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Phenotypic diversity in durum wheat landraces and cultivars from Morocco and North America

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Abstract

Studying the phenotypic diversity of landraces and older advanced cultivars, along with their distribution, is important for breeding and germplasm conservation. To this sense, we analyzed the phenotypic diversity and spreading of 108 durum wheat accessions, including 56 landraces (LANs), 15 Moroccan cultivars (MCs), and 37 North American cultivars (NACs), using thirteen phenotypic descriptors. The collection studied was phenotypically very diverse (Shannon-Weaver index, *H'*mean=0.66). Spike color (*H'mean*=0.95), glume hairiness and spike waxiness (*H'mean*=0.89), peduncle attitude (*H'mean*=0.82), awn color (*H' mean*=0.75), and spike density and grain color (*H'mean*= 0.73) were the most diverse traits. The results also showed that NACs (*H'mean*=0.78) and the LANs (*H'mean*=0.69) were more diverse than MCs (*H'mean*=0.53). Multiple correspondence analyses explained 19.31% of the total variability and demonstrated a clear distinction between genotypes of Morocco and North America and between the LANs and MCs. These results of phenotypic diversity and distribution of studied genotypes can make a major leap forward in national breeding programs and germplasm collection expeditions.

Keywords: landraces and advanced cultivars; phenotypic diversity; distribution; durum wheat.

Abbreviations: CRRA_regional centre of the agricultural research; INRA_national institute of the agronomic research; MAPM-DREF_ ministry of agriculture, maritime fisheries, rural development and water and forests; FAO_food and agriculture organization; H'_shannon-weaver index; MCA_multiple correspondence analysis; NACs_north american cultivars; MCs_moroccan cultivars; LANs_landraces; CIMMYT_international maize and wheat improvement center; ICARDA_the international center for agricultural research in the dry areas; DUS_distinction, uniformity, and stability; UPOV_International Union for the Protection of New Varieties of Plants; Hs_the intrapopulation genetic diversity; Ht_total gene diversity; Gst_ coefficient of gene differentiation.

Introduction

Durum wheat (*T. turgidum ssp.* durum) is a well-known cereal in the Mediterranean region, used to produce a range of traditional products including bread, couscous, pasta, and semolina. Durum wheat is widely cultivated, accounting for about 60% of the world's durum wheat area, due to its ability to adapt to different agroclimatic conditions (Royo et al., 2017). Mediterranean countries, such as Italy, Spain, France, and Greece, as well as West Asian and North African countries like Morocco, Algeria, Tunisia, and Libya, are the main producers and consumers of this crop (Royo et al., 2021). Durum wheat has been a staple food in these regions for a long time. In Morocco, durum wheat is a fundamental element of the cereal consumption pattern and an essential component of local food security. It is used to make semolina and pasta in the industrial sector and bread in urban and rural areas (Nassif et al., 2012). Recently, the demand for durum wheat in quantity and quality has increased. Despite producing and growing about 2.2 million tons of durum wheat per year in an area of more than 1 million hectares (MAPM-DREF, 2019), the country heavily relies on imports to meet its consumption demand, which can sometimes go up to 90 kg per person per year (Taghouti et al., 2017b). Still, importing durum wheat is no longer a sufficient solution to the growing demand for grain in the global market. Moreover, in the coming decades, unforeseen challenges such as climate fluctuations and population growth in 2050 (FAO, 2017), could negatively impact the productivity and availability of durum wheat in the global market. Therefore, it is critical to focus on improving durum productivity and quality in future breeding programs in Morocco.

Increasing genetic diversity in modern durum wheat cultivars is crucial for improving the crop's productivity and addressing the challenges posed by climate change and food security issues (Christov et al., 2022). This new genetic diversity provides breeders with the ability to develop advanced cultivars with desirable traits. Nevertheless, the replacement of landraces with modern cultivars often leads to reduced genetic diversity in harsh environments. Ex-situ conservation of plant genetic resources, particularly those rich in landraces and local and foreign cultivars, is therefore seen as a valuable source of this new genetic diversity. The reuse and reintroduction of these resources are important tools for addressing future challenges in durum wheat production.

Lately, exploring landraces and old durum wheat varieties held in gene banks has become a popular trend in breeding programs. This renewed interest is due to the genotypes' adaptability to traditional farming systems and consumers' preference for traditional and organic products, which are perceived as "safer" and "healthier" foods (Mefleh et al., 2022). Re-utilizing these resources will help prevent their neglect and restore genetic diversity that has been lost due to the replacement of traditional varieties with more productive ones. As a result, incorporating new genetic diversity from landraces and old varieties into modern durum wheat cultivars has become a priority in Moroccan breeding programs.

Recent studies have focused on characterizing and evaluating the genetic diversity of landraces and old advanced cultivars, revealing that these resources contain desirable alleles that can be utilized in breeding programs to improve productivity, quality, and resistance to biotic and abiotic factors (Rasheed et al., 2016; Zhao et al., 2019; Khalid et al., 2019; Zhang et al., 2021; Chegdali et al., 2024). This is particularly relevant to Moroccan genetic resources, which exhibit significant diversity in promising glutenin alleles related to gluten strength (Chegdali et al., 2020). Local varieties are a treasure trove in terms of genetic diversity, desirable adaptive traits, and technological quality, making them a valuable resource for breeding programs (Amallah et al., 2015). Similarly, Taghouti et al. (2017a) reported that local old durum wheat is a good source of needed genes for future cultivar improvement. This genetic richness is largely attributed to traditional cultivation practices, the diversity of growing regions, and the appreciation of genetic material by local farmers (Zarkti et al., 2010a). Therefore, characterizing and evaluating these adapted and unexploited resources would be a beneficial step for Moroccan durum wheat breeding programs.

Phenotypic characterization is a method used to determine the genetic diversity of crop genetic resources. It involves qualitative and quantitative descriptors and is an essential tool for selecting parents for crosses and designing breeding programs (Schut et al., 1997). This method relies solely on visual observation of visible traits such as phenotypic traits of the plant, ear, and grain (Khlestkina et al., 2004; Dagnaw et al., 2022; Yirgu et al., 2022). Phenotypic characterization is widely used as a first step in assessing genetic diversity and population genetic structure in durum wheat studies (Jain et al., 1975; Pecetti et al., 1992; Hailu et al., 2010; Mengistu et al., 2015; Ouaja et al., 2021; Iannucci et al., 2022; Gadissa and Gudeta, 2023). Shannon-Weaver index (*H'*) serves as a key parameter for assessing the extent of phenotypic diversity (Shannon and Weaver, 1949). Additionally, utilizing information on genetic diversity, the frequency distribution of traits, and the application of multiple correspondence analysis (MCA) are appropriate approaches for effective parental selection in designing breeding programs. valuating genetic diversity aids in predicting the utilization of genetic resources, while the analysis of trait frequency distribution and MCA reveals distinctions between genotypes concerning various traits.

Evaluating the genetic diversity of Moroccan durum wheat is crucial for breeding programs seeking to enhance important agricultural traits, including high yield, grain quality, and stress resistance. Morocco harbors over 3000 durum wheat entries at the National Gene Bank, making it a significant center of diversity for this crop in North Africa. However, studies based on phenotypic characterization to assess genetic diversity remain insufficient. The phenotypic distribution between landraces and old advanced cultivars, crucial for determining future collection missions and improvement strategies, has not been well understood. To fill this gap, we conducted a study using 13 phenotypic descriptors to analyze the genetic diversity and phenotypic distribution of durum wheat landraces and cultivars from Morocco and North America.

Results

Percentage frequency of phenotypic classes of individual traits

Table 1 presents the frequency distribution of phenotypic classes for traits among all accessions, NACs, MCs, and LANs. The results show significant phenotypic variability among the accessions in the collection and the three groups studied.

In this study, 62.37% of the accessions reached the heading stage at a median date. Median dates were more common among MCs and NACs, while most LANs were late to reach the heading stage. In terms of plant height, the medium and tall classes were the most abundant. Within the groups, medium and tall plants were the most prevalent in LANs (80%) and MCs (64.29%), while the majority of NACs had medium or very tall heights.

In addition to heading date and plant height, we analyzed other traits of the spike, including density, color, and wax. Among the accessions, 58.11% had dense spikes, 36.5% had medium spikes, and just over 5% had loose spikes. Regarding spike density prevalence within groups, NACs and LANs had the highest proportion of dense spikes, whereas most MCs had medium or dense spikes. For spike color, we observed dominance of light brown, followed by white. In the groups, most MCs and NACs had white or light brown spikes, while LANs were generally distinguished by light brown and dark brown color. For spike waxiness, the waxy and non-waxy types had approximately the same percentage of occurrence in this collection, the same distribution was also observed in NACs. Among the other two groups, waxy spikes were more frequent in LANs, and non-waxy types were more prevalent in MCs.

In terms of peduncle attitude distribution, we found that NACs and LANs were largely characterized by the straight form, while MCs were mainly distinguished by the curved shape. As for the phenotypic characteristics of the beards and the awn, most accessions have had a beard of straight shape with an

Table 1. Phenotypic class frequencies of studied traits for all accessions, North American cultivars, landraces, and Moroccan cultivars.

Traits	Class	All Accessions (%)	North American Cultivars (%)	Moroccan Landraces (%)	Moroccan Cultivars (%)
Days to Heading	Early	1.8	5.41	0	0
	Medium	62.37	56.76	30.36	100
	Late	35.83	37.84	69.64	0
Plant Height	Very Short	0	0	0	0
	Short	8.4	21.62	3.57	0
	Medium	43.43	32.43	17.86	80
	Long	11.49	13.51	14.29	6.67
	Very Long	36.68	32.43	64.29	13.33
Spike Density	Lax	5.39	10.81	5.36	0
	Medium	36.5	37.84	25	46.67
	Dense	58.11	51.35	69.64	53.33
Spike Color	White	34.72	37.84	19.64	46.67
	Light Brown	40.83	37.84	44.64	40
	Dark Brown	24.46	24.32	35.71	13.33
Spike Waxiness	Wax	44.62	51.35	62.5	20
	Non-Wax	55.38	48.65	37.5	80
Spike Shape	Tapering	54.07	48.65	53.57	60
	Parallel	27.04	5.41	35.71	40
	Clubbed	0	0	0	0
	Fusiform	18.89	45.95	10.71	0
Beard Shape	Straight	68.4	67.57	64.29	73.33
	Medium	28.31	24.32	33.93	26.67
	Curved	3.3	8.11	1.79	0
Peduncle Attitude	Straight	53.07	51.35	67.86	40
	Bent	36.04	35.14	19.64	53.33
	Crooked	10.89	13.51	12.5	6.67
Awn Color	White	4.02	5.41	0	6.67
	Light Brown	42.37	56.76	30.36	40
	Dark Brown	14.58	13.51	3.57	26.67
	Dark	39.02	24.32	66.07	26.67
Awn Attitude	Appressed	75.53	70.27	69.64	86.67
	Medium	24.47	29.73	30.36	13.33
	Spreading	0	0	0	0
Glume Hairiness	Non-Hairy	19.9	40.54	12.5	6.67
	Medium	41.7	29.73	55.36	40
	Hairy	38.4	29.73	32.14	53.33
Kernel Color	White	37.21	21.62	50	40
	Amber	56.81	67.57	42.86	60
	Red	5.98	10.81	7.14	0
Kernel Shape	Round	0	0	0	0
	Ovate	0.6	0	1.79	0
	Oblong	91.62	83.78	91.07	100
	Elliptical	7.79	16.22	7.14	0

appressed attitude. For awn color, the most common classes in the collection were light brown and black. The NACs and MCs showed a predominance of light brown awns, while the LANs exhibited a prevalence of black color.

As for the distributing glume hairiness for the collection, accessions showed all three classes of hairiness, with different and decreasing percentages as follows medium, hairy, and not hairy. The same distribution occurred with the LANs. For cultivars, we observed the abundance of hairless glumes for NACs and hairy or medium glumes for MCs.

Regarding grain characteristics, we observed that amber grains were the most common color between accessions, followed by white-colored grains, while the red color was infrequent within accessions. For the groups, golden kernels were the most common color in NACs and MCs, while white and amber grains were the most prevalent classes in LANs. For grain shape, the oblong shape showed a broad and relatively uniform distribution in most accessions of the collection.

Estimating Genetic Diversity: Shannon-Weaver Index

To assess genetic diversity within the durum wheat accessions, we calculated the Shannon-Weaver diversity index (*H'*) for all accessions and within NACs, LANs, and MCs, and the results are summarized in Table 2. The *H'mean* value of 0.66 indicated a substantial level of genetic diversity across the collection. Notably, NACs had the highest *H'mean* value of 0.78, while MCs showed the lowest value at 0.53.

At the collection level, the smallest mean-diversity index (*H'mean*=0.19) was obtained for grain shape while the highest (*H'mean*=0.95) was observed for grain shape, while the highest

Table 2. Estimates of Shannon-Weaver index (H') for all accessions, North American cultivars, Landraces, and Moroccan cultivars based on the traits used in the study.

Traits	H' Values for All accessions	H' Values for North American cultivars	H' Values for Moroccan landraces	H' Values For Moroccan ultivars
Days to Heading	0.44	0.77	0.56	0
Plant Height	0.61	0.83	0.61	0.39
Spike Density	0.73	0.87	0.69	0.63
Spike Color	0.95	0.98	0.95	0.9
Spike Waxiness	0.89	0.99	0.95	0.72
Spike Shape	0.60	0.62	0.68	0.49
Beard Shape	0.64	0.74	0.66	0.53
Peduncle attitude	0.82	0.89	0.77	0.8
Awn Color	0.75	0.79	0.54	0.9
Awn Attitude	0.49	0.55	0.56	0.36
Glume Hairiness	0.89	0.99	0.87	0.8
Kernel Color	0.73	0.76	0.82	0.61
Kernel Shape	0.19	0.32	0.25	0
Means	0.66	0.78	0.69	0.53
±SE	0.2	0.05	0.05	0.08

H': Shannon-Weaver index; SE: Standard error.

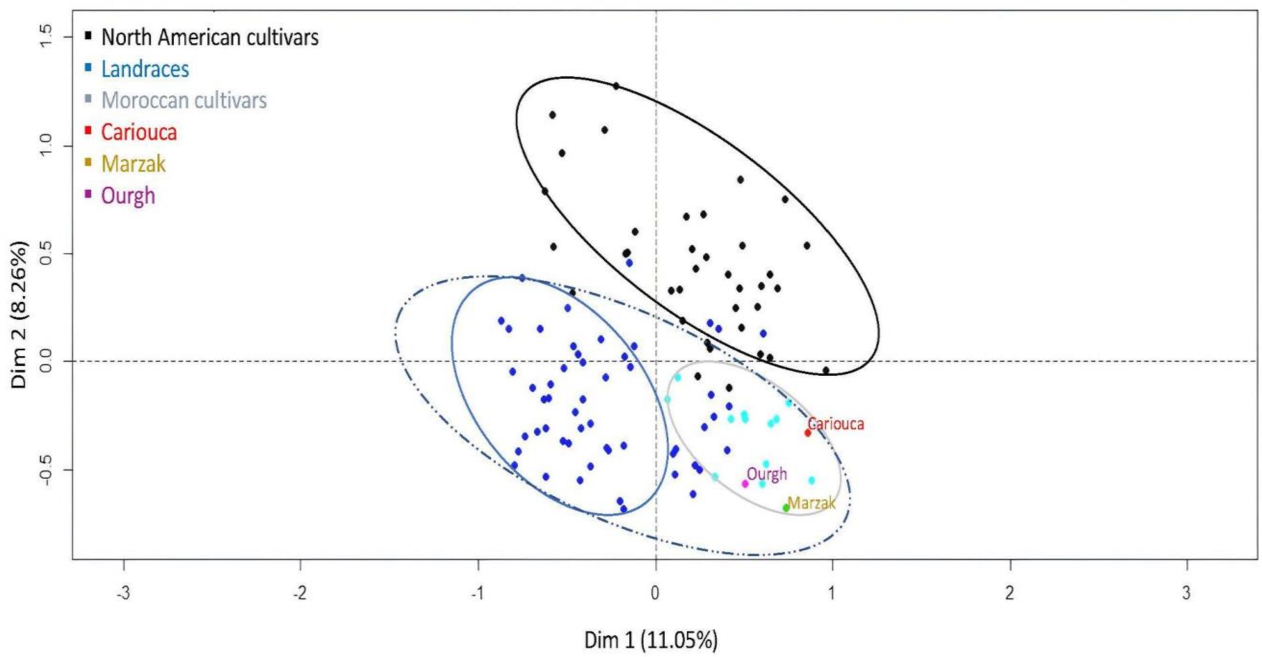

Fig 1. Multiple correspondence analysis elucidates the distribution of Moroccan and North American durum wheat landraces and cultivars based on thirteen phenotypic traits.

($H'mean$=0.95) was obtained for spike color. Most phenotypic characters exhibited a high level of diversity ($H'mean$>0.5), except for heading date, awn attitude, and grain shape, which were below 0.5. In NACs, the lowest H' was calculated for grain shape (H'=0.32), while the smallest was obtained for spike waxiness and glume pubescence (H'=0.99). In LANs, the smallest H' was obtained for the grain shape (H'=0.25), and the highest H' was registered for color and the waxiness spike (H'=0.95). In MCs, H' ranged from completely monomorphic traits (H'=0) for heading date and grain shape to highly polymorphic traits for spike color and grain color (H'=0.9). This group showed less variation (H'<0.5) for heading date, plant height, spike shape, and awn attitude. Across all three groups, we observed that most of the phenotypic traits were highly polymorphic (H'>0.50), except for grain shape.

Estimation of genetic parameters: Nei's gene diversity indices

The parameters used for the estimation of gene diversity (*Nei's*) in this study were total gene diversity (*Ht*), gene diversity within the population (*Hs*), and coefficient of gene diversity (*Gst*). The results of Nei's indices are provided in Table 3.

The *Ht* values ranged from 0.1545 for grain shape to 0.6566 for plant height, with an average of 0.52. Meanwhile, the *Hs* average was 0.47, with the highest value found in spike color (0.6312) and the lowest in grain shape (0.1456). As for *Gst*, values varied between 0.3402 for days to heading and 0.0095 for beard shape, with an average contribution of 0.09 to total diversity (Table 3).

Multiple correspondence analysis

Multiple correspondence analysis (MCA) was exploited to see the distribution of NACs, MCs, and LANs based on thirteen phenotypic traits. Fig. 1 shows this distribution, including the considered controls such as "Marzak", "Cariouca" and "Ourgh". The MCA biplot accounted for 19.31% of the total variance. The two dimensions that explained the highest percentages of variance were dimension 1 (Dim1) and dimension 2 (Dim2), which accounted for 11.05% and 8.26% of the total variance, respectively. Dim 1 separated the 108 accessions into two groups: the first group consisted of NACs, while the second group consisted of Moroccan accessions, including LANs and MCs. Dim 2 distinguished MCs from LANs. The controls, namely "Marzak," "Cariouca," and "Ourgh," were grouped with the MCs.

Discussion

A strong phenotypic variability was observed between these stored durum wheat accessions. This finding is consistent with previous research conducted by Zarkti et al. (2010a and b, 2012) and Chegdali et al. (2020, 2022a and b, 2024), which also reported diversity in agro-morphological, biochemical, and molecular characteristics of accessions from the same gene bank. These results show the importance of maintaining plant genetic resources in gene banks, such as the Moroccan gene bank, and the potential role it could play in supporting local breeding programs aimed at developing new, more efficient wheat varieties.

For the phenotypic class frequencies, MCs and NACs exhibited earlier heading dates and shorter plant heights compared to LANs. This implies that these traits have been targeted in durum wheat breeding programs, with the incorporation of genes related to these traits into advanced cultivars. This aligns with the findings of Taghouti et al. (2017b) and Chentoufi et al. (2014), who reported decreases in heading date and plant height from landraces to advanced cultivars.

Spike density is a strong distinguishing phenotypic characteristic (Pecetti et al., 1992). Most spikes in this study were medium to dense, which is similar to the distribution found by Sourour et al. (2010) in a Tunisian durum wheat collection. For the waxiness, waxy spikes were more frequent in NACs and LANs, while non-waxy spikes were more prevalent in MCs. This pattern is also observed in a Spanish durum wheat collection (Ruiz and Aguiriano, 2004). In contrast, glaucous appearance is often dominant over non-glaucous (Clarke et al., 1994; Huang et al., 2017; Würschum et al., 2020). Indeed, this trait increases tolerance to diseases, drought, and heat (Clarke et al., 1994; Huang et al., 2017; Bi et al., 2017; Würschum et al., 2020). Therefore, NACs and LANs could be essential sources of Wax genes that can help mitigate biotic and abiotic stresses and enhance yield, unlike MCs. Concerning spike shape, the tapered form was the most common in LANs and MCs, as observed by Zarkti et al. (2012) and Othmani et al. (2015) for Moroccan and Tunisian genotypes, respectively. Fusiform and tapered classes were prevalent in NACs, as noted by Bayles and Clark (1954) in cultivars grown in the United States in 1949 and by McKevith (2004), who observed the dominance of the fusiform class, preferred by farmers because it is easier to manage.

Beard color is among the most commonly used criteria by producers to justify their choice (Nassif et al., 2012). Our study found that black beards were more prevalent in LANs, while light brown beards were more dominant in MCs and NACs. Sahri et al. (2014) also found that Moroccan landraces tend to have black beards. Additionally, Jain et al. (1975) observed that black beards were more common in Southwest European and North African landraces, while other colors were more prevalent in other origins.

The distribution of glume hairiness is a dominant and inherited monogenic trait (McIntosh 1988). However, contradictory results have been obtained regarding the predominance of hairy glumes. Some studies have reported the dominance of hairy glumes (Bekele, 1984; Eticha et al., 2005; Al Khanjari et al., 2008), while others have noted the predominance of hairless glumes (Bechere et al., 1996; Hailu et al., 2010; Mengistu et al., 2015). In the present study, we observed a distinct pattern in glume hairiness distribution. NACs exhibited a dominance of hairy glumes, LANs displayed medium hairiness, and MCs had hairless glumes.

The color of durum wheat grain, particularly amber, is crucial for assessing semolina quality in pasta and couscous production. Amber color indicates high quality and predicts a yellow end-product, attributed to carotenoids and anthocyanins accumulation (Banach et al., 2022; Ficco et al. 2014; Banach et al. 2022). Our study found amber grains more prevalent in NACs and MCs, whereas LANs displayed a mix of white and amber grains. Several studies have highlighted that improved cultivars tend to have a higher pigment content compared to LANs (Digesù et al. 2009; Mengistu et al. 2015; Ficco et al. 2014). Therefore, breeding programs could potentially enhance quality by prioritizing the selection of amber-colored grains.

As for grain shape, the oblong shape is entirely observed monomorphic, indicating strong selection pressure for this trait. This finding is similar to Hailu et al. (2010), who reported that the reduced genetic diversity and the monomorphism of accessions might be attributed to human intervention.

The mean value of *H'mean* for the genetic diversity estimate was 0.66, indicating relatively high phenotypic diversity within the collection of durum wheat accessions. Except for heading date and awn and kernel shape, all traits exhibited diversity indices greater than 0.60, demonstrating substantial genetic diversity in each trait. Comparing to previously reported diversity indices for Moroccan durum wheat collections, no significant changes were observed. The estimate is slightly higher than that reported by Sahri et al. (2014), and slightly lower than that found by Chentoufi et al. (2014) and Amallah et al. (2016). Furthermore, it is lower than those observed by Negassa (1986), Eticha et al. (2005), Teklu and Hammer (2009), and Mengistu et al. (2015) for Ethiopian durum wheat collections, as well as those reported by Sourour et al. (2010) and Ouaja et al. (2021) for Tunisian collections. These findings confirm the significant genetic diversity of landraces in

Table 3. Nei's gene diversity indices within accessions for the studied phenotypic descriptors.

traits	*Ht*	*Hs*	*Gst*
Days to Heading	0.4823	0.3182	0.3402
Plant Height	0.6566	0.5319	0.1899
Spike Density	0.5262	0.5096	0.0315
Spike Color	0.6530	0.6312	0.0334
Spike Waxiness	0.4942	0.4295	0.1310
Spike Shape	0.5988	0.5344	0.1075
Beard Shape	0.4510	0.4467	0.0095
Peduncle Attitude	0.5766	0.5437	0.0571
Awn Color	0.6453	0.5870	0.0904
Awn Attitude	0.3697	0.3573	0.0336
Glume Hairiness	0.6391	0.5949	0.0692
Kernel Color	0.5353	0.5088	0.0495
Kernel Shape	0.1545	0.1456	0.0574
Means	0.5262	0.4735	0.0973
±SE	0.0365	0.0343	0.0233

Ht: Total gene diversity; Hs: Intrapopulation genetic diversity; Gst: Coefficient of gene differentiation. SE: Standard error.

Morocco, highlighting the central role of the country as a hub of genetic diversity in North Africa.

The estimated *H'mean* reveals that NACs have the highest genetic diversity (*H'mean*= 0.78), followed by LANs (*H'mean*= 0.69) and MCs (*H'mean*= 0.51). This indicates a greater genetic diversity in NACs, with an increase in diversity observed from MCs to NACs, through landraces. This result contradicts the findings of Chentoufi et al. (2014), who reported a decrease in genetic diversity from local to international populations. However, some studies investigating the distribution of alleles related to yield and quality have concluded that modern cultivars exhibit greater diversity than landraces and local cultivars (Zhao et al., 2019; Zhang et al., 2021), which supports our findings. This is likely due to the large origin of these cultivars and their cultivation sites. This result is consistent with the findings of Bechere et al. (1996) and Mengistu et al. (2015), who observed that phenotypic diversity varies according to the altitude and origin where these genotypes are cultivated. The low genetic diversity within MCs may be due to the fixation of the phenotypic traits studied in most genotypes during selection. Its H'*mean* is comparable to that found by Chentoufi et al. (2014) in local modern varieties.

Previous studies conducted on durum wheat populations in Morocco have produced varying results for polymorphic traits, depending on the methodology used, such as UPOV and International Plant Genetic Resources Institute (IPGRI). Sahri et al. (2014) reported that spike type (*H'*=0.77), grain color, and spike shape (*H'*=0.74), spike length, and thousand kernel weight (*H'*=0.71) were the most polymorphic traits, while Chentoufi et al. (2014) found that heading date (*H'*=0.92), plant height (*H'*=0.91), spike form (*H'*=0.88), grain color (*H'*=0.78), spike density (*H'*=0.76), and spike length (*H'*=0.73) showed the highest global diversity index. Similarly, Amallah et al. (2016) reported high polymorphism for several traits, including grain size (*H'*=0.93), spike length (*H'*=0.88), beard length (*H'*=0.85), thousand kernel weight (*H'*=0.84), grain number per spike (*H'*=0.83), specific weight (*H'*=0.82), maturity time (*H'*=0.78), and plant height (*H'*=0.74). In this study, we found that spike color (*H'mean*=0.95), glume hairiness and spike waxiness (*H'mean*=0.89), peduncle attitude (*H'mean*=0.82), awn color (*H'mean*=0.75), and spike density and grain color (*H'mean*=0.73) were the most polymorphic phenotypic traits. The wide diversity observed in these traits may be utilized in wheat breeding programs, and breeding prospects and strategies are suggested.

The gene diversity indices of *Hs* and *Ht* estimated by *Nei* also showed significant gene diversity, which is consistent with the results of *H'mean*. Similar findings were observed by Hailu et al. (2010). The *Gst* value for the groups was 0.0973, indicating that 9.73% of the total genetic diversity was distributed among the groups. This moderate contribution was significant compared to the findings of Hailu et al. (2010).

The MCA biplot explained 19.31% of the total variance, indicating significant variation among the accessions. The analysis confirmed the existing differences between the three groups of durum wheat, with clear distinctions observed between NACs and Moroccan genotypes and between MCs and LANs. These findings may be explained by the impact of selection and improvement evolution on improved cultivars compared to landraces, both internationally and nationally, and the evolution between cultivar-cultivars and cultivar-landraces. For instance, the clear dispersion observed between North American and Moroccan genotypes could be attributed to developing breeding programs for cultivars with local adaptations to specific environments. On the other hand, the convergence and intermix between LANs and MCs support the hypothesis of the mobilization of important phenotypic traits from landraces to cultivars, notably cultivars created through the collaboration of national breeding programs and the international breeding programs of CIMMYT and ICARDA. In previous studies, Jain et al. (1975) found a considerable genetic distance between the North American and Moroccan genotypes, while Chentoufi et al. (2014) and Mengistu et al. (2018) concluded that a distinction existed between farmer's traditional and improved varieties of durum wheat.

Materials and Methods

Plants material

The plant material used in this study comprised 108 accessions of durum wheat. All genotypes were provided by the National Gene Bank of Morocco affiliated with the Regional Centre of the Agricultural Research (CRRA) of Settat. The collection of durum wheat accessions consisted of 15 old Moroccan cultivars (MCs), 56 landraces (LANs), and 37 North American cultivars (NACs) from Canada and USA (**Supplementary Table 1**).

The Moroccan cultivars have been developed through collaborative efforts led by national breeding programs, the International Maize and Wheat Improvement Center (CIMMYT), and the International Center for Agricultural Research in the Dry Areas (ICARDA). In contrast, the landraces were collected from various harsh environmental systems in Morocco. Foreign cultivars were kept in the germplasm bank to increase genetic diversity in local breeding programs and to improve grain yield and quality, and this is the reason why used in the present study. For the subsequent tests, the accessions were studied according to these geographic and genetic origins as described above, i.e., Moroccan cultivars, landraces, and North American cultivars.

The 108 genotypes tested here represent the most productive genotypes from a primary sample of 280 accessions characterized by agro-morphological markers and some of these genotypes were screened by biochemical and molecular markers (Chegdali et al., 2022b). All seeds used in this study were derived from a single spike.

Experimental site and design

The trial was conducted during the 2016/2017 agricultural season at the experimental station of Sidi El Aidi. The experimental protocol was an augmented design with non-replicated accessions but replicated checks (Federer and Raghavarao, 1975). The plots consisted of three rows of 1 m in length. The spacing between plots and blocks was 0.50 m and 1 m, respectively. The checks, consisting of three local varieties named "Marzak," "Cariouca," and "Ourgh," were included in each incomplete block.

Phenotypic description

The phenotypic description of the genotypes was done according to the standard norms of new variety registration (Gupta et al., 2017), described in the guideline test of "distinction, uniformity, and stability (DUS) on durum, dicoccum, and the other Triticum species," according to the instructions of the International Union for the Protection of New Varieties of Plants (UPOV, 2012). Each accession was characterized based on phenotypic classes of the visual traits listed in Table 1. For quantitative descriptors, the traits were measured and categorized into classes. Measurements were obtained for three plants per accession.

Data analysis

Phenotypic classes were scored according to the phenotypic description of Gupta et al. (2017). Microsoft Excel was used to calculate the frequencies of each class for each trait. Based on these frequencies, the Shannon-Weaver index (*H'*) was calculated for each trait to estimate the phenotypic diversity for the entire collection and the three subcollections using the following formula:

$$H = -\sum_{i=1}^{n} \rho i \; log \, \rho i$$

Shannon-Weaver index (named H') was calculated:

$$H' = -\sum_{i=1}^{n} (\rho i \; ln \, \rho i) \; / \ln(n)$$

Where ρi: frequency of the i^{th} class in a trait, n: number of phenotypic classes of each trait.

A multiple component analysis (MCA) and an ascending hierarchical classification, based on the results of MCA, were carried out to highlight the structure of our collection of the different qualitative and quantitative traits.

All the statistical analyzes were carried out with the R-cran software (//cran.r-project.org/).

As for the genetic parameters describing the differentiation of population parameters, the intrapopulation genetic diversity (*Hs*), total gene diversity (*Ht*), and coefficient of gene differentiation (*Gst*) were calculated based on the formulas of Nei (1978) and Nei and Chesser (1983), where allele and locus signified respectively class and trait:

For each trait:

Hs = sum (H exp) / nb pop

Ht = 1 - sum (pi mean * pi mean)

Gst = 1 - *Hs* / *Ht*

Where, H exp: H is calculated with a bias for each pop, H nb = H is calculated without bias (Nei 1978), and H obs = H observed.

On all traits:

HS = sum (*Hs*) / trait nb

HT = sum (*Ht*) / trait nb

GST = 1 - HS / HT

Where, (nb): Non-biased estimators according to Nei and Chesser (1983).

The analysis and the test of these parameters were done with Genetix software (Genetix version 4.05; https://kimura.univ-montp2.fr/genetix/).

Conclusion

The study of the phenotypic diversity of Moroccan and North American durum wheat landraces and cultivars based on thirteen qualitative and quantitative traits revealed a significant diversity, particularly for traits such as spike color, glume hairiness, and peduncle attitude. The results also showed that NACs and LANs were more diverse than MCs. Multiple correspondence analysis highlighted the differences between Moroccan and North American genotypes and between LANS and cultivars. These findings could open up promising avenues in national breeding programs and germplasm collection missions by emphasizing the importance of maintaining diverse genetic material in national gene bank.

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Supplementary Material

Supplementary Table 1.

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