Correlation and path coefficient analysis for the yield and its related components in some genotypes of durum wheat (*Triticum durum Desf.*).

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Abstract

The study was conducted during the 2024-2025 growing season at the research farm of the College of Agricultural Engineering Sciences, University of Duhok. This study was carried out according to R.C.B.D. with three replications to study some genetic parameters on 10 genotypes of durum wheat. The analysis of variance showed highly significant differences among the genotypes for the traits studied, number of grains per spike (120.525), number of spikes per plot (15611.485), and grain yield (9177.875), at the 1% level. High heritability in a broad sense, coupled with high genetic advance, was recorded for grain yield (46.365) and no. spike per plot. (74.579).A highly significant and positive correlation between grain yield and the number of grains per spike (0.90) was found between spike weight and the number of grains per spike, as well as between spike weight and the number of spikes per plot, indicating that selection for more grains per spike will directly and strongly improve yield. The results exhibited the direct effect of the number of spikes per plot and the number of grains per spike on grain yield, indicating that choosing more grains per spike will significantly increase the yield.

Keywords: Correlation, Path coefficient, Durum wheat genotypes, Yield components.

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1.Introduction

Durum wheat (*Triticum durum Desf.)* is a globally strategic cereal crop, fundamental to food security and human nutrition, particularly within the Mediterranean basin, North Africa, and West Asia. Its economic and culinary importance is derived from unique grain qualities, notably high protein content, hardness, and yellow carotenoid pigments—which make it the preferred raw material for pasta, couscous, and various traditional foods [32] [40]. Despite this critical role, global productivity is challenged by a persistent yield gap in several major producing regions. Constraints include limited availability of improved cultivars adapted to local agro-ecological zones, insufficient research investments, and increasing vulnerability to abiotic stresses such as drought, which are exacerbated by climate change [37]. Enhancing genetic yield is an urgent priority for sustaining production in the face of a growing global population and shifting climatic patterns.

In Iraq, as in many countries with similar semi-arid climates, wheat is a cornerstone of agriculture and food security. Although national cultivation areas are substantial, average yields remain below potential, necessitating heavy reliance on imports to satisfy domestic demand [41].This underscores the critical need for developing superior, locally adapted durum wheat varieties that can perform reliably under the region's specific environmental pressures.

breeding programs increasingly focus on indirect selection for heritable and stable yield components that exhibit consistent causal relationships with final grain output.

To achieve this, plant breeders rely on statistical tools to decipher trait relationships. Correlation analysis is fundamental for identifying which morphological and physiological traits are associated with grain yield. For instance, studies in bread wheat have shown that kernel yield per plant is significantly correlated with traits like thousand-kernel weight and biomass yield [5]In durum wheat, similar positive associations have been reported for thousand-kernel weight and spike components, while negative correlations with foliar diseases highlight a key biotic constraint [11] [15] However, correlation does not distinguish between direct and indirect causes. Path coefficient analysis, which partitions correlation coefficients into direct and indirect effects, is therefore essential for elucidating the causal pathways underlying yield formation [21] [23] . This analysis can reveal, for example, that while several traits may correlate with yield, the direct effects of biomass yield and harvest index are paramount [15], providing clearer targets for selection.

The success of such an analytical breeding approach is predicated on the presence of sufficient genetic variation within the breeding germplasm. Research indicates that promising variability exists for key traits in durum wheat. Studies report significant genotypic coefficients of variation (GCV) for grain yield and grains per spike, and high heritability coupled with high genetic advance for components like thousand-grain weight, suggesting strong potential for effective phenotypic selection [22] [27] This available diversity, often sourced from wild relatives and landraces, forms the essential raw material for genetic gain [31] .

Despite these established methodologies and the recognized importance of component trait analysis, there remains a need for targeted studies that apply integrated correlation and path analyses to diverse durum wheat genotypes under specific, stress-prone agro-ecologies like those found in Iraq. A comprehensive understanding of which yield components exert the strongest direct effects on grain yield under local conditions is crucial for designing efficient, trait-based selection indices. This study aims to estimate the genotypic correlation and path coefficient, and heritability for yield and its related components of durum wheat.

2. Materials and Methods

The study was conducted during the 2024-2025 growing season at the research farm of the College of Agricultural Engineering Sciences, University of Duhok.10 durum wheat genotypes (ZINAKO, Artukler, MEKI-3, FRAT-93, Cham-3, SEVEVO, Iraq-7, AKSAD-65, SMETO, SARDAR) were involved in this study. The site is located at geographic coordinates 36.8679° N, 42.9489° E, at an elevation of 681 m above sea level. The soil was classified as silty clay. Fertilizer applications recommended doses for different growth stages to supplement the baseline soil fertility. Nitrogen-phosphorus-potassium (NPK) fertilizer was applied at sowing, and urea was supplied in two dose applications: the first when plants reached approximately 30 cm in height, and the second before the flowering stage.

The experimental design was a randomized complete block design (RCBD) with three replications. Each plot consisted of a single 3-meter row, with 30 cm between rows and 40 cm between plots. A seeding rate of 18.5 grams was used for each genotype per plot.

Meteorological data, including monthly rainfall totals, average temperatures, and relative humidity percentages, were recorded throughout the growing season. Due to a rainfall deficit in March 2025, supplementary irrigation was applied using a sprinkler irrigation system to maintain adequate soil moisture. At the maturity stage following traits were studied:-

- Grain Yield (GY): Total weight (g) of threshed grains per plot.
- Spike Weight (SW): Weight (g) of the main spike.
- Number of Grains per Spike (NGS): Total grains counted on the main spike.
- Number of Spikes per Plot (NSP): Average number of fertile spikes per plot, based on a count of ten plants.
- Thousand-Grain Weight (TGW): Weight (g) of 1000 randomly sampled seeds.

2.1 Statistical analysis and the estimation of genetic parameters:

Statistical analysis was done for all traits according to the [10] to estimate the following genetic components:

2.2 Variance of components.

Variance of components including genotypic and phenotypic variances, heritability, genotypic and phenotypic coefficients of variation, and genetic advances were estimated according to [27] [31]

Phenotypic and Genotypic Variance

For genotypic variance:

$$\sigma^2 = \frac{MSV-MSE}{r}$$

Where:

MSG = mean sum of squares for genotypes

MSE = mean sum of squares for error

r = number of replications

According to PCV and GCV values,> 20% regarded as high, PCV and GCV values between 10 and 20% medium, and PCV and GCV < 10% low. [20].

genotypic coefficient of variation according to [18]

$$GCVy. = \frac{\sigma^2 g}{Y^-} \times 100$$

Where:

GCV = is the genotypic coefficient of variation.

PCV = is the phenotypic coefficient of variation.

δg = is the genotypic standard deviation.

δp = is the phenotypic standard deviation.

y- = the meaning of the population.

Phenotypic, genotypic Correlation coefficient:

The phenotypic, genotypic correlation coefficient is calculated according to the formula below. [10] Genetic correlation coefficient (rG)

$$rG= \frac{\sigma G \times GY}{\sqrt{\sigma^2 Gx+\sigma^2 Gy}}$$

Heritability

The concept of heritability explains whether differences observed among individuals arose as a result of differences in genetic makeup or due to environmental forces. According to [5]. heritability, estimates can be placed in the following categories: low heritability< 40%, medium heritability 40-59%, moderately high 60-79% and remarkably high heritability 80% or more.

$$H^2_{.b.s}\ \% = \frac{\sigma^2\ g}{\sigma^2\ p} X\ 100$$

Where:
H^2b.s= heritability in a broad sense.
σ^2 G = Genetic Variance.
Σ^2 P = Phenotypic Variance.

Expected Genetic Advance:

Estimates of Expected Genetic Advance: under selection (GA) refers to improvement in genotypic value for the new population, the base population under one cycle of given selection intensity [7].

$$GA\ \% = \frac{GA}{\bar{Y...}} \times 100$$

Where:
$h\bar{y}$ ... = General mean.

Path coefficient analysis

The path coefficients between grain yield (y) and each of spike weight (x1), No. of grains per spike (x2), No. of spikes per plot (x3), Grain weight (x4), and separated into direct and indirect results by using path coefficient analysis. [29].

[21]have suggested the following scale to determine the importance of direct and indirect effects.

Value of direct or indirect effect rate of scale:

Negligible	0.00 to 0.09
Low	0.10 to 0.19
Moderate	0.20 to 0.29
High	0.30 to 0.99
Very high	More than one

Results and discussion

Analysis of Variance

The results of the analysis of variance for the wheat genotypes across the studied traits are presented in (table 1) The results exhibited that the genotypes had a highly significant effect on the number of grains per spike(120.525), number of spikes per plot(15611.485), and grain yield (9177.875) at the 1% level. A significant effect at the 5% level was found for the 1000-grain weight(170.499). However, no significant effect was observed for spike weight (0.365).This indicated the presence of a considerable amount of diversity among the genotypes for the studied traits These results align with the results found by [9] [30][38]

Table(1): Analysis of variance of the durum genotypes.

Source variation	**M.S.**					
	d.f	Weight	Grains/Spike	Spike Per plot	Grain Yield	Grain weight
Block	2	1.016	31.964	5920.300	2393.039	324.560
Genotypes	9	0.365	** 120.525	** 15611.485	** 9177.875	* 170.499
Error	18	0.239	12.297	4020.151	1742.749	61.117

Genotypes	Spike Weight	No.of	No.of	Grain Yield	1000

*Significant at 0.05 probability
**Significant at 0.01 probability

Performance of mean genotypes

Table (2) presents the mean values of various durum wheat genotypes. The results show that the Among the genotypes evaluated, Genotype 7 recorded the highest mean for number of spikes per plot (421.000), which was significantly greater than most other entries. It also showed (251.573) among all genotypes, though its 1000-grain weight was moderate (38.927). Genotype 6 excelled in number of grains per spiker (36.600) and maintained high values for grain yield and 1000-grain weight. In contrast, Genotype 2 and Genotype 9 showed lower performance in several traits. Genotype 2 had the lowest grain yield (86.757), while Genotype 9 recorded the lowest number of spikes per plot (149.000) and low grain yield (78.050).Overall, Genotype 7 demonstrated superior or competitive mean performance. strong performance in spike weight (1.867), number of grains per spike (34.500), grain yield (218.680), and 1000-grain weight (42.067.Genotype 3 also performed well, particularly in grain yield (154.823) and 1000-grain weight (42.357), while Genotype 5 achieved the highest grain yield

across all measured traits, particularly in spike production and yield components, making it a promising genotype under the conditions of this study. Genotype 5 also stands out for its exceptional grain yield. These findings align with previous studies emphasizing the importance of selecting genotypes with balanced performance in yield-related traits, as supported by research such as [8] [17] [36].

Table (2): Mean Performance of the genotypes

		Grains Per spike	Spike Per plot		Grain weight
1	a 0.667	c 14.067	bc 263.000	bc 146.040	c 24.127
2	a 1.333	b 27.300	bc 238.667	c 86.757	bc 29.147
3	a 1.567	ab 30.867	b 300.333	ab 154.823	ab 42.357
4	a 1.767	ab 31.200	bc 243.000	ab 177.663	bc 29.393
5	a 1.600	ab 31.367	bc 242.667	a 251.573	abc 38.927
6	a 1.400	a 36.600	b 303.000	ab 203.710	ab 41.473
7	a 1.867	a 34.500	a 421.000	ab 218.680	ab 42.067
8	a 1.833	ab 31.200	b 286.667	ab 174.207	a 45.330
9	a 1.700	ab 34.600	c 149.000	c 78.050	abc 36.720
10	a 1.500	ab 33.567	ab 343.667	ab 203.330	bc 27.187

The values followed by the same Latter for each trait are not significantly different from each other.

Variance components

Table 3 displays the variance component estimated to be 10 genotypes for the traits studied. The data showed that the phenotypic coefficient of variance was the genotypic coefficient of variance for the studied traits, which indicates that the environmental factors had a great impact on these traits. This finding aligns with [14] [16] [11] [25]. based on the finding [5]the heritability estimate for all the studied traits where low for 1000 grain weight indicating that the environmental factor has greater impact on the expression of this traits while Hight for no of grain per spike moderate and moderate for grain yield and no of spike per plot this finding are aligned with [12] [25] [34]. The genetic advance as a percentage reported by Allard 1960 was high for grain yield, no of grain per spike, no of spikes per plot, while moderate for other traits. These results are consistent with [25].

Table (3) variance component estimated for 10 genotypes for the traits studied.

Genetic parameters	Studied traits				
	Grain yield	Spike weight	No. of grains per spike	No. of spike per plot	1000 grain weight
σ^2G	2478.375	0.042	36.076	3863.778	36.461
S.E	1317.358	0.058	17.180	2259.022	25.075
σ^2E	1742.749	0.239	12.297	4020.151	61.117
S.E	551.106	0.076	3.889	1271.283	19.327
σ^2P	4221.124	0.281	48.373	7883.929	97.578
%H^2b.s	58.714	14.947	74.579	49.008	37.366
EGA	78.581	0.163	10.685	89.641	7.604
EGA%	46.365	10.717	35.003	32.118	21.315
GCV	29.374	13.456	19.675	22.271	16.927
PCV	38.334	34.806	22.783	31.814	27.691

Table (4) Genotypic correlations between grain yield and its component traits

Genotypic correlation

The table(4) displays the genotypic correlations between grain yield and its component traits. The analysis revealed a highly significant and positive correlation between grain yield and the number of grains per spike (0.90), indicating that selection for more grains per spike will directly and strongly improve yield. A significant positive correlation was also found between spike weight and the number of grains per spike, as well as between spike weight and the number of spikes per plot. Furthermore, a significant positive correlation was observed between spike weight and 1000-grain weight. On the other hand, no significant genotypic correlation was found between grain yield and spike weight, grain yield, and the number of spikes per plot, or grain yield and 1000-grain weight. Similarly, no significant correlation was detected between the number of grains per spike and the number of spikes per plot, the number of grains per spike and 1000-grain weight, or the number of spikes per plot and 1000-grain weight. Overall, the results demonstrate that among the traits studied, the number of grains per Spikes are the most critical and direct genotypic determinant of final grain yield in this population. The independent correlations of spike weight with both grains per spike and spikes per plot suggest it is a useful integrative trait, but it does not show a direct genetic link to final yield in this dataset. These findings are consistent with the results from studies done by[1] [2][6] [3].

Genotypic path coefficient analysis

Direct and indirect effect of grain yield on spike weight, No. of grains per spike, No. of spikes per plot and 1000 grain weight. presented in Table 5, the results showed that the spike weight had a positive indirect effect on yield (0.034)and a positive indirect effect through No. of grains per spike, no. of spikes per plot, and 1000 grain weight with (0.015,0.007, and 0.012)respectively, resulting in a total correlation (0.068).Concerning the number of grains per spike, the results revealed a positive direct effect on yield (0.002) and a positive indirect effect through the number of spikes per plot, spike weight, and 1000-grain weight, resulting in a correlation of 0.090.The number of spikes per plot showed a positive direct effect on yield (0.003)and an indirect effect through spike weight No. of grains per spike and 1000 grain weight, resulting in a low correlation (0.197).1000 grain weight has exhibited a positive direct effect on yield

Table (5) The direct and indirect genotype path coefficient analysis between yield and other traits

Source of variance	Grain yield	Spike Weight	No.of grains per spike	No.of Spikes per plot	1000 Grain weight
grain yield	1.000	0.069	0.90	0.197	0.100
spike weight		1.000	** 0.265	** 0.040	* 0.171
No .of grains / spike			1.000	0.060	0.185
No. of spike/ plot				1.000	0.069
1000 grain weight					1.000

(0.013) and a positive indirect effect through spike weight No. of grains and No. of spike per plot with (0.71,0.006, 0.10)Respectively resulting in a low correlation (0.100, the results showed that the ratio on yield ranged between 0.187 Indirect effect such as no. of spikes per plot and (0.001)on no of grains per spike. These results are consistent with [4] [13][22] [39]

Conclusion

Based on the analysis, considerable genetic diversity exists among the durum wheat genotypes. Genotypes 7 and 5 demonstrated superior performance, particularly for grain yield and its key components. The high phenotypic variance and low heritability for some traits indicate.

significant environmental influence on their expression. Genotypically, grain yield was most strongly and directly determined by the number of grains per spike. Therefore, selecting genotypes with high grains per spike, like Genotype 7 and Genotype 5, is recommended for improving yield in breeding programs under similar conditions.

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