

Genetic variability of some agronomic traits in a collection of wheat (*Triticum turgidum* L. sp.pl.) genotypes under South Mediterranean growth conditions

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Highlights

- The genetic variability of 9 traits of 60 wheat varieties was investigated.
- There was significant variability among wheat genotypes for all measured traits.
- There were wheat varieties that showed the highest phenotypic and genotypic coefficient of variation.
- Some wheat genotypes may be desired allele reservoirs.
- Some traits can be an alternative in wheat selection.

Abstract

Some agronomic traits' genetic variability was investigated in 60 tetraploid wheat accessions (*Triticum turgidum* L. sp.pl.) under rainfed conditions. The results indicated the presence of sufficient variability for all measured traits. The highest phenotypic and genotypic coefficient of variation was recorded for yield and awn length. High heritability coupled with high genetic advance and high expected response to selection recorded for thousand-grain weight, awn length, and the number of grains per spike. Cluster

analysis grouped the 60 wheat genotypes into five clusters. Clusters are relatively formed according to the geographical origin of the genotypes. Cluster III carried entries having the best combinations for all the traits, in which genotypes PI 127106, PI 192658, PI 29051, and PI 67343 can represent an important reservoir of useful genes for the development of new wheat cultivars. Thousand-grain weight, biomass, awn length, and harvest index could be used as a selection criterion for hybridization programs in the future.

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Introduction

Wheat provides food and nutrition security for millions of people belonging to the world's population. Durum wheat is the only tetraploid species with significant agricultural importance because of its use for human consumption; it is one of the most cultivated crops in the Mediterranean basin, several abiotic stresses impose its culture; these unpredictable constraints generally arise during the last stages of the cereal development cycle leading to a great loss of yield and reduce the rate of genetic gain in productivity. For these reasons, new wheat varieties that can adapt to future challenges must be developed. More efficient use of biodiversity in breeding programs is essential to this progress (Mackay *et al.*, 2016). The genetic variability, genetic gain, and heritability estimations are of great importance in plant breeding programs. Heritability provides evidence for genetic control for the expression of a given trait and phenotypic reliability to predict its breeding value (Ullah *et al.*, 2012).

Current intensive agricultural practices opt for high species, and varieties characterised by a higher yield, leading to a reduction in the diversity of agro-ecosystems and a risk of loss of important alleles characterizing the gene pool adapted to specific environments (Rao *et al.*, 2009). As a result of drift and selection, genetic diversity has been lost, which has reduced the improvement potential of wheat in modern agricultural systems (Allard *et al.*, 1996; Ruiz *et al.*, 2012). Wild forms and other related wild species constitute a crucial alternative in breeding programs (Moragues *et al.*, 2006; Peleg *et al.*, 2008) because of their great

variability in terms of phenological and morphological traits. *Triticum turgidum* is a species of monocotyledonous plants of the Poaceae family; they are tetraploid kinds of wheat ($2n=28$) of the AABB genome, is a neglected and underutilised species, which appears to have survived over the centuries in subsistence farming systems in the world, it can be used for the improvement of durum wheat in breeding programs. Understanding gene expression and the mode of inheritance of traits is necessary to choose an appropriate selection methodology for effective improvement (Vineela *et al.*, 2013). An effective breeding program depends on the variation present in the gene pool for yield-enhancing traits. The efficacy of selection relies on sufficient diversity of donor parents; however, the variability of the genetic pool of the starting material has a considerable impact on the response to selection (Falconer and MacKay, 1996). Awareness of heritability makes it possible to predict the genetic component of the offspring and, consequently, to better evaluate the extent of the genetic improvement by following an appropriate selection (Tuhina-Khatun, 2007). The selection of wheat varieties suitable for semi-arid environments is based on their yield in these areas, although this is more effective if associ-

ated morphological and physiological traits assist it. Grain yield is influenced by several agronomic and physiological traits (Chen *et al.*, 2012; Liu *et al.*, 2015).

The objective of this study is to investigate the phenotypic variability of some agronomic traits and their relationship with yield by evaluating heritability and genetic advance in a collection of 60 accessions of wheat (*T. turgidum* L sp.pl.) cultivated in South Mediterranean conditions to select the more desirable traits which may contribute to the improvement of durum wheat yield.

Materials and methods

Plant materials

The plant material studied consists of a collection of 60 accessions of four tetraploids (*Triticum turgidum* L. Subspecies) obtained from The Research Centre for Cereal and Industrial Crops of Foggia (Italy). The accessions are from 26 countries (Table 1).

Table 1. The 60 accessions of durum wheat used for the evaluation (collection population).

Code	Accession*	Origin	Code	Accession*	Origin
G1	Citr 11390	United States	G18	PI 210845	Iran
G2	PI 68287	Azerbaijan	G19	PI 223171	Jordan
G3	PI 113393	Iraq	G20	PI 266846	England
G4	PI 191599	Morocco	G21	PI 272564	Hungary, Pest
G5	PI 192641	Morocco	G22	PI 278647	England
G6	PI 254206	Iran	G23	PI 286547	Ecuador
G7	PI 278350	Italy	G24	PI 289606	England
G8	PI 290530	Hungary, Pest	G25	PI 290512	Portugal
G9	PI 306665	France, Herault	G26	PI 306549	Romania
G10	PI 576854	Turkey	G27	PI 330554	England
G11	PI 624429	Iran, Bakhtaran	G28	PI 330555	England
G12	PI 127106	Afghanistan	G29	PI 349051	Georgia
G13	PI 67343	Australia	G30	PI 352487	Germany
G14	PI 192658	Morocco	G31	PI 352488	Italy
G15	PI 184526	Portugal	G32	PI 352489	Cyprus
G16	PI 352514	Azerbaijan	G33	PI 361757	Denmark
G17	PI 362067	Romania	G34	PI 366117	Egypt. Sinai
G37	PI 56263	Portugal	G35	PI 387479	Ethiopia
G38	PI 134946	Portugal	G36	PI 566593	United States
G39	PI 157983	Italy, Sicily	G52	Citr 7665	Russian Feder
G40	PI 157985	Italy, Sicily	G53	PI 70738	Iraq
G41	PI 173503	Turkey, Ardvin	G54	PI 94755	Georgia
G42	PI 185723	Portugal, Leira	G55	PI 283888	Iran
G43	PI 191104	Spain	G56	PI 341800	Russia
G44	PI 191145	Spain, Baleares	G57	PI 499972	Georgia
G45	PI 191203	Spain	G58	PI 532501	Former Soviet Union
G46	PI 286075	Poland	G59	PI 573182	Turkey
G47	PI 221423	Portugal	G60	PI 585017	Georgia
G48	PI 352544	Switzerland			
G49	PI 290522	Germany			
G50	PI 290526	Hungary, Pest			
G51	PI 341391	Turkey, Burd			

*Citr and PI number indicate the accession number in USDA National Small Grains Collection, Aberdeen, Idaho, USA.

Field trials

The experiment was laid out in a randomized complete block design with three replications at the National Agronomic Research Institute of Algeria (INRAA), Constantine Research Unit (36° 17' N, 6° 38' E and 640 m above sea level), during the 2013-2014 and 2014-2015 crop seasons. Plot dimensions were 4 rows, 1 m long, and 20 cm apart. Soil preparation, planting date, fertilizer application, and weed control were exactly as recommended for the region. Seeds were sown in early January, 100 kg/ha of 46% triple superphosphate was applied for sowing and pointing, and 130 kg/ha of 46% urea was released. Weeds were chemically controlled with Cossack® OD (mesosulfuron-methyl (mesomaxx) + iodosulfuron-methyl-sodium + mefenpyr-diethyl) at the rate of 1/ha. All agronomic practices were carried out uniformly for all treatments.

The morphological traits measured were: Number of days to heading (DH, days) was counted as the number of calendar days from April 1st to when 50% of the spikes were halfway out from the flag leaf. Plant height (PH, cm), spike (SpL) and awn (AwL) length, and the number of grains per spike (KNS) were measured at maturity. Thousand-grain weight (TKW, g), aboveground biomass (BIO, q/h), and grain yield (GY, q/h). Harvest index (HI, %) was derived as 100 times the ratio of grain yield to aboveground biomass:

$$HI(\%) = 100 \frac{\text{yield}}{\text{biomass}} \quad (1)$$

Data analysis

Collected data were subjected to an analysis of variance according to the additive model in a complete block design with three replicates as per Steel and Torrie (1982) (Table 2) as follows:

$$Y_{ij} = \mu + G_i + B_j + e_{ij} \quad (2)$$

where Y_{ij} is the observed value of the measured trait for i th genotype and j th block, μ is the overall mean for the measured trait, G_i is the i th genotype effect, B_j is the j th block effect, and e_{ij} is the residual associated with i th genotype and j th block.

Phenotypic (σ^2_p) and genotypic (σ^2_g) variance components were derived from the expected mean square according to Aquaah (2009) as follows:

$$\sigma^2_g = \frac{MSg - MSe}{b} \quad (3)$$

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

where t is the tabulated value at 5% probability with $(b-1)(g-1)$ df of the residual, b is the number of blocks, and σ^2_e is the residual mean square. Based on the estimates of phenotypic (σ^2_p), genotypic (σ^2_g), and environmental (σ^2_e) variances, phenotypic (PCV) and genotypic coefficients of variation (GCV) were obtained according to the method outlined by Cruz *et al.* (2012):

Table 2. Analysis of variance model.

Source	DF	Mean square	F test ratio
Genotype	2	MSg	MSg/MSe
Block	59	MSb	MSb/MSe
Residual	59	MSe	-

DF, degree of freedom; MS, grand mean of trait of interest.

$$PCV(\%) = 100 \frac{\sigma_p}{\bar{x}} \quad (4)$$

$$GCV(\%) = 100 \frac{\sigma_g}{\bar{x}} \quad (5)$$

Broad-sense heritability was calculated using variance components according to Aquaah (2009):

$$h^2_{bs}(\%) = \frac{\sigma^2_g \times 100}{\sigma^2_g + \sigma^2_e} \quad (6)$$

The expected response to selection expressed as a percent of the grand mean RS (%) was calculated according to Cruz *et al.* (2012) as follows:

$$RS(\%) = S h^2_{bs} / Ms \quad (7)$$

where Ms: the grand mean of trait of interest, S: differential to selection.

The genetic advance as a percentage of the mean was calculated according to the method given by Comstock and Robinson (1952) according to the formula:

$$GA\%_{ave} = GA \times 100 / Ms \quad (8)$$

where GA: genetic advance; Ms: grand mean of trait of interest.

Analysis of variance (ANOVA) and mean comparison, correlation, Cluster, and PCA analysis were performed using Minitab17.

Results and discussion

Climatic data

Rainfall was 451.9 and 509.3 mm during 2013-14 and 2014-15 growing seasons, respectively. Rainfalls were almost similar during the study period, but their distribution was not uniform, which relatively influenced the agronomic traits studied (Table 3).

Each year was characterised by exceptional meteorological events. For example, during 2013-2014, winter minimum temperatures were milder, and 196.4 mm of rain was concentrated in spring, whereas during 2014-2015, large portions of the total rainfall occurred at the beginning of the wheat season, leaving the rest of the growing season in drought, which may explain the higher grain yields and plant height recorded during the first season.

Phenotypic variation

Figure 1 shows the study results for the 9 traits during the two seasons. The results of the analysis of variance indicated a significant genotype effect, suggesting the presence of significant variation among genotypes for all measured traits (Table 4).

This variability deserves to be exploited for selection purposes to improve the performance and adaptation of wheat to the environmental fluctuations that characterise the growing regions in Algeria. Several studies (Mengistu *et al.*, 2016; Birhanu *et al.*, 2017; Mansouri *et al.*, 2018) had reported a higher range of variability in agronomic traits in *T. turgidum* and *T. turanicum* (Ikanović *et al.*, 2014; Iannucci and Codianni, 2019).

The results revealed a wide range of genetic variability among

genotypes for studied agronomic traits (Table 5). Except for BIO, all the traits in the present study exhibited a high broad-sense heritability. The highest value was recorded for TKW (99.28%), followed by DH (98.66%), AwL (91.88%), and KNS (91.60%). AwL, TKW, and KNS also show the highest genetic advance (GA) values with 83.04%, 51.25%, and 36.14%, respectively. While DH displayed the lowest GA value (8.02%). The phenotypic variance (σ^2_p) of all traits was higher than the genotypic variance (σ^2_g); likewise, the phenotypic coefficient of variation (PCV) was also higher than the genotypic coefficient of variation (GCV), which implies that the expression of these characters is modulated by the genotype effect more than that of the environment which makes possible a selection based on phenotypic values. Similar observations were also reported by Sriram Ajmera *et al.* (2017) in rice and observed by Fellahi *et al.* (2013) in durum wheat. The highest PCV was recorded for GY (40.37%), followed by AwL (39.74%) which also displayed the highest GCV with 36.75% and 38.10%, respectively. PH exhibits the lowest PCV and GCV (15.09% and 13.78%). The expected response to selection was relatively moderate for bio (13.93%) and high for the remaining traits; the observed values were over 20.00% for plant height, over 30.00% for KNS, HI%, and DH, and over 50.0% for AwL (87.96%), TKW (64.48%) and GY (63.87%). Heritability is indicative of the degree of expression of the genotype through the phenotype. It represents the proportion of phenotypic variability that is genetic; this proportion is heritable and fixable in whole or in part. The Highest heri-

tability was recorded to TKW and DH (>90%) which suggests that these traits are the expression of additive genes. Comparable data were reported for Khorasan wheat by Iannucci and Codianni (2019); High values of heritability are reported by Majumder *et al.* (2008); Singh and Upadhyay (2013) for these characters;

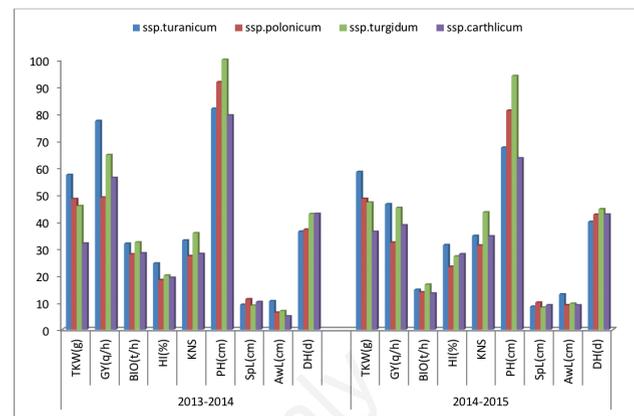


Figure 1. Mean values of agronomic traits in the two growing seasons. TKW, thousand-grain weight; GY, grain yield; BIO, biomass; HI, harvest index; KNS, number of grains per spike; PH, plant height; SpL, spike length; AwL, awn length; DH, number of days to heading.

Table 3. Monthly rainfall and mean maximum and minimum temperatures for two growing seasons for Constantine (Algeria).

	2013-2014			2014-2015		
	Tmax (C°)	Tmin (C°)	Rainfall (mm)	Tmax (C°)	Tmin (C°)	Rainfall (mm)
Sept	28.9	15.7	23.0	33.1	17.2	12.8
Oct	28.5	13.5	26.8	27.0	11.9	13.0
Nov	15.7	6.5	86.2	20.9	8.2	25.1
Dec	12.9	2.3	29.6	12.5	3.2	105.4
Jan	14.0	3.5	42.8	12.3	1.5	113.0
Feb	16	3.2	31	11	2.1	121
Mar	14.3	4.2	131.7	16.0	4.6	85.8
Apr	21.8	6.2	5.7	22.5	7.2	5.2
May	25.3	9.3	60.3	27.3	10.7	18.8
Jun	31.1	14.4	14.8	30.7	14.2	9.2
Sum	-	-	451.9	-	-	509.3

Table 4. Analysis of variance mean squares of 9 measured traits in 60 accessions of *Triticum turgidum* sp.pl.

Source	2013-2014			2014-2015		
	Block	Genotype	Residual	Block	Genotype	Residual
DF	2	59	59	2	59	59
TKW	2.88	395.34***	0.95	31.67	335.16***	11.56
GY	243.92	1664.4***	107.28	26.34	518.22***	82.72
BIO	19458	18596.5***	3951	3140.44	2697.4***	1063.23
HI	1.43	80.77***	7.55	53.05	90.69***	14.41
KNS	25.57	134.92***	4	10.16	198.73***	35.84
PH	483.79	482.36***	29.87	463.68	749.53***	114.02
SpL	9.4	12.61***	0.59	0.09	9.26***	0.65
AwL	0.38	24.81***	0.71	2.09	21.48***	0.7
DH	1.2	115.47***	0.52	4.21	49.09***	2.36

***Highly significant ($P < 0.0001$). DF, degree of freedom; TKW, thousand-grain weight; GY, grain yield; BIO, biomass; HI, harvest index; KNS, number of grains per spike; PH, plant height; SpL, spike length; AwL, awn length; DH, number of days to heading.

Muhammad *et al.* (2017) reported high broad-sense heritability for spike length (43%), grains spike⁻¹ (88%), 1000-grain weight (95%), biomass yield (89%), grain yield (96%) and harvest index (86%). The high heritability indicates that the characters were less influenced by the environment (Kumar *et al.*, 2014). The highest heritability values coupled with high genetic advance were observed for TKW, AwL, and KNS, indicating a major role of additive gene action for these traits; similar findings were reported by Ajmal *et al.* (2009); Bilgin *et al.* (2011); Nishant *et al.* (2018). The effectiveness of selection for a character is best when it exhibits high heritability and High genetic advances together (Larik *et al.*, 2000). Heritability insinuates the magnitude of improvement in a trait achieved under particular selection conditions; its efficiency is better when used to calculate genetic advance (Shukla *et al.*, 2004). Nwangburuka and Denton (2012) noted that heritability estimates with the genetic progress are more reliable and meaningful than their individual examination. High heritability coupled with moderate genetic advance was recorded for DH, indicating the predominance of non-additive gene action in the expression of this character. Similar results in wheat were also reported by Prasad *et al.* (2006). According to Burton and Devane (1953), estimating the genotypic and phenotypic coefficients of variation and heritability gives the best information to disclose desirable traits through selection. In this context, Deshmukh *et al.* (1997) consider that the phenotypic coefficients of variation whose value is greater than 20% are high, those whose value is between 10 and 20%, are average and those in the value is less than 10% are low. Accordingly,

moderate PCV and GCV were recorded for DH and PH, indicating less scope for selection as they are under the influence of the environment. High PCV and GCV were obtained for the remaining traits, which suggests the possibility of improving these traits through selection based on phenotypic expression. In a study of sixty-eight durum wheat genotypes, Wolde *et al.* (2016) observed high values of PCV and GCV for productive tillers per plant, the number of kernels per spike, and weight of thousand kernels, grain yield, and harvest index. The CV_p are higher in value and more valuable than the CV_g for all the traits; this was also the case for all the traits, indicating that environmental effects influence these characters. Similar records were obtained by Alemu *et al.* (2020) for Sixty-four durum wheat landraces. In another study, Osman *et al.* (2012) reported that the influence of the environment on the expression of a trait is determined by the difference between the genotypic and phenotypic coefficients of variation. Large differences suggest that the variability in the trait measured depends on an environmental effect, while small differences reflect a strong genetic effect. TKW, PH, KNS, and DH exhibit small differences between the PCV and GCV, suggesting that selection based on these characters would be effective for future crossing programs. GY and HI% showed a higher difference between PCV and GCV, indicating that the expression of these traits is more subject to the environmental effect.

Trait relationship

The relationships between traits (Table 6) indicated that AwL

Table 5. Genetic variability parameters for 9 agronomic traits of 60 wheat genotypes (*Triticum turgidum* L. sp.pl.) were evaluated in 2013-14 and 2014-15 crop seasons.

	TKW	GY	BIO	HI	KNS	PH	SpL	AwL	DH
σ^2_e	0.95	107.3	3951	7.55	4	29.87	0.59	0.71	0.52
σ^2_g	131.5	519	4882	24.4	43.6	150.8	4.01	8.03	38.32
σ^2_p	132.4	626.3	8833	32.0	47.6	180.7	4.60	8.74	38.84
h^2_{bs} %	99.28	82.87	55.27	76.4	91.6	83.47	87.2	91.9	98.66
σ_p	11.51	25.03	93.98	5.65	6.90	13.44	2.14	2.96	6.23
σ_g	11.47	22.78	69.87	4.94	6.61	12.28	2.00	2.83	6.19
PCV %	24.08	40.37	31.14	27.4	22.2	15.09	21.6	39.7	15.91
GCV %	23.99	36.75	23.15	23.9	21.2	13.78	20.1	38.1	15.80
S (H-L)	31.27	59.08	220	14.5	18.5	34.85	5.21	7.76	16.60
RS (%)	64.48	63.87	13.93	39.8	49.0	24.33	36.8	88	41.23
GA	24.49	19.5	31.58	9.83	11.3	26.61	3.57	6.18	3.14
GA _{mn} %	51.25	31.46	10.46	47.6	36.1	29.86	35.9	83.0	8.02

TKW, thousand-grain weight; GY, grain yield; BIO, biomass; HI, harvest index; KNS, number of grains per spike; PH, plant height; SpL, spike length; AwL, awn length; DH, number of days to heading; σ^2_e , σ^2_g , σ^2_p , environmental, genotypic, and phenotypic variances; PCV and GCV phenotypic and genotypic coefficients of variation; S (H-L), differential to selection; GA, genetic advance.

Table 6. Phenotypic correlation coefficients for 9 characters of 60 *Triticum turgidum* sp.pl. genotypes

Traits	TKW	GY	BIO	HI	KNS	PH	SpL	AwL
GY	0.533***	-----						
BIO	0.325*	0.737***	-----					
HI	0.496***	0.798***	0.242 ns	-----				
KNS	0.060 ns	0.469***	0.292*	0.469***	-----			
PH	0.061 ns	0.018 ns	0.292*	-0.242 ns	0.335*	-----		
SpL	-0.005 ns	-0.347*	-0.199 ns	-0.294*	-0.41**	0.007 ns	-----	
AwL	0.698***	0.578***	0.263*	0.636***	0.156 ns	-0.244 ns	-0.334*	-----
DH	-0.531***	-0.230 ns	-0.028 ns	-0.322*	-0.145 ns	0.251 ns	-0.242 ns	-0.324*

***Highly significant (P<0.001); **significant (P<0.005); *(P<0.05); ns, not significant. TKW, thousand-grain weight; GY, grain yield; BIO, biomass; HI, harvest index; KNS, number of grains per spike; PH, plant height; SpL, spike length; AwL, awn length; DH, number of days.

Table 7. Distribution of 60 wheat genotypes in different clusters.

Clusters	Accessions									
I (20 genotypes)	G1	G2	G3	G4	G5	G6	G8	G9	G11	G12
	G18	G21	G23	G32	G34	G45	G49	G56	G59	G60
II (15 genotypes)	G7	G16	G17	G28	G36	G29	G48	G50	G51	G52
	G53	G54	G55	G57	G58	-	-	-	-	-
III (7 genotypes)	G10	G13	G14	G15	G20	G25	G30	-	-	-
IV (8 genotypes)	G19	G24	G26	G27	G41	G43	G46	G47	-	-
V (10 genotypes)	G22	G31	G33	G35	G37	G38	G39	G40	G42	G44

exhibited significant and positive correlation coefficients with GY, TKW, BIO HI, and KNS. These results suggested AwL as an indirect selection criterion to improve grain yield. On the other hand, DH exhibited negative and significant phenotypic correlations with TKW; these results corroborated with those of Mohsin *et al.* (2009), Muhammad *et al.* (2017), and Nishant *et al.* (2018).

Cluster analysis

The Euclidean distance was calculated using standardised traits data. The dendrogram of 60 genotypes was constructed using Ward’s method: 5 major groups were constructed based on multivariate analysis (Figure 2). The clusters are relatively formed according to the geographical origin of the genotypes (Table 7). Cluster I contained the maximum number of genotypes (20), most of which are of Afro-Asian origin and belonging to the subspecies turanicum (10) and polonicum (5) - noting that most of the accessions from Iran and adjacent regions are in this cluster. Clusters V contained 10 genotypes, most (90%) of which are of European origin - also noting that the genotypes belonging to *T carthlicum* are concentrated in cluster II. The distribution of the accessions within the other clusters has no apparent relationship in terms of geographic origin. Iannucci and Codianni (2019), in a study on a collection of 77 Khorasan wheat, identified six clusters which included 7, 22, 1, 5, 35, and 7 accessions. The relative differences among clusters are indicated in (Figure 3). Clusters III enclosed the shortest and earliest genotypes had the highest GY, TKW, HI, AwL, and

Table 8. Eigenvectors and Eigenvalues of the first four principal components of 9 traits.

Principal components	PC1	PC1	PC1	PC1
Eigenvalues	3.61	1.9	1.24	0.73
Proportions	40.2	21.2	13.9	0.08
Cumulative	40.2	61.4	75.2	83.4
TKW	0.379	-0.270	-0.323	0.003
GY	0.485	0.114	-0.061	0.117
BIO	0.312	0.271	-0.388	0.527
HI	0.446	-0.073	0.24	-0.325
KNS	0.255	0.459	0.099	-0.613
PH	-0.02	0.454	-0.579	-0.21
SpL	-0.214	-0.342	-0.507	-0.261
AwL	0.417	-0.206	0.161	0.182
DH	-0.198	0.510	0.236	0.286

TKW, thousand-grain weight; GY, grain yield; BIO, biomass; HI, harvest index; KNS, number of grains per spike; PH, plant height; SpL, spike length; AwL, awn length; DH, number of days to heading.

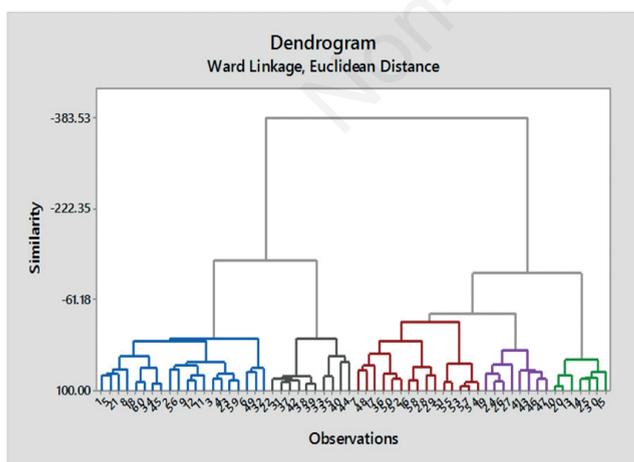


Figure 2. Hierarchical cluster analysis dendrogram (Ward’s method) of the mean values of the 9 agronomic traits (TKW, thousand-grain weight; GY, grain yield; BIO, biomass; HI, harvest index; KNS, number of grains per spike; PH, plant height; SpL, spike length; AwL, awn length; DH, number of days to heading) for the 60 *Triticum turgidum* sp.pl. genotypes.

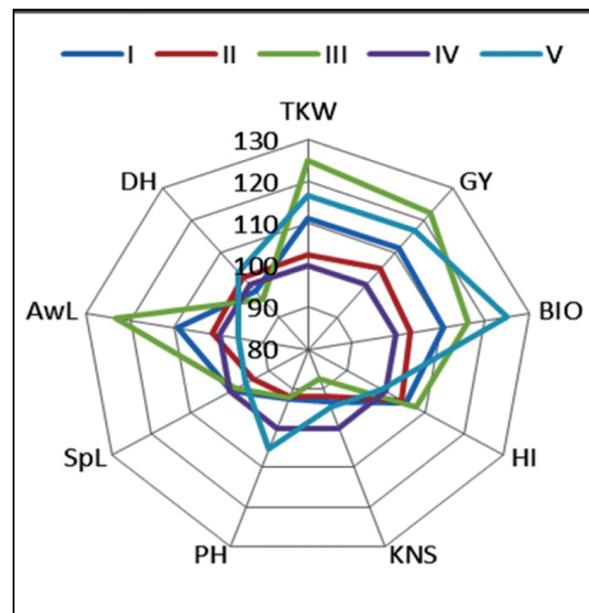


Figure 3. Relative deviation of the performance of clusters (C) CI, CII, CIII, and CV as a percent of mean values of CIV for the measured traits. TKW, thousand-grain weight; GY, grain yield; BIO, biomass; HI, harvest index; KNS, number of grains per spike; PH, plant height; SpL, spike length; AwL, awn length; DH, number of days to heading.

high BIO. Cluster V included the latest and tallest genotypes, with the highest BIO, moderate GY, TKW, and low AwL. Khan *et al.* (2013) reported significant and large indirect effects of days to heading and plant height on grain yield. Cluster III carried entries having the best combinations for GY, TKW, BIO, HI, and AwL. Therefore, selecting suitable genotypes among the 7 available within this cluster would be beneficial; it represents an important reservoir of economically useful genes for the development of new wheat cultivars. In particular, we identified: PI 127106 from Turkey, PI 192658 from Morocco, PI 290512 from Portugal, and PI 67343 from Australia. These findings were in accordance with Iannucci and Codianni (2019) results concerning the last accession.

Principal component analysis

The presence of solid differences among 60 wheat genotypes in the present study was also further confirmed by PCA. The principal component analysis revealed that four principal components (PC1-PC4) exhibited Eigenvalue near or higher than one and have accounted for 83.4% of the total variation, which indicated a very strong correlation among the characters being studied (Table 8). Chahal and Gosal (2002) reported that traits influence clustering with the largest absolute value within the first principal component. Therefore, in the present study, the edification of the different clusters of genotypes results from the relatively high contribution of a few traits. Hence, the first principal component (PC1) accounted for 40.2% of the variation. Thus PC1 represents an overall TKW, GY, AwL, and HI effect because the coefficients of whose terms have the same sign and are not close to zero. However, variability among genotypes was attributed to those discriminatory traits.

Conclusions

The results revealed a wide range of variability among wheat genotypes for multiple agronomic traits, allowing us to take advantage of beneficial alleles that were excluded from the domesticated gene pool. The highest heritability recorded for almost all studied characters demonstrates that these traits could be successfully transferred to offspring. Thousand-grain weight (TKW), number of grains per spike (KNS), and awn length (AwL) had high heritability coupled with high genetic advance, which implies that these traits could be used as a selection criterion to select upland accession genotypes for a notable improvement in cultivation in changing environments. *Furthermore*, 7 accessions enclosed in cluster III carried the best combinations of desirable traits for high GY and other useful characteristics that can be further used in durum wheat breeding programs. The development of varieties adapted to the arid conditions depends on improving potential yield and yield evaluation in different environments. The information obtained from this collection of genotypes will help select parents to develop high-yield durum wheat lines in breeding programs.

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