

# Multivariate analysis of agro-morphological and quality traits of a durum wheat collection under rainfed Algerian conditions

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## ABSTRACT

This study assesses the variability, heritability, and correlation of some agro-morphological and quality traits in 125 durum wheat germplasm and groups them into clusters. These germplasms include landraces and cultivars from a variety of countries. The field experiment was conducted at the Algiers experimental station during the 2020-2021 season using an augmented randomized complete block design, with data collected for 11 quantitative traits. The analysis of variance revealed significant differences between the genotypes for the majority of the traits examined. Plant height, flag leaf area, thousand-kernel-weight, number of kernels/spikes, sedimentation volume, yellow index, and wet and dry gluten all showed high heritability coupled with high to moderate genetic advance as a percentage of the mean. The principal components analysis explained 46.67% of the total variation in the first two axes, allowing the identification of traits that significantly contributed to this variation. Pearson correlation coefficients revealed strong associations between plant height and days to heading, which affects seed yield improvement, as well as protein content, gluten content, and sedimentation volume, which influence durum wheat nutritional quality. Cluster analysis divided the 125 durum wheat germplasm samples into five clusters based on trait similarities. Genotypes in clusters II, IV, and V exhibit superior agronomic and quality traits, making them valuable resources for breeding and crossing programs aimed at improving durum wheat. The findings also highlight the value of Algerian landrace germplasm and its potential for use in the genetic improvement of other external genetic materials, particularly in terms of quality trait parameters.

**Keywords:** durum wheat, variability, multivariate analysis, quality traits, landraces, yield

## INTRODUCTION

Durum wheat (*Triticum turgidum* L. ssp. *Durum*, Desf.) is considered the world's most important cereal, particularly in the Mediterranean basin and North America, where the majority of global production is concentrated (Royo et al. 2009). In Algeria, durum wheat is consumed in a variety of forms, including semolina and pasta. It is grown on 1.49 million hectares, producing 2.58 million tons and yielding 1.8 t/ha (FAO, 2021). The primary objectives of a

breeding program are grain yield and quality. The end-use quality of durum wheat products is closely related to grain quality, such as protein content and gluten quality, which is influenced by wheat variety, environmental factors, and GxE interactions (Troccoli et al., 2000; Magallanes-López et al., 2017). The phenotypic characterization of diverse genetic resources is an important first step in determining genetic diversity across multiple traits. This process is a

valuable management tool for validating the identity of a specific accession (Aghaee et al., 2010). Moreover, it provides a foundation for crop improvement of various desirable traits (Ambati et al., 2020).

The two international centers, CIMMYT and ICARDA, have made significant contributions to expanding the genetic pool of current durum wheat cultivars through global germplasm exchange (Royo et al., 2009). According to Hernández-Espinosa et al. (2019), local varieties play a fundamental role in enriching the genetic diversity of durum wheat owing to their adaptive characteristics, resilience to biotic and abiotic stresses, and ability to produce good grain yields under low-input farming systems and possession of suitable quality traits such as nitrogen content and wheat color analysis. Therefore, local varieties can significantly contribute to the development of new durum wheat varieties and broaden their genetic base (Kendal et al., 2019). Well-established multivariate statistical methods are useful for identifying germplasm, organizing variability across a large number of accessions, and investigating relationships between breeding materials (Mohammadi and Prasanna, 2003). Multivariate analysis is a statistical method used to investigate data with multiple variables (Dudhe et al., 2020). This method employs techniques like principal component analysis, correlation analysis, cluster analysis, and genetic parameter analysis.

Understanding the interrelationships between different traits assists breeders in direct and indirect selection of traits that are difficult to measure and have low heritability (Arya et al., 2017). Heritability estimates of the trait to be improved in a germplasm collection help to select superior genotypes by assessing the extent to which traits are transmitted from one generation to the next (Deepika et al., 2021). In this context, this study evaluates the genetic variability of a durum wheat collection using various phenological, agro-morphological, and quality parameters. The relationships between these traits are also assessed using a correlation matrix. Genotypes with significant agronomic and qualitative traits are identified using cluster analysis.

## MATERIALS AND METHODS

### *Plant material, site and experimental design*

The plant material contains 125 durum wheat genotypes, including both landraces and modern cultivars. It includes 120 test entries and 5 checks from various countries and research centers. Table 1 lists the plant materials and their respective countries. The experiment was carried out during the 2020-2021 cropping season at the National Agronomic Research Institute of Algeria's experimental station in Algiers (36°68'N, 3°11'E, 18.5 m above sea level) under rainfed conditions. The site's climate is defined by an annual cumulative rainfall of 474.2mm. The mean annual temperature ranges from 8.6 °C in January to 30.8 °C in June. The field experiment was carried out using an augmented randomized complete block design (ARCB) with 4 blocks, each containing 30 test entries and 5 checks (Waha, Cirta, Sigus, Beni Mestina, and Gta/dur), which were repeated twice in each block, for a total of 160 experimental plots.

**Table 1.** List of 125 durum wheat genotypes used for evaluation

Country/Research Center	Number of genotypes
Algeria	22
Tunisia	3
Morocco	1
Spain	2
France	7
Italy	7
Cyprus	1
Syria	6
Iran	1
Jordan	1
USA	2
Mexico	28
Australia	2
CIMMYT	13
ICARDA	29

Each genotype was sown in 2 rows of 1-meter length and 0.25 m apart with a seed rate of 10 g. All recommended crop management practices were implemented to ensure a healthy crop stand.

#### **Phenological and agro-morphological traits**

Five traits were measured: days to 50% heading (DTH, days), which was counted from the date of sowing to the time when 50% of the spikes were halfway out from the flag leaf, and plant height (PH, cm), which was measured at maturity from the soil surface to the tip of the spike, excluding awns. At the heading stage, the distance from the base to the tip of the leaf was calculated using the formula  $FLA (cm^2) = 0.606 (L \times l)$ , where L represents the total length of the leaf, l is the average width of the leaf, and 0.606 is the regression coefficient described by Spagnoletti-Zeuli and Qualset (1990). Other parameters measured were thousand-kernel-weight (TKW, g) and number of kernels per spike (NKS). A mean value for each genotype's agro-morphological parameters was calculated based on the sampling of three plants from each plot.

#### **Quality traits evaluation**

Grains harvested from each elementary plot were used for quality parameter analysis, with two repetitions to calculate the mean value for each genotype. The yellow color index 'b' and brightness 'L' were measured from flour semolina using a reflectance colorimeter (Minolta Chroma Meter, CR-200) according to the AACC Method 14-22 (AACC, 2000). Gluten strength was determined by the SDS volume of sedimentation (Sodium Dodecyl Sulfate) according to the AACC method 56-70, as described by Axford et al. (1979). The process involves combining 6 g of ground material with 50 ml of distilled water, agitating it for 15 seconds, and repeating the process three times every 2 minutes. Then, 50 ml of the prepared SDS-lactic acid solution (which consists of 1 L of 30% SDS and 20 ml of 88% diluted lactic acid solution) is added. After 15 seconds of agitation, which is repeated four times every 2 minutes, the mixture is allowed to settle for 20 minutes before the sedimentation volume in ml is measured directly from the graduated cylinder.

Grain nitrogen content was determined using the standard Kjeldhal method, and the percentage of protein content (PC) was calculated by multiplying Kjeldhal nitrogen by 5.7 and expressing it on a dry weight basis. Wet gluten content was determined using the AACCI Method 38-12A; 10 g of flour and 5.5 ml of 2% saline solution were mixed and placed in a gluten washer (Glutomatic® 2200, Perten Instruments, USA). The resulting wet gluten was weighed and expressed as a percentage of pure flour. The dry gluten content was obtained by drying the wet gluten in the Glutork 2020 at 150 °C for 4 minutes. The wet gluten (WG) and dry gluten (DG) were calculated using the formulas listed below; the results are expressed on a dry matter basis:

$$WG (\%) = [(Weight\ of\ wet\ gluten) / (Weight\ of\ flour)] \times 100,$$

$$DG (\%) = [(Weight\ of\ dry\ gluten) / (Weight\ of\ flour)] \times 100.$$

#### **Statistical analysis**

The 'augmentedRCBD' R package (Aravind et al., 2021) was used in R Studio 4.1.2 to conduct variance analysis on the measured traits. The formula proposed by Johnson et al. (1955) and Acquah (2012) was used to calculate the phenotypic variance ( $\sigma^2_p$ ), genotypic variance ( $\sigma^2_g$ ), broad sense heritability ( $h^2_{BS}$ ), genetic advance (GA), and genetic advance as a percentage of the mean (GAM):

$$PCV = 100 \times \frac{\sqrt{\sigma^2_p}}{\mu}$$

$$GCV = 100 \times \frac{\sqrt{\sigma^2_g}}{\mu}$$

$$h^2_{BS} = 100 \times \frac{\sigma^2_g}{\sigma^2_p}$$

$$GA = h^2_{BS} \times k \times \sigma_p$$

where,  $\sigma^2_p$  is the phenotypic variance,  $\sigma^2_g$  is the genotypic variance,  $\mu$  is the grand mean of the trait, and k is the efficacy of selection, which is 2.06 at 5% selection intensity.

The values of PCV and GCV were categorized as low (0–10%), moderate (10–20%) and high (>20%), according to Sivasubramanian and Menon (1973). The value of  $h^2_{BS}$  is classified as low (0–30%), moderate (30–60%) and high (>60%) according to Robinson et al. (1949).

For  $GAM = (GA/\mu) \times 100$ , GAM was categorized as low (0-10%), moderate (10-20%) and high (20% and above, according to Falconer and Mackay (1996). Principal component analysis (PCA) was carried out using the R packages 'FactoMineR' (Lê et al., 2008) and 'Factoshiny' (Kassambara and Mundt, 2017). Pearson correlation analysis was executed using the R packages 'corrplot' (Wei et al., 2017). To group durum wheat genotypes based on measured traits, cluster analysis using Ward's method based on Euclidean distances was performed using the R packages 'factoextra' and 'cluster' (Kassambara, 2017).

## RESULTS

### *Analysis of variance*

Analysis of variance for 11 trait studies revealed a significant variation ( $P < 0.01$ ) among genotypes (treatments) divided into three components: checks, tests, and test versus checks (Table 2). Both checks and tests showed significant variation ( $P < 0.01$ ) across all traits. The test versus check was significant ( $P < 0.01$ ) for all traits except the flag leaf area. Based on the mean square values obtained for these components, the impact of the test versus check has the greatest influence on traits such as PH, L, NKS, TKW, and DTH, followed by the effect of checks, with tests ranking last. In contrast, for parameters b, PC, SDS, FLA, WG, and DG, the effect of checks caused the most variation, followed by the effect of the test on b, PC, FLA, and DG, and test versus check on SDS and WG. Significant differences between genotypes can be attributed to the germplasm's high variability and diverse geographic origins. The observed significant differences between blocks could be attributed to environmental factors and plot borders.

### *Descriptive statistic and variation among durum wheat germplasm*

The experimentation results reveal significant variation across all traits (Table 3). The average DTH was 97.03 days, with the earliest being genotype T111 from ICARDA (83.68 days) and the latest being landrace T82 from Algeria (117.87 days). Similarly, PH levels varied from 72.21 cm for genotype T24 from Mexico to 148.08

cm for landrace T78 from Algeria. Genotypes with taller and later headings also had a larger FLA. NKS showed significant variation, with values ranging from 35.42 to 78.4 kernels per spike. Certain genotypes from CIMMYT, ICARDA, Mexico, Italy, and Algeria demonstrated high TKW. Among them, genotype T122 from Iran had the highest value, 65.13 g. In terms of quality traits, 26 genotypes had PCs ranging from 14 to 16%, including some landraces from Algeria and Cyprus. The highest PC was detected in genotype T59 from France, while the lowest was found in genotype T94 from Mexico.

This study discovered that genotype T121 from Tunisia had high values for b, WG, and DG. On the other hand, landrace T72 from Algeria had the highest SDS value. For the parameter L, most genotypes have values close to the average. The highest coefficient of variation was found for SDS (28.15%) and the lowest for L (1.80%).

### *Genetic parameters analysis*

Table 3 summarizes the results for variance components and genetic parameters. SDS shows the highest PCV (28.46%) and GCV (28.42%). Moderate PCV and GCV were reported for b, PH, NKS, FLA, TKW, DG, and WG. The traits PC, DTH, and L had low values for PCV and GCV, respectively. The broad sense heritability ranged from 62.2 for FLA to 99.79 for b, indicating that all traits were highly heritable (>60%). GAM was classified as high for PH, FLA, NKS, TKW, b, SDS, WG, and DG, medium for PC and DTH, and low for L. PH, FLA, TKW, NKS, SDS, b, WG, and DG all showed high heritability coupled with relatively high GAM; DTH, PC, and L exhibited high heritability but moderate to low GAM, respectively.

### *Principal component analysis (PCA)*

In the current study, 11 principal components (PCs) were extracted, with a cumulative variance of 100% explained in Figure 1(a) (Table 4). The PCA focused solely on the first two principal components (PCs), which accounted for 46.67% of the total variation: 32.84% and 13.83% for axes 1 and 2, respectively. Figure 1 (b) shows that the most important traits with the greatest

**Table 2.** Mean squares and significance levels for the 11 traits studied in durum wheat genotypes using ANOVA analysis

Source	Df	b	PC	PH	L	NKS	DTH	TKW	SDS	FLA	WG	DG
Block (ignoring Treatments)	3	5.37 **	3.79 **	420.72 **	2.69 **	28.03 *	47.24 **	8.17 *	95.36 **	46.71 **	64.93 **	6.61 **
Treatment (eliminating Blocks)	124	7.47 **	1.64 **	300.5 **	2.87 **	72.55 **	56.86 **	34.91 **	195.08 **	25.77 **	18.16 **	2.47 **
Check	4	10.91 **	9.37 **	115.31 **	3.91 **	105.52 **	98.41 **	33.2 **	619.43 **	125.55 **	54.08 **	11.95 **
Test	119	7.54 **	1.47 **	296.86 **	2.52 **	70.29 **	53.92 **	31.85 **	181.2 **	23.02 **	18.44 **	2.31 **
Test versus Check	1	1.71 **	1.17 **	2728.44 **	48.46 **	272.13 **	365.75 **	402.23 **	436.05 **	4.91 ns	30.79 **	2.2 **
Error	32	0.02	0.15	2.32	0.03	7.92	7.96	2.15	0.56	8.7	1.29	0.17

(Df) degrees of freedom, (b) yellow index, (PC) protein content, (PH) plant height, (L) brightness, (NKS) number of kernels per spike, (DTH) days to heading, (TKW) thousand-kernel-weight, (SDS) sedimentation volume, (FLA) flag leaf area, (WG) wet gluten, (DG) dry gluten  
ns: not significant, \*  $P < 0.05$ , \*\*  $P < 0.01$

**Table 3.** Descriptive statistics, variance components and genetic parameters for the 11 traits studied

Traits	Min	Max	Mean $\pm$ SD	CV (%)	$\sigma^2_p$	$\sigma^2_g$	GCV (%)	PCV (%)	$h^2BS(\%)$	GA	GAM (%)
DTH	83.68	117.87	97.03 $\pm$ 7.25	7.47	53.92	45.96	6.99	7.57	85.23	12.91	13.31
PH	72.21	148.08	94.68 $\pm$ 17	17.96	296.86	294.54	18.13	18.2	99.22	35.27	37.25
FLA	18.79	43.99	28.02 $\pm$ 4.87	17.38	23.02	14.32	13.51	17.13	62.2	6.16	21.98
NKS	35.42	78.4	54.23 $\pm$ 8.36	15.42	70.29	62.36	14.56	15.46	88.73	15.35	28.3
TKW	26.93	65.13	41.87 $\pm$ 5.69	13.59	31.85	29.7	13.02	13.48	93.25	10.86	25.93
b	8.63	24.38	15.07 $\pm$ 2.69	17.85	7.54	7.53	18.2	18.22	99.79	5.65	37.51
L	82.14	92.84	89.56 $\pm$ 1.61	1.80	2.52	2.49	1.76	1.77	98.68	3.23	3.61
SDS	16.48	83.11	47.29 $\pm$ 13.31	28.15	181.2	180.64	28.42	28.46	99.69	27.68	58.54
PC	9.92	16.46	13.08 $\pm$ 1.23	9.40	1.47	1.32	8.78	9.27	89.8	2.25	17.17
WG	25.21	48.34	34.56 $\pm$ 4.27	12.36	18.44	17.15	11.98	12.42	93	8.24	23.84
DG	9.18	17.29	12.04 $\pm$ 1.51	12.54	2.31	2.15	12.17	12.64	92.75	2.91	24.18

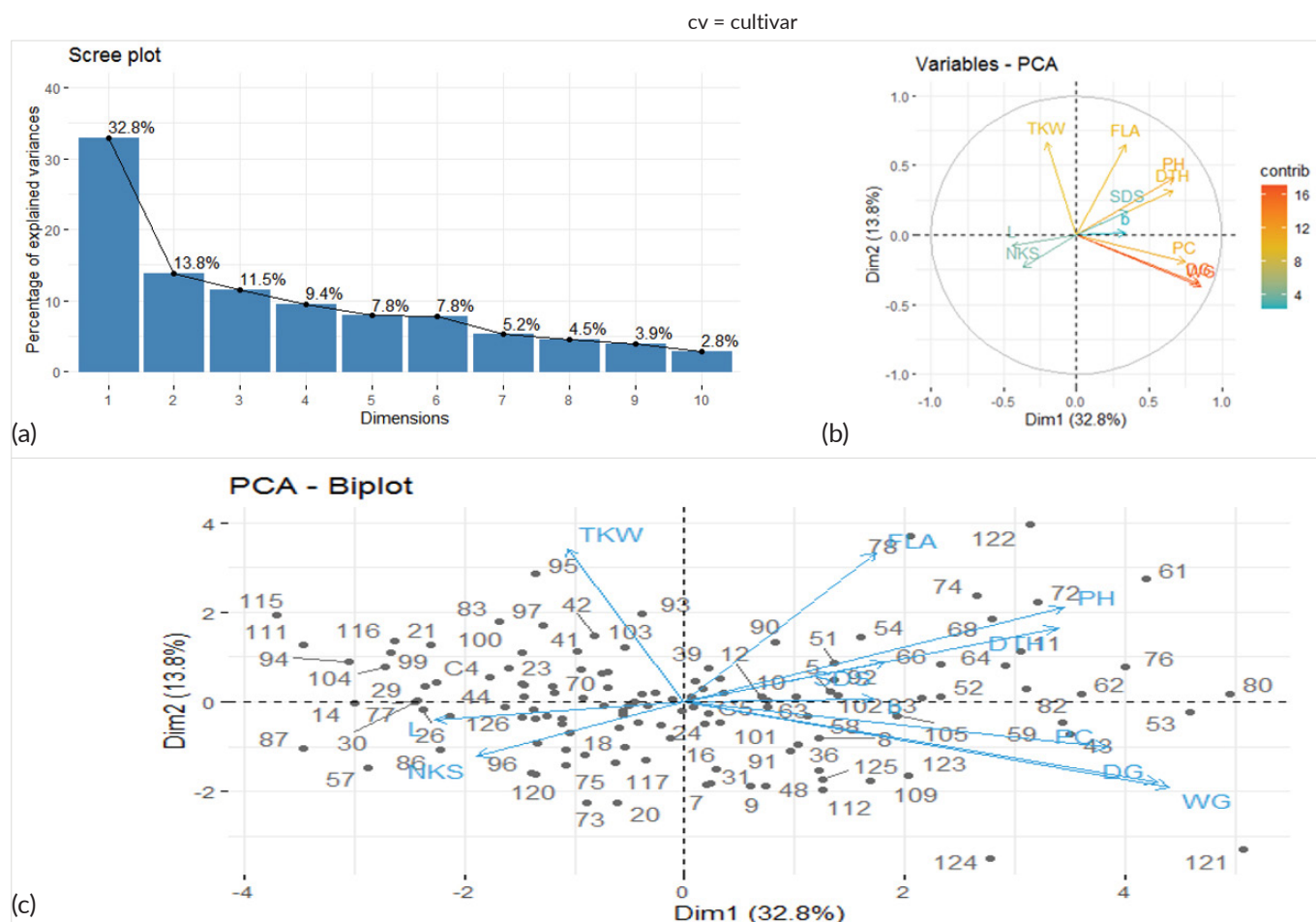
(SD) standard deviation, (CV) Coefficient of variation, ( $\sigma^2_p$ ) variance phenotypic, ( $\sigma^2_g$ ) variance genotypic, (GCV) genotypic coefficient of variation, (PCV) phenotypic coefficient of variation, ( $h^2BS$ ) broad sense heritability, (GA) genetic advance, (GAM) genetic advance as a percentage of the mean

effect on the first principal component were WG, DG, PH, DTH, and PC, which had relatively long vectors, indicating significant variation between genotypes. In the second principal component, TKW and FLA were the most influential traits. The cosine of the angles between the vectors reveals a strong positive correlation between PH and DTH, NKS and L, and the PC, WG and DG. In contrast, the vectors representing the quality components had completely opposite directions as TKW and NKS, indicating a negative correlation.

The biplot in Figure 1(c) shows the distribution of 125 durum wheat germplasm based on 11 quantitative traits. Specifically, genotypes T121 (Tunisia), T61 (ICARDA), T76, T80, and T53 (Algerian landraces), and T62 (Italy) have high principal component scores along the first axis, indicating elevated values for parameters such as PH, DTH, PC, WG, DG, SDS, and b.

**Table 4.** Principal components of the 11 traits studied in 125 durum wheat genotypes

Traits	PC1	PC2
b	0.34	0.01
WG	0.86	-0.37
PC	0.75	-0.20
DG	0.84	-0.35
PH	0.67	0.41
L	-0.44	-0.08
NKS	-0.37	-0.23
DTH	0.66	0.32
TKW	-0.21	0.67
SDS	0.35	0.17
FLA	0.34	0.65



**Figure 1.** (a) Scree plot explaining the percentage of variance for 11 PCs, (b) PCA-variables, (c) PCA-biplot showing the contribution of 11 parameters to the total variability of 125 durum wheat germplasm

In contrast, genotypes like T122 (Iran), T71 and T95 (Italian cultivars), and T72, T78, and T74 (Algerian landraces) have high scores along the second principal component axis, indicating higher values on TKW or FLA. The remaining genotypes are spread across the plot, indicating significant variation in the measured parameters.

#### Phenotypic correlation between traits analyzed

Correlation analysis establishes the association between the studied traits and helps to determine strategies for improving trait combinations. In this study, the Pearson correlation coefficient values (Table 5) show that PH was positively and very significantly correlated with DTH (0.58). NKS was negatively correlated with PH (-0.30). FLA showed a positive correlation with PH and DTH (0.39 each). PC was positively and significantly associated with PH (0.39), WG (0.62), and DG (0.60) but negatively associated with the NKS and TKW (-0.25 and -0.23, respectively). A strong positive correlation was observed between WG and DG (0.97). Furthermore, b was positively correlated with SDS (0.25) but negatively with L (-0.28).

#### Cluster analysis

Table 6 lists the clusters, the number of genotypes in each cluster, and their major characteristics. Ward's method was used to divide the 125 genotypes into five clusters, as shown in Figure 2. The number of genotypes in each cluster varied from 3 to 52. Tables 6 and 7 show that Cluster I consists of 52 genotypes from Algeria (8), CIMMYT (6), Mexico (15), ICARDA (13), Italy (3), Syria (4), France (2), and Tunisia (1), all with trait values close to the mean. Cluster II includes 32 genotypes distinguished by early heading and short plant height. The genotypes include cultivars from Algeria (3), CIMMYT (3), France (1), Italy (2), ICARDA (11), Mexico (8), Spain and Syria (1 each), and two genotypes from the United States.

Cluster III contains 26 genotypes, including three cultivars from Algeria, seven landraces from Algeria, one landrace from Spain, Jordan, and Cyprus, as well as cultivars from Italy, Iran, and Tunisia (1 each), four from France and ICARDA, and two from Mexico. These genotypes are distinguished by their tall plant height, late heading, large flag leaf area, low brightness values, and certain good-quality traits.

Table 5. Pearson correlation coefficients for the 11 traits studied

Traits	FLA	PH	DTH	PC	WG	DG	b	SDS	TKW	L	NKS
FLA	1	0.39***	0.39***	0.14 ns	0.09 ns	0.12 ns	0.00 ns	0.16 ns	0.16 ns	-0.08 ns	-0.07 ns
PH		1	0.58***	0.39***	0.42***	0.41***	0.00 ns	0.18*	0.05 ns	-0.16 ns	-0.30***
DTH			1	0.33***	0.41***	0.37***	0.16 ns	0.18*	-0.09 ns	-0.28**	-0.10 ns
PC				1	0.62***	0.60***	0.17 ns	0.27**	-0.23*	-0.25**	-0.25**
WG					1	0.97***	0.27**	0.15 ns	-0.28**	-0.26**	-0.19*
DG						1	0.24**	0.15 ns	-0.25**	-0.21*	-0.19*
b							1	0.25**	-0.13 ns	-0.28**	-0.09 ns
SDS								1	-0.03 ns	-0.12 ns	-0.09 ns
TKW									1	0.05 ns	-0.11 ns
L										1	0.27**
NKS											1

ns: not significant, \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$

Cluster IV contains three genotypes, one from Tunisia and two from CIMMYT. These genotypes are distinguished by high levels of protein content, wet gluten, dry gluten, and kernels per spike. Cluster V contains genotypes with

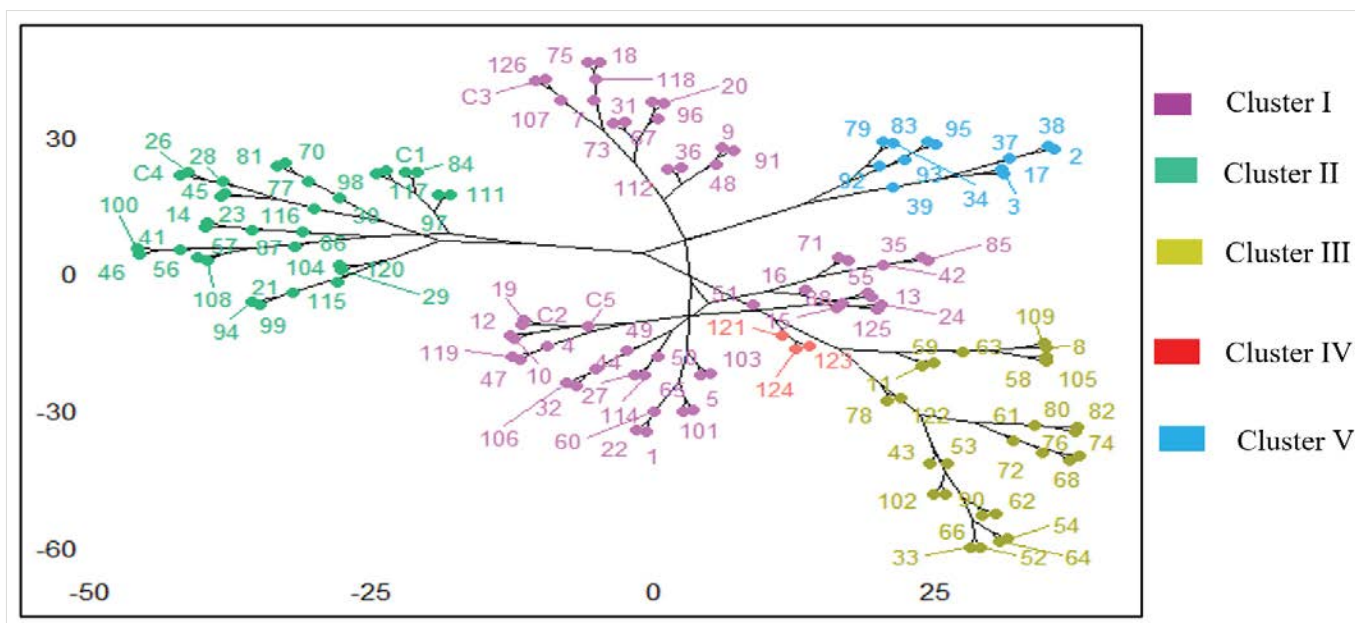
high values for b, SDS, and thousand kernel weight. This cluster includes two genotypes from Australia, three from Mexico, two from CIMMYT, one each from Italy, Syria, ICARDA, and Algeria, and one landrace from Morocco.

**Table 6.** Cluster, number of genotypes and major characteristics in each cluster

Cluster	Genotypes	Cluster character
I	52	Near-average performance of all traits
II	32	Shorter, earliness
III	26	Taller, tardiness, wide flag leaf area, low brightness and good quality parameters
IV	3	High protein with gluten content and high number of kernels/spike
V	12	High yellow index with sedimentation volume and heavier grain weight

**Table 7.** Cluster means value for the 11 traits studied

Cluster	Genotypes	b	WG	PC	DG	PH	L	NKS	DTH	TKW	SDS	FLA
I	52	14.54	34.86	13.15	12.15	89.10	89.38	53.82	94.61	41.15	46.06	26.28
II	32	13.60	30.75	11.99	10.71	86.59	90.87	58.37	94.05	42.26	40.24	28.05
III	26	16.14	38.74	13.98	13.47	117.53	88.27	49.32	106.32	42.10	51.13	31.86
IV	3	14.17	44.72	15.61	16.02	106.38	91.50	62.07	99.34	28.75	55.90	28.87
V	12	19.22	31.87	13.12	10.99	88.00	89.17	53.65	94.68	46.72	60.96	26.90



**Figure 2.** Visualization of 125 durum wheat genotypes grouped into 5 clusters



## DISCUSSION

Eleven quantitative traits were analyzed, revealing significant variation among 125 durum wheat germplasm in terms of agro-morphological and quality trait studies. The analysis of variance using the augmented randomized complete block design revealed significant differences for almost all of the traits studied, favoring selection for further use in breeding programs. ARCBD is commonly used in situations where a large number of genotypes must be evaluated, particularly when there is a limited supply of seeds available, as in our study. Previous studies on durum wheat have also found significant variation in phenotypic characterization (Alemu et al., 2020; Dave et al., 2021; Dagnaw et al., 2022). This variability allows for the development of varieties appropriate for various agroecological zones (Chegdali et al., 2022). This study's landraces from Algeria, Cyprus, Spain, Morocco, and Jordan share common traits such as an extended vegetative period, taller plant height, larger leaf area, and superior technological quality traits, in contrast to certain cultivars from CIMMYT, ICARDA, and Mexico, which exhibit the opposite characteristics. This suggests that the aim of these research centers may be to increase grain yield without taking other criteria into account.

Phenotypic and genotypic variations within a crop population are critical for successful plant breeding (Mabuza et al., 2022). Almost all of the traits studied showed moderate values (10-20%) for both GCV and PCV, with the exception of DTH, L, and PC, which had low (0-10%) PCV and GCV values. According to Alemu et al. (2020), low PCV and GCV values (<10%) indicate that the environment significantly affects the expression of traits. In our study, PC, DTH, and L had low PCV and GCV values, indicating that selecting these traits may be difficult. The findings indicate that PCV estimates were slightly higher than GCV for all traits studied. Furthermore, it should be noted that genotype factors have a significant influence on the expression of these parameters, albeit with minimal environmental effects. Similar results were obtained by Mohammed et al. (2012), Taneva et al. (2019) for DG, WG, PC, and SDS and Wolde et al. (2016) for DTH, PH, NKS and TKW.

Broad-sense heritability is expressed as a proportion of the ratio of genotypic to phenotypic variance. In this study, heritability values were found to be high (>60%) for agro-morphological traits. Our findings are consistent with those of Robbana et al. (2021), who examined 189 Tunisian durum wheat lines for DTH, PH, FLA, and TKW; Haddad et al. (2021) for DTH and TKW, and Mansouri et al. (2018) for PH and DTH. Heritability values were also high for quality traits (>60%), indicating that genetic improvement for industrial quality is possible (Zaïm et al., 2017). Similar results were obtained by Dave et al. (2021), who reported similar results for SDS and PC, as did Lamara et al. (2021) for WG and DG. The extremely high heritability values of variables indicate that environmental factors have no influence on the phenotypic variation of these traits (Dudhe et al., 2020). Estimates of genetic advancement aid in understanding the types of gene activity involved in the development of various polygenic traits (Dutamo et al., 2015).

According to Eid (2009), heritability alone is insufficient to pass down a specific trait from generation to generation. Advanced genetics must also be present. A favorable condition for selection is the presence of high genetic advance combined with high heritability estimates, implying the presence of additive gene effects controlling the trait (Ogunniyan et al. 2014). High heritability was associated with high GAM for PH, FLA, TKW, NKS, SDS, b, WG, and DG. Arya et al. (2017) reported similar results for PH, TKW, and NKS. These results suggest that these traits are controlled by additive genes and that selection may be effective. Taneva et al. (2019) found that protein content and wet gluten had high to moderate heritability but low genetic advance, indicating the presence of non-additive gene action and a significant influence of the environment on trait expression. In general, heritability values based on single-year environmental data are high because genotype and environmental variance are confounded, and selection based on these values can be misleading (Haddad et al., 2021). Thus, multi-year experiments are required to validate the heritability estimates for the traits under consideration.

Principal component analysis (PCA) is a multivariate analysis technique used to assess diversity in durum wheat accessions and identify the key traits that explain the majority of the overall variation (Al Lawati et al., 2021). In this study, PCA analysis explained a variation of 46.67% of the total variance for the first two axes, demonstrating trait diversity. This result is consistent with the findings of Alemu et al. (2020), who found that the first and second PCs explained 46.68% of the total variability in 64 Ethiopian durum wheat. The graph of the PCA variable shows a negative relationship between yield-related traits and quality traits. Gebrewahid et al. (2021) reported a negative relationship between agronomic and grain-quality traits, which may present difficulties in developing and introducing high-yielding genotypes with desirable grain-quality characteristics. According to the results of the PCA-biplot, a number of genotypes, including T121, T61, T76, T80, T53, T62, T122, T71, T95, T72, and T78, have higher principal component scores and contribute significantly to overall diversity. As a result, depending on the desired outcome, such as grain yield or quality, it is critical to include these genotypes as parents in the wheat improvement program.

To develop an effective breeding strategy, it is important to understand how different traits are related using a correlation matrix (Anwar et al., 2009). The differences in the results of various durum wheat studies, which use correlation as a multivariate analysis method to discover relationships between studied parameters, can be attributed to variations in durum wheat varieties and environmental factors (Singh et al., 2018).

Haddad et al. (2021) also reported a positive correlation between DTH and PH, as in the present study. The authors also reported that tall cultivars showed delayed heading but produced more straw. These two traits are desirable in a breeding program designed to increase cereal yields. Frih et al. (2021) and Khan et al. (2013) found that a large number of grains has a negative impact on grain size. This result is explained by the compensatory effect of the two yield components, which is consistent with our findings. PC and PH showed a strong positive correlation. Babay

et al. (2019) reported similar results for Tunisian durum wheat. According to Simpson et al. (1983), the leaves (40%), stem (23%), glumes (23%), and roots (16%) all contribute to nitrogen redistribution and incorporation at the grain level.

The significant negative correlation observed between PC and TKW is consistent with the findings of Al-Nggar et al. (2020) and Gebrewahid et al. (2021). According to Bogard et al. (2008), the negative correlation between TKW and PC could be attributed to genetic incompatibility (linkage, pleiotropy) and nitrogen-carbon competition for photosynthetic energy. A negative correlation was found between L and b. Babay et al. (2019) found similar results with some Tunisian durum wheat cultivars, as did Kendal et al. (2019) with 133 Turkish durum wheat populations. A strong positive correlation was found between PC, WG, DG, and SDS. According to Conti et al. (2011), doughs with high protein content and strong gluten yield excellent rheological properties suitable for pasta production. These traits could be used as criteria for higher-quality pasta because they are strongly and directly associated.

Cluster analysis is an appropriate method for determining familial relationships, specifically the degree of genetic distance between genotypes (Singh et al., 2018). The significant variation in cluster means across all traits suggests that each trait had a significant impact on genotypic grouping. In the present study, the 125 germplasm of durum wheat were divided into five clusters. Each contains genotypes of various origins. The presence of genotypes from various origins in the same cluster can be attributed to similar environmental conditions and the exchange of plant materials between breeders. Notably, research institutions such as CIMMYT and ICARDA engage in extensive germplasm exchange on a global scale. This practice aims to create lines with desirable criteria by combining beneficial traits from various germplasm sources. Kabbaj et al. (2017) examined the genetic diversity of durum wheat landraces and modern germplasm. The study discovered that genotypes from various countries, including Australia, Italy, Algeria,

Spain, France, Canada, and the United States, were clustered together despite geographical differences and varying environmental conditions. The study focuses on the strict rheological standards set by the pasta industry, which has led durum wheat breeders to maintain limited hybridization programs. These programs frequently rely on a standard set of cultivars to provide quality traits.

This study also shows that genotypes from different countries are grouped in the same cluster, as shown by clusters IV and V, and are distinguished by their favorable technological traits. If the goal is to produce high-quality pasta, using these genotypes as donor parents is ideal. Furthermore, because these two clusters have high NKS and TKW, genotypes from clusters IV and V can be used as breeding material if the objective is only fixed to increase the number of kernels per spike and grain weight, as well as overall grain yield. Cluster III contained genotypes that described a long vegetative period, allowing for the production of a significant amount of biomass. These genotypes can be used in semi-arid regions to produce high straw yields suitable for livestock feeding. This is especially important because these regions in Algeria typically use the cereal system in conjunction with livestock farming. Genotypes in cluster II can be used as genetic bases in a selection program to develop early varieties in semi-arid areas, allowing for better water use, particularly during grain filling, and avoiding drought at the end of the cycle. According to Dudhe et al. (2020), selecting genotypes with multiple desirable traits and belonging to different clusters is consistently advantageous in terms of cluster mean values. In our study, genotypes in clusters II, IV, and V show a combination of favorable quality attributes as well as moderate to good phenology, morphology, and yield components. As a result, crossing these genotypes could be a promising breeding strategy.

## CONCLUSION

The results presented in this study emphasize the variations in agro-morphological and quality traits among different types of durum wheat, including a combination of traditional landraces and modern cultivars. This variability allows breeders to choose appropriate plant materials based on specific desired traits, which can

then be incorporated into improvement programs. Plant height, flag leaf area, thousand-kernel-weight, number of kernels/spike, sedimentation volume yellow index, and wet and dry gluten showed a combination of high heritability and a relatively high genetic advance as a percentage of the mean. This result indicates that selecting these traits in early generations could be an effective strategy. The principal component analysis yielded a cumulative variance of 46.67% for the first two principal axes. This analysis enabled us to discern that traits such as PH, DTH, PC, WG, DG, TKW and FLA have a major contribution to this variation. The Pearson correlation analysis demonstrated robust connections between desirable traits, such as plant height and days to heading, which play a vital role in increasing grain yield, as well as between protein content, gluten content, and gluten strength, which contribute to enhancing the nutritional value of durum wheat.

The 125 durum wheat germplasm was categorized into five distinct clusters using cluster analysis, which relied on trait similarities among genotypes. This enables the identification of multiple promising genotypes that display distinct traits, such as elevated protein content and thousand kernel weight, early maturity, and reduced plant height. Integrating landraces into breeding initiatives helps preserve genetic diversity and introduce valuable traits. This approach assists small-scale farmers in adjusting to difficult environmental conditions, guaranteeing the nutritional quality of crop varieties, and decreasing reliance on external resources. Conducting multiple trials in different environments is crucial for studying how different genotypes interact with their environments, assessing how well genotypes perform in relation to specific parameters, and determining the heritability of traits that are relevant to selection criteria.

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