlation of this trait with plant height was positive and highly significant, as well as the genetic correlation of this trait with the number of days from sowing to physiological maturity was positive and highly significant across the three seeding rates, this result matched with the results of many studies [16, 18, and 19]. The genetic correlation of this trait was also highly significant with the area of the flag leaf and spike length in the three seed rates, except for the genetic link, which was insignificantly positive in the seed rate of 190 kg ha⁻¹. Munir [20] obtained similar results regarding the correlation with the area of the flag leaf.

Plant height (cm)

Tables (1, 3 and 5) show that the trait of plant height is genetically highly positive with the total yield across the three seed rates. These results are in agreement with what was found by [21], and this trait also showed a highly significant positive genetic correlation with the number of tillers for seed rates of 130 kg ha⁻¹ and 190 kg ha⁻¹, this trait was also genetically negatively significant with the characteristics of spike length and flag leaf area across seed rates 130 kg ha⁻¹ and 160 kg ha⁻¹.

Flag leaf area (cm²)

Tables (1, 3 and 5) showed that the genetic correlation of this trait was negative and highly significant with grain yield across the three seed rates, except at the seed rate of 190 kg ha⁻¹ which was significant and positive. This result is consistent with what was found by [3]. The genetic correlation of this trait differed with the number



of tillers between negative and positive and according to the seed rates, as it was insignificant negative in the seed rate of 130 kg ha⁻¹ and insignificantly positive in the seed rate of 160 kg ha⁻¹, while the genetic correlation was negative highly significant at the rate of the seed is 190 kg ha⁻¹, which indicates that it is not possible to adopt this trait as a fixed criterion for diagnosing the optimal compositions in increasing yield or tolerating environmental stress. This trait was positively and highly significantly correlated with spike length genetically in seed rates of 130 kg ha⁻¹, 160 kg ha⁻¹ and 190 kg ha⁻¹, except for the genetic correlation, which was highly negative and highly significant in seed rate 190 kg ha⁻¹.

Number of tillers (tiller m⁻²)

From tables (1, 3 and 5), it is clear that the characteristic of the number of tillers was genetically positively and significantly associated with the grain yield in the seed rates of 130 and 190 kg ha⁻¹, while the correlation of this trait was genetically positive and insignificant in the seed rate of 160 kg ha⁻¹. This result agreed with [22] who found that the grain yield is genetically positive and morally related to the number of tillers in the plant, and [6] who obtained positive and significant genetic associations for this trait with the grain yield in the barley crop, as well as the results of [5] showed a positive and significant genetic correlation between grain yield and the number of tillers in their study on some genotypes of durum wheat, this trait was genetically negative and significantly associated with spike length in seeding rate 130 kg ha⁻¹ and 160 kg ha⁻¹.

Spike length

Genetic correlations of this trait with the yield were negative, highly significant in all three seed rates and did not reach the level of significance at the seed rate of 190 kg ha⁻¹. This result did not agree with [15, 23, and 24] who indicated that there is a positive correlation of this trait with the two traits of grain yield, as well as highly significant positive genetic correlations for this trait with the number of days until flowering 50%, the number of days to physiological maturity and the area of the flag leaf on the genetic level in seed rates 130 kg ha⁻¹ and 160 kg ha⁻¹, with the exception of the genetic correlation, which was not significant positive with the number of days until flowering 50% and highly negative with flag leaf area in the seeding rate 190 kg ha⁻¹, while the genetic correlation for this trait was significant negative with the number of tillers in seed rates of 130 and 160 kg ha⁻¹, while the genetic correlation was significantly positive.

Number of days to physiological maturity

Genetic correlation of this trait with grain yield was negative and highly significant in seed rates 130 and 160 kg ha⁻¹, while the genetic correlation in seed rate 190 kg ha⁻¹ for this trait with grain yield was positive and highly significant. [7 and 8] have found a positive correlation between these two traits, as increasing seeding rates leads to a decrease in the production of secondary branches and these secondary



branches are by nature late in maturity and thus will work to make the maturity date more homogeneous within plants of the same genotype. It is clear that the high density of the seeds led to showing the natural relationship between the maturity date and the yield, because prolonging the ripening date prolongs the period of filling the bean, which is positively reflected in the yield. In all seed rates, except for the genetic correlation at the seed rate of 190 kg ha⁻¹, it was positive, not significant. This result agreed with [10].

Crop Growth Rate (CGR) (gm m⁻²day⁻¹)

Genetic correlation in this trait with the grain yield was positive and highly significant in all three seed rates (Tables 2, 4 and 6). This result agreed with [10], who obtained positive genetic associations for this trait with the grain yield in the wheat crop. The shorter genotypes may be characterized by high growth rates during the period from planting to flowering, and the reason for this may be due to the negative genetic correlation between the two characteristics of plant height and flowering date (Table 1 and 3), reflected on the increase in the growth rate of the crop during that period .This trait was genetically positively and highly correlated with the biological yield and in all seed rates, as well as the genetic correlation with the characteristics of the number of spikes and the number of grains of the spike was positive and highly significant in the seed rates of the three tables (2, 4 and 6). On the contrary, the genetic correlation of this trait with the weight of 1000 grains was negative highly significant across the three seed rates, and the genetic correlations for this trait were positive and significant with the biological yield across the three seed rates. These results agreed with what [10] found.

Number of spikes m⁻²

genetic correlation of this trait with the grain yield is demonstrated in Tables (2, 4 and 6). It was positive and highly significant in all three seed rates. This result agreed with [25]. It was noted that there is a positive and significant genetic link between the grain yield and the number of spikes in the plant. The trait with the biological yield and the growth rate of the crop took a similar behavior, as the genetic correlation of these two traits was positive and highly significant across the three seed rates. This trait was also positively and highly correlated with the number of grains per spike at the genetic levels and across seeding rates. These results agreed with [26, 27 and 17]. This trait showed highly significant negative genetic correlations with the weight of 1000 grains across all seeding rates, the later tillers produce

smaller grains [28] and should be taken into account when applying direct selection for this trait in such associations because it will be accompanied by a possible decrease in mean grain weight

Number of grains spike ⁻¹

This trait was genetically positive and highly significant correlation with the trait of grain yield and at all seed rates of 130, 160 and 190 kg ha⁻¹ (table 2, 4 and 6). This result agreed with [11, 29, and 30], this trait also showed similar correlations with the



biological yield and the growth rate of the crop, as the genetic correlation of the two traits was significant and positive across the three seed rates, as many researchers obtained similar results, including [15, 17, and 26].

1000 grain weight (gm)

There was genetically negative and highly significant correlation with grain yield across all three seed rates. This trait was also genetically and highly significant negatively correlated with the number of spikes and in all three seed rates, this result agreed with [31]. If they found a negative correlation between the number of spikes and the weight of the bean, this trait was also correlated with the biological yield and the growth rate of the crop with a high negative correlation to the significance across the genetic level and at all seed rates.

Biological yield (tons ha⁻¹)

biological yield trait was genetically positive and highly correlated with grain yield and across all three seed rates (Tables 2, 4 and 6). The biological yield trait also showed a significant positive genetic correlation with harvest index at seed rates 130 and 160 kg ha⁻¹, and at seed rate 190 kg ha⁻¹, the genetic correlation was significant negative for this trait with harvest index.

Harvest index

harvest index was genetically positive and highly significant correlated with all three seed rates except for the seed rate of 190 kg ha⁻¹ (Tables 2, 4 and 6). These results are in agreement with the findings of [15, 17, 26, 27].



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Table (1): Genetic correlations between field traits under seed rate 130 kg ha⁻¹ for the season 2019-2020

traits	Fotal grain yield tons ha ⁻¹	Spike length cm	Number of tillers m ⁻²	Flag leaf area cm ⁻²	Plant height cm	Number of days to physiological maturity	Number of days to 50% flowering
Number of days to 50% flowering	- 0.990**	0.984**	-0.306n.s	0.979**	- 0.961**	0.847 **	1.000
umber of days to hysiological maturity	- 0.894**	0.778**	-0.203n.s	0.628**	- 0.671**	1.000	
lant height cm	- 0.994**	-0.992**	0.965**	- 0.915**	1.000		
lag leaf area cm ⁻²	- 0.820**	0.935**	-0.072n.s	1.000			
umber of tillers m2	0.597**	-0.469**	1.000				
pike length	- 0.975**	1.000					
otal grain yield	1.000						

%1 significant level **

%5 significant level *

Table (2): Genetic correlations between yield traits under seed rate 130 kg ha⁻¹ for the season 2019-2020

traits	total grain yield (tons ha ⁻¹)	Harvest index	iological yield (tons ha ⁻ 1)	Crop Growth Rate (gm m ⁻² day ⁻¹)	0	Number of grains spike ⁻¹	Number of spikes m ⁻²
Number of spikes	0.966103 **	0.973642**	0.997805 **	0.982051 **	-0.823591 **).823423 **	1.000
Number of grains spike	0.974099 **	0.962944 **	0.980013 **	0.967782 **	-0.312650n.s	1.000	
1000 grain weight	-0.597492**	-0.531305 **	-0.691861 **	-0.645590 **	1.000		
Crop Growth Rate	0.958021 **	0.987274 **	0.993584 **	1.000			
Biological yield	0.961197 **	0.998698 **	1.000				
Harvest index	0.986064 **	1.000					
total grain yield	1.000						-

%1 significant level **

%5 significant level *



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Table (3): Genetic correlations between field traits under seed rate 160 kg ha-1 for the season 2019-2020

traits	Fotal grain yield tons ha ⁻¹	pike length cm	Number of tillers m ⁻²	Flag leaf area cm ⁻²	Plant height cm	Number of days to physiological maturity	Number of days to 50% flowering
Number of days to 50% flowering	-0.960610**	0.986753**	-0.709228**	0.862368**	-0.958167**	0.663343**	1.000
Number of days to physi ological maturity	-0.983296**	0.773982**	0.041116 n.s	0.636309**	0.119517n.s	1.000	
Plant height	0.341853**	-0.703750**	0.135278n.s	- 0.996848**	1.000		
Flag leaf area	-0.784326**	0.907302**	0.002369n.s	1.000			
Number of tillers	0.301330n.s	-0.372403**	1.000				
Spike length	-0.966883**	1.000					
Total grain yield	1.000						

%1 significant level **

%5 significant level *

Table (4): Genetic correlations between yield traits under seed rate 160 kg.ha-1 for the season 2019-2020

traits	total grain yield (tons ha ⁻¹)	Harvest index	Biological yield (tons ha ⁻¹)	Crop Growth Rate (gm m ⁻² day ⁻¹)	1000 grain weight (gm)	umber of grains spike ⁻¹	umber of spikes m ⁻²
Number of spikes	0.808556 **	0.092845 n.s	0.975991**	0.955878**	0.987134 **	0.612945**	1.000
Number of grains spike	0.878598 **	0.629930 **	0.794551**	0.836025**	0.415715**	1.000	
1000 grain weight	-0.701159 **	0.052809 n.s	-0.916491**	-0.885214**	1.000		
Crop Growth Rate	0.948138 **	0.405113 *	0.989319**	1.000			
Biological yield	0.875543**	0.236988 n.s	1.000				
Harvest index	0.678064 **	1.000					
Total grain yield	1.000						

%1 significant level **

%5 significant level *



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Table (5): Genetic correlations between field traits under seed rate 190 kg ha⁻¹ for the season 2019-2020

traits	Total grain yield tons ha ⁻¹	Spike length cm	Number of tillers m ⁻²	Flag leaf area cm ⁻²	0	Number of days to physiological maturity	Number of days to 50% flowering
Number of days to 50% flowering	0.966054 **	0.218186 n.s	0.978099**	0.153916n.s	0.876872**	0.997955**	1.000
Number of days to physiological maturity	0.956581**	0.315269 n.s	0.975944**	0.056615 n.s	0.926554**	1.000	
Plant height	0.587232**	0.207228 n.s	0.527679**	-0.098139n.s	1.000		
Flag leaf area	0.416647*	- 0.951481**	-0.504113**	1.000			
Number of tillers	0.698051**	0.614065 **	1.000				
Spike length	-0.235258 n.s	1.000					
Total grain yield	1.000						

%1 significant level **

%5 significant level

Table (6): Genetic correlations between yield traits under seed rate 190 kg ha⁻¹ for the season 2019-2020

traits	total grain yield (tons ha ⁻¹)	Harvest index	Biological yield (tons ha ⁻¹)	Crop Growth Rate (gm m ⁻² day ⁻¹)	1000 grain weight (gm)	Number of grains spike ⁻¹	Number of spike m ⁻²
Number of spikes	0.970748**	0.034406 n.s	0.931124 **	0.911182 **	-0.691232**	0.963049 **	1.000
Number of grains spike	0.991751**	0.101493 n.s	0.910198 **	0.921700 **	-0.517174**	1.000	
1000 grain weight	0.528536**	0.755905 **	-0.871946**	-0.830990**	1.000		
Crop Growth Rate	0.800959**	- 0.420285**	0.995836 **	1.000			
Biological yield	0.828827**	- 0.387588*	1.000				
Harvest index	0.198664n.s	1.000					
Total grain yield	1.000						

%1 significant level **

%5 significant level I *



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