

Agro-morphological Characterization of Azerbaijan Durum Wheat Accessions by Multiple Statistical Analysis

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Abstract

The present investigation was conducted, using biometrical analysis, to estimate the genetic diversity of biomorphological traits in 69 durum wheat accessions. The traits evaluated were plant height, number of fertile tillers, spike length, number of spikelets, number of grains per spike, grain weight per spike, grain yield and 1000 kernel weight. Analysis of variance demonstrated significant differences between durum wheat samples for the all the traits studied. Coefficient variation indicated that grain yield, spike length and grain weight per spike resulted from high genetic diversity between the traits studied. Correlation analysis showed that genotypes with high yield, had high numbers of grains per spike, high grain weight per spike and high 1000 kernel weight. Cluster analysis classified genotypes into seven main groups, so that genotypes with different characteristics were located in separate groups. Results showed that there was adequate genetic variability in Azerbaijan durum wheat germplasm to support breeding for improved grain yield and that indirect selection for high yield can be conducted in early generations using traits that include number of grains per spike, grain weight per spike and 1000 kernel weight.

Keywords: Durum wheat, genetic diversity, multiple statistical, morphological traits

Introduction

Durum wheat (*Triticum turgidum* L. var. *durum*) is the only tetraploid species of wheat of commercial importance in wide cultivation today (Shewry, 2009). Despite

its smaller growing area and lower annual production than hexaploid wheat, durum wheat has long remained an important food resource for the human diet. It is used in different parts of the world for a range of food products, such as pasta, couscous, unleavened bread, bulgur, and mote, among others (Nachit, 1992). Turkey and Canada are the countries producing most, each with an estimated 2 million ha (USDA, 2015), followed by Algeria, Italy and India, each cultivating over 1.5 million ha (Bonjean *et al.*, 2016). Syria belonged to this group of large producers, but the recent unrest has greatly reduced crop production. France, Greece, Morocco, Pakistan, Portugal, Kazakhstan, Russia, Spain and Tunisia cultivate durum wheat on areas from 0.5 to 0.8 million ha annually (USDA, 2015). Azerbaijan, Iraq and Iran combined grow durum wheat on over 0.7 million ha (Bonjean *et al.*, 2016).

Information on genetic diversity and the relationships among and between individuals, populations, plant varieties, animal breeds and species is important to plant and animal breeders for the improvement of crop plants and animal breeds, for conservation biology and for studies of the evolutionary ecology of populations. It is essentially the first step towards plant breeding for crop improvement and is immediately available from germplasm, regarded as a reservoir of variability for different characteristics (Wondifraw, 2016).

Morphological markers are based on visually accessible traits such as flower colour, seed shape, growth habits and pigmentation; this does not require expensive technology, but does often require large tracts of land for field experiments. These marker traits are often susceptible to phenotypic plasticity; conversely, this allows assessments of diversity in the presence of environmental variation, which cannot be neglected in determining genotypic variation. These types of markers are still advantageous and are indeed mandatory in distinguishing adult plants from genetic contaminations in the field, for example, spiny seeds, bristled panicle and variants in flower and leaf colouration (Govindaraj *et al.*, 2015).

As for the gene bank of Azerbaijan, however, little has been done to characterize durum wheat accessions based on studies of a large number of qualitative and quantitative traits and the interrelationships among those traits with greatest effect on genotype discrimination. More information, however, is needed to identify adapted accessions suitable for a breeding programme for durum wheat in Azerbaijan. Therefore, the main objectives of this investigation were, firstly, to evaluate the morphological traits of 69 durum wheat accessions for use in describing the genetic variation of accessions from several countries preserved in Azerbaijan's national gene bank and, secondly, to study the relationships between the traits studied using multiple statistical analysis.

Materials and methods

In this study, we used durum wheat (*Triticum durum* L.), 69 accessions by base collection of the Azerbaijan National Gene Bank (Table 1). The study was conducted at the Genetic Absheron Experimental Station of Genetic Resources Institute of the ANAS. Experiments were conducted on the basis of RCBD experimental design with three replications during the autumn season of 2018-2019. Each accession was planted in a 1m long plot with a between-row spacing of 25 cm and within-row spacing of 10 cm. Observations were recorded on 10 randomly selected competitive plants for eight morphophysiological traits: plant height (cm), Number of fertile tillers, spike length (cm), number of spikelets per spike, number of grains per spike, grain weight per spike (gr), grain yield per plot (g) and 1000 kernel weight. SPSS and PAST programmes were used for statistical analyses of correlation, principal component analysis and genotype clustering.

Table 1. Names of variety and pedigree of the durum wheat used in this study

<i>N</i> <i>o.</i>	Variety name	Pedigree	<i>N</i> <i>o.</i>	Variety name	Pedigree
1	Mut.leucurum	tur.luzit x leucomelan	36	Erythromelan	murciense x leucomelan
2	Murciense	erythroleuc x murciense	37	Leucomelan	murciense x leucomelan
3	Murciense	tur.luzit x miltur	38	Apulicum	melanopus x murciense
4	Murciense	lut x murciense	39	Hordeiforme	melanopus x murciense
5	Affine	Bezostaya 1 x leucur	40	Leucomelan	leucurum x mut.apulicum
6	Mut.murciense	graecum x aegyption	41	Hordeiforme	melanopus x murciense
7	Obscurum	lut(Azəri x niloticum)	42	Mut. Murciense	leucurum x mut. apulicum
8	Obscurum	graecum x niloticum	43	Mut.alexandrinum	leucurum x murciense
9	Hordeiforme	Azəri x Sevinc	44	Melanopus	melanopus x hordeiforme
10	Melanopus	tur.albojadur x hostion	45	Hordeiforme	mut.hordeiforme x leucurum
11	Africanum	albidium x lybic	46	Lybicum	boeuffix x leucurum
12	Melanopus turgid	Bezostaya 1 x erythromelan	47	Coerulescens	mut.lybicum x leucurum

13	Mut.lybicum	albidium x lybicum	48	Erythromelan	mut.hordeiforme x leucurum
14	Mut.lybicum	coerules x polnic	49	Hordeiforme	apulicum x graecum
15	Niloticum	Abşeron	50	Reinchebachii	apulicum x graecum
16	Obscurum	lutescens x obscurum	51	Mut.apulicum	mut.apulicum x graecum
17	Obscurum	hostianum x obscurum	52	Mut.lybicum	lybicum x lutescens
18	Obscurum	hostianum x erythrospermum	53	Etyhromelan	hordeiforme x leucomelan
19	Albooscurum	Bezostaya 1 x lybicum	54	Leucurum	niloticum x leucurum
20	Albooscurum	erythrospermum x obscurum	55	Mut.hordeiforme	lutescens x sarı buğda
21	Alboprivinciale	Abşeron	56	Mut.hordeiforme	lutescens x erythromelan
22	Alboprivinciale	Bezostaya 1 x lybicum	57	Niloticum	erythrospermum x apulicum
23	Mut.africanum	albidum x lybicum	58	Mut.hordeiforme	hordeiforme x lutescens
24	Aegiptiacum	Bezostaya 1 x niloticum	59	Affine	affine x erythromelan
25	Lubicum	Azəri x coerulecens	60	Hordeiforme	sarı buğda x lutescens
26	Hordeiforme	apulicum x hordeiforme	61	Affine	şərq x milturum
27	Affine	leucomelan x affine	62	Mut.murciense	sevinc x velutinum
28	Hordeifirme	Azəri x erythromelan	63	Murciense	sevinc x velutinum
29	Murciense	Bezostaya 1 x lybicum	64	Aegiptiacum	sevinc x velutinum
30	Affine	murciense x leucurum	65	Murciense	sarı buğda x gürgənə
31	Murciense	murciense x leucurum	66	Hordeiforme	hordeiforme x erythrospermum
32	Leucomelan	apulicum x leucomelan	67	Murciense	hordeiforme x erythrospermum
33	Niloticum	apulicum x murciense	68	Leucurum	leucurum x milturum

34	Murciense	apulicum x murciense	69	Hordeiforme	leucurum x milturum
35	Melanopus	leucomelan x melanopus			

Results and discussion

The descriptive statistics for the traits of the wheat genotypes evaluated are listed in Table 2. The coefficient of variation for most of the traits displayed high diversity among the genotypes studied. The high coefficient variation in most of the traits studied is very useful for germplasm improvement. In this study the highest CV was observed in grain yield, at 61.52 %. The traits' spike length, grain weight per spike, number of grains per spike and 1000 kernel weights also displayed high genetic diversity. The high variation in plant height indicates that breeders can use cultivars of appropriate height in breeding programmes for mechanized harvesting and to counter lodging risk. Similar results were obtained by Babaie Zarch et al. (2013). The high genetic diversity of the traits studied in our research indicates that selection for increased value may be highly effective.

Table 2. Statistical indicators of traits in the durum wheat accessions studied

Traits	Min.	Max.	Mean	Standard error of mean	Standard deviation	Coefficient variation (CV%)
Plant height	75.30	173	130.387	2.759	22.916	17.575
Number of fertile tillers	3.20	4.20	3.631	0.03	0.253	6.97
Spike length	5.5	27.80	8.699	0.329	2.734	31.43
Number of spikelets	16	35.20	24.278	0.395	3.289	13.55
Number of grains per spike	16.40	70.20	47.971	1.221	10.149	21.16
Grain weight per spike	1.0	3.98	2.235	0.069	0.57	25.5
Yield	1.0	13.52	2.373	0.176	1.46	61.52
1000 kernel weight	30.04	76.10	47.191	1.112	9.236	19.57

Spike length and number of grains per spike are important to grain yield. Genetic variance was observed at 7.13. Arya et al. (2018), Yadav et al. (2006), Nagireddy and Jyothula (2009) and Kaul and Singh (2011) demonstrated high heritability with high genetic advance for these traits. This indicates a substantial contribution of

additive genetic variance in the expression of these characters and may be useful in hybridization and selection for higher grain yield.

Selection programmes to increase 1000 kernel weight as a principal component of grain yield may play an important role in improving grain yield. This research indicated high genetic diversity for this trait. Analysis of variance demonstrated a significant difference between the wheat genotypes for all traits studied. The results of correlation (Table 3) between the traits measured demonstrated a significant positive relationship between plant height, number of spikelets per spike, number of grains per spike and grain weight per spike.

Significant positive correlation was recorded between grain yield, number of grains per spike, grain weight per spike and 1000 kernel weight. Hence, these traits may be considered key yield components in selection processes for the breeding of durum genotypes for high yield.

The cluster analysis based on Ward's method classify all the durum wheat accessions studied in 7 main groups (Fig. 1). The genotypes No.37 and 65 were grouped into the first cluster, which had the lowest mean for plant height and the highest 1000 kernel weight. This group also shows that in plants of low height, this reduced height increases 1000 kernel weight, one of the traits affecting yield. The cultivars in this group are suitable for breeding programme to create plant varieties of low height.

11 genotypes were clustered into the second group, consisting of genotypes with the greatest spike length of the genotypes studied. Cluster III consisted of 4 cultivated types: No. 12, 41, 44 and 45, principally characterized by high traits in plant height, grain weight per spike and grain yield. These genotypes are strongly recommended as high yield parents for use in future selection programmes. Cluster IV, comprising 15 durum wheat samples, demonstrated high grain weight per spike. In total, 8 samples were grouped in cluster V and 12 wheat samples in cluster VI. Finally, cluster VII contained 17 genotypes, comprising 24.63% of all the genotypes examined. Conducting multivariate analysis, Singh et al. (2018) studied 35 genotypes, which were grouped into 6 clusters based on genetic divergence value.

The results of this research introduced information about the genetic structure of durum wheat accessions in Azerbaijan which should be considered in the further collection of genetic resources and which demonstrate a wide spectrum of agronomic variability in the genotypes investigated.

Table 3. Simple coefficients of correlation between the traits of durum wheat accessions studied

Traits	Plant height	Number of fertile tillers	Spike length	Number of spikelets	Number of grains per spike	Grain weight per spike	Yield	1000 Kernel weight
Plant height	1							
Number of fertile tillers	-0.062	1						
Spike length	-0.078	0.018	1					
Number of spikelets	0.244*	-0.130	0.117	1				
Number of grains per spike	0.247*	-0.020	0.262*	0.464**	1			
Grain weight per spike	0.269*	0.160	0.258*	0.145	0.677**	1		
Yield	0.069	0.126	0.174	0.054	0.429**	0.684**	1	
1000 Kernel weight	0.054	0.297*	0.004	-0.328**	-0.286*	0.475**	0.328**	1

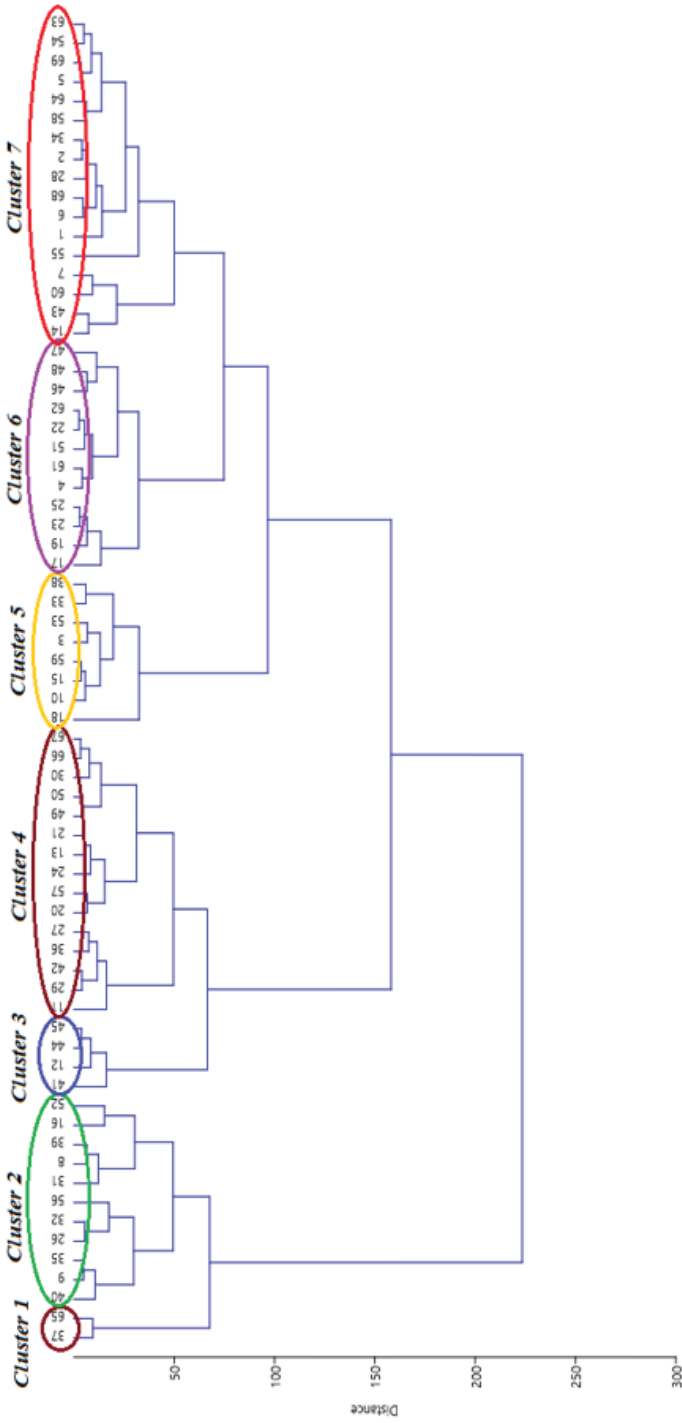


Fig 1. Grouping the durum wheat accessions based on morphological traits using the UPGMA method. Symbols for the ecotypes are presented in Table 1.

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