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Morphological Diversity of Some Qualitative Traits in Tetraploid Wheat Landrace Populations Collected in the South of Tunisia

Slim Amine[1] • Ayed Sourour[2*] • Slama-Ayed Olfa[2] • Robbana Cyrine[1] • Jaime A. Teixeira da Silva[3] • Slim-Amara Hajer[2]

[1] National Gene Bank of Tunisia, Boulevard du Leader Yasser Arafat, Charguia I, 1080, Tunis, Tunisia
[2] Genetic and Plant Breeding Laboratory, Department of Agronomy and Biotechnology, National Agronomic Institute of Tunisia, 43, Avenue Charles Nicole, 1082 Tunis, Tunisia
[3] Faculty of Agriculture and Graduate School of Agriculture, Kagawa University, Miki-cho, Ikenobe 2393, Kagawa-ken, 761-0795, Japan

Corresponding author: * **ayedsourour@yahoo.fr**

ABSTRACT

When indigenous Tunisian durum wheat germplasm were evaluated by quantitative parameters, significant richness was observed. There are few reports on genetic variation of Tunisian durum wheat landraces based on morphological and qualitative traits. A total of 368 accessions of durum wheat (*Triticum durum* Desf.) were evaluated in 3 different regions in the south of Tunisia: Soukra (66 accessions), Matmata (145 accessions) and Toujene (157 accessions) using 9 qualitative traits. Phenotypic diversity indices (*H′*) were calculated for different traits and collection regions. Polymorphism was high for awn anthocyanin coloration (*H′* = 1.18), spike glaucosity (0.89), hairiness on the external surface (0.88), awn colour (0.78), and awn length in relation to the spike (0.77). However, *H′* estimates were relatively low for awn length (0.14), length of brush hair in dorsal view (0.30) and shoulder width (0.37). The pattern of variation of individual traits varied among regions. The Shannon-Weaver diversity index (*H′*) estimates for Matmata and Toujene, 0.75 and 0.61, respectively, were best among the three regions. Principal component analysis (PCA) explained 45.64 and 45.31% of total variability in Matmata and Toujene, respectively. This analysis classified the 145 Matmata accessions into two groups and the 157 Toujene accessions into four groups according to their similarity. These values showed that this germplasm has a relatively important diversity, confirming that Tunisia is one of the principal durum wheat centres of diversity.

Keywords: Index variability, PCA, phenotypic diversity, *Triticum durum*
Abbreviations: ACA, anthocyanin coloration of awn; **AL**, awn length; **ALE**, awn length in relation to spike; **AC**, awn color; **EG**, spike glaucosity; **HGl**, hairiness on external surface (lower glume); **UPOV**, International Union for the Protection of New Varieties of Plants; **LBH**, length of brush hair in dorsal view; **PCA**, principal component analysis; ***H′***, Shannon-Weaver diversity index; **SB**, shape of beak (lower glume); **SW**, shoulder width (lower glume)

INTRODUCTION

Genetic diversity within a species is essential for its survival and adaptation to changing environments. For this reason, many plant scientists and conservation specialists have deplored the continued loss of genetic diversity, and some have attributed this loss to the widespread adoption of modern varieties, displacing primitive varieties and traditional landraces of crops and other domesticated plant species in gene-rich developing countries (Jana 1999).

Tunisia, like other countries of the Mediterranean basin, is an area rich in crop biodiversity. It is characterised by a high diversity of climatic, edaphic and agronomic conditions. With reference to *Triticum durum*, several studies have shown that the diversity found in tetraploid wheat germplasm collections partly accounted for the geographic provenance of the materials in terms of country gene pools (Medini *et al*. 2005; Ayed and Slim-Amara 2009; Ayed *et al*. 2010). Durum wheat landraces are characterised by a specific adaptation to the environmental conditions of the cultivation area, tolerance to biotic and abiotic stresses and constant yields (Daaloul *et al.* 1998; Deghaïs *et al*. 2007). However, many genotypes are subject to the process of disappearance due to an increase in population, food consumption and climate changes. In fact, the breeding strategy has changed and is actually meant for intensive agriculture. New durum wheat varieties, characterised by high genetic potential, have replaced many landraces that had already completely disappeared. For this reason, in the last few years some initiatives aimed at collecting and preserving genetic resources have been carried out at the regional level. This work aimed to evaluate the phenotypic variability for 9 qualitative parameters in 368 accessions of tetraploid wheat collected from south of Tunisia by the thematic group of cereal and food legumes of the Tunisian National Gene Bank.

MATERIALS AND METHODS

The experiments presented in this manuscript were performed at the National Gene Bank of Tunisia.

A total of 368 accessions of durum wheat (*Triticum durum* Desf.) were used for this study. These accessions are collected from 3 different regions in south of Tunisia: Soukra (66 accessions), Matmata (145 accesions) and Toujene (157 accessions). Each accession was sown in the field in a 1-m line and interplant spacing of 0.25 m.

Data were recorded for 9 characters using durum wheat descriptors of Bioversity International and UPOV (International Union for the Protection of New Varieties of Plants) (**Table 1**). Phenotypic frequency distributions of the characters were calculated for all material.

The Shannon-Weaver diversity index (*H′*) was computed using phenotypic frequencies to assess the phenotypic diversity for each character. The Shannon-Weaver diversity index, as described by Hutchenson (1970), is given as:

$$H' = - \sum_{i=1}^{n} pi. \ln pi$$

where pi is the proportion of accessions in the i^{th} class of an n-

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Short Communication

Table 1 Qualitatively measured traits.

Characters	Code / Description
ACA	1 Absent or very weak
	3 Weak
	5 Medium
	7 Strong
	9 Very strong
AL	1 Very short
	3 Short
	5 Medium
	7 Long
	9 Very long
EG	1 Absent
	3 Weak
	5 Medium
	7 Strong
	9 Very strong
ALE	1 Shorter
	2 Equal
	3 Longer
AC	1 Whitish
	2 Light brown
	3 Brown
	4 Black
HGl	1 Absent
	2 Sparse
	3 Intermediate
	4 Strong
SW	1 Narrow
	2 Medium
	3 Broad
SB	1 Straight
	2 Slightly curved
	3 Moderately curved
	4 Strongly curved
LBH	1 Short
	2 Medium
	3 Long

ACA: anthocyanin coloration of awn; **AL**: awn length; **ALE**: awn length in relation to spike; **AC**: awn color; **EG**: spike glaucosity; **HGl**: hairiness on external surface (lower glume); **LBH**: length of brush hair in dorsal view; **SB**: shape of beak (lower glume); **SW**: shoulder width (lower glume).

class character and n is the number of phenotypic classes for a character. Finally, in order to better classify the 368 accessions, a principal component analysis (PCA) was carried out on the correlation matrix. It was calculated on the mean data of the three replications using STATISTICA 7.0.

RESULTS AND DISCUSSION

Estimates of diversity indices, *H's*

Polymorphism was common, to varying degrees, for most traits, thus indicating a wide distribution of variability among these landraces. In general, the proportion of polymorphic entries or H' estimates for individual traits was different for each region. Estimates of H's for individual traits are presented in **Table 2**. These estimates ranged from 0.14 for AL to 1.18 for ACA for all regions. While most traits showed relatively high ($H' > 0.60$) levels of polymorphism, a few of these traits (e.g., AL, ALE) displayed low H' estimates. However, a low H' estimate may reflect unequal frequencies of different classes rather than the absence of the desirable class for a particular trait. The average H' estimate for Tunisia, based on traits evaluated in this study, was 0.63. This estimate is relatively higher than the one reported for wheat landraces of Oman (0.52) (Al Khanjari *et al*. 2008), but lower than Ethiopian wheat landraces (0.81) (Negassa 1986) and Mediterranean wheat landraces (0.79), which was based on 27 traits (Jana *et al*. 1990).

The H' estimates for the three regions (Toujene, Matmata and Soukra) showed that Matmata and Toujene showed the highest values, 0.75 and 0.61, respectively. Polymorphism was high for ACA (0.99), EG (0.89), HGl (0.88), AL (0.77) and AC (0.77) in Matmata. However, in Toujene, ACA (0.76), AL (0.69), ALE (0.69) and LBH (0.69) had the highest diversity index. In Soukra, the best indices are observed for ACA (1.18), AC (0.78), HGl (0.76), SB (0.68) and EG (0.64). Ayed and Slim-Amara (2009) evaluated 111 Tunisian durum wheat accessions for six qualitative traits. That germplasm had an average diversity index of about 0.77. This index, calculated for each parameter, revealed that spike density ($H' = 0.86$), HGl ($H' = 0.80$) and glume colour ($H' = 0.79$) showed the highest diversity index.

Table 2 Index diversity (H') of each trait for the three regions.

Characters	*H'*		
	Soukra	**Matmata**	**Toujene**
ACA	1.18	0.99	0.76
AL	0.14	0.77	0.69
EG	0.64	0.89	0.39
ALE	0.14	0.67	0.69
AC	0.78	0.77	0.67
HGl	0.76	0.8	0.37
SW	0.37	0.56	0.66
SB	0.68	0.58	0.57
LBH	0.30	0.65	0.69
Average *H'*	0.55 ± 0.34	0.75 ± 0.14	0.61 ± 0.13
	Average = 0.63 ± 0.10		

ACA: anthocyanin coloration of awn; **AL**: awn length; **ALE**: awn length in relation to spike; **AC**: awn color; **EG**: spike glaucosity; ***H'***: Shannon-Weaver diversity index; **HGl**: hairiness on external surface (lower glume); **LBH**: length of brush hair in dorsal view; **SB**: shape of beak (lower glume); **SW**: shoulder width (lower glume).

Table 3 Projection of the qualitative traits on axes 1 and 2 of the principal components analysis (Matmata), i.e., **Fig 1A**.

	Factor 1	**Factor 2**
ACA	-0.59998	-0.08578
AL	0.184409	-0.90887
EG	-0.825582	-0.130447
ALE	0.13704	-0.926528
AC	-0.466347	0.000349
HGl	-0.844818	-0.046135
SW	-0.403766	-0.054677
SB	0.318851	0.214809
LBH	0.238453	0.025301

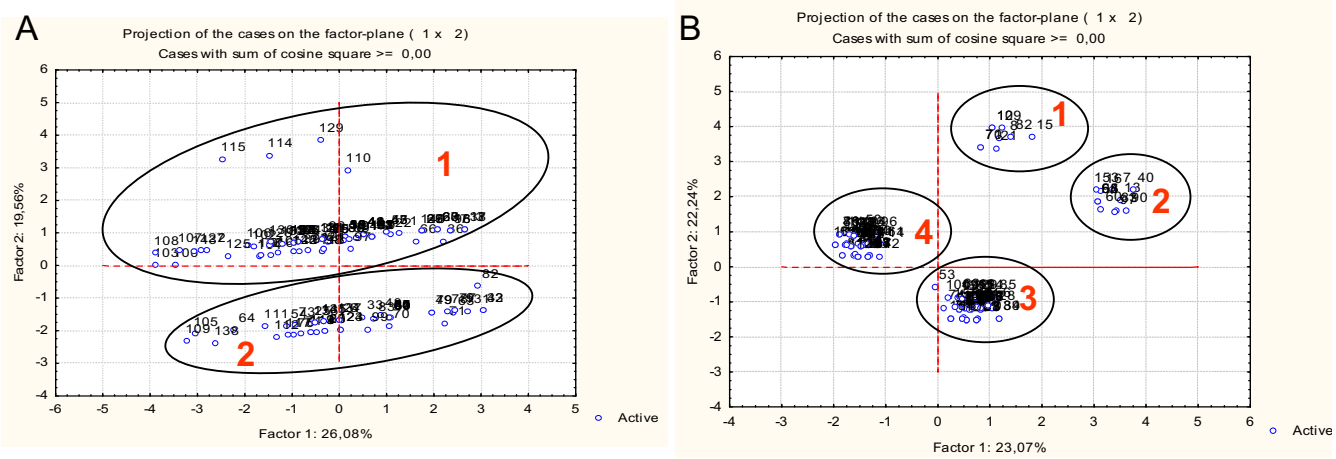
Table 4 Projection of the qualitative traits on axes 1 and 2 of the principal components analysis (Toujene), i.e., **Fig 1B**.

	Factor 1	**Factor 2**
ACA	0.16944	-0.001647
AL	-0.749587	0.634107
EG	-0.652545	-0.742251
ALE	-0.75	0.640111
AC	0.157093	0.024467
HGl	-0.652545	-0.742251
SW	0.046269	0.201888
SB	0.184555	-0.023157
LBH	0.102731	-0.213523

Genotype classification

PCA was performed with standardised mean values for each of the 9 quantitative traits and subpopulations. PCA was only calculated for the two regions witch presented the best diversity index, i.e., Matmata and Toujene.

In the region of Matmata, the PCA explained 45.64% of total variation of accessions (**Fig. 1A**). The first PCA axis explained 26.08% of total variability and the most associated traits were EG and HGl. The second PCA axis explained 19.56% and was mostly related to ALE and AL (**Table 3**). The 145 accessions were classified into 2 important groups. The first group was formed by accessions that are characterised by a slightly curved beak and medium brush hair in dorsal view. The second group is constituted by accessions that present a very long awn and an awn lon-



Matmata

Group 1				Group 2	
1	34	69	114	4	79
2	35	72	115	6	80
3	36	76	116	9	81
5	37	85	118	24	82
7	38	86	120	25	83
8	39	88	121	29	84
10	41	89	122	32	87
11	42	90	125	33	99
12	44	91	126	40	105
13	45	92	127	43	109
14	46	93	128	48	111
15	47	94	129	49	112
16	50	95	130	54	113
17	51	96	132	55	117
18	52	97	133	60	119
19	53	98	134	63	123
20	56	100	139	64	124
21	57	101	140	65	131
22	58	102	142	70	135
23	59	103	143	71	136
26	61	104	144	73	137
27	62	106	145	74	138
28	66	107		75	141
30	67	108		77	
31	68	110		78	
Total = 97 accessions				Total = 48 accessions	

GRAND TOTAL = 145 accessions

Toujene

Group 1	Group 2	Group 3			Group 4		
8	7	1	72	128	2	59	108
9	13	4	74	129	3	61	111
10	16	5	80	131	6	62	115
12	40	11	84	133	14	64	125
15	58	17	85	135	18	68	127
21	60	19	86	136	24	69	124
70	65	20	87	138	25	73	130
71	83	22	88	140	28	75	121
82	90	23	91	141	29	76	132
	94	26	92	145	30	77	134
	97	27	95	146	32	78	137
	153	31	99	147	33	79	139
		35	100	148	34	81	142
		36	105	149	37	89	143
		38	106	150	41	93	144
		39	109	151	42	96	
		47	110	152	43	98	
		48	112	154	44	117	
		49	113	155	45	118	
		51	114	156	46	120	
		52	116	157	50	101	
		53	119		54	102	
		63	122		55	103	
		66	123		56	104	
		67	126		57	107	
Total = 9 accessions	Total = 12 accessions	Total = 71 accessions			Total = 65 accessions		

GRAND TOTAL = 157 accessions

ger than the spike.

In the region of Toujene, PCA explained 45.31% of total variation of accessions (**Fig. 1B**). The first PCA axis explained 23.07% of total variability and was mostly related to ALE and AL. The second PCA axis explained 22.24% and is associated with EG and HGl (**Table 4**). The 157 accessions were partitioned into 4 groups. The first group is formed by accessions characterized by broad shoulder width while the second group is constituted by accessions with a light brown awn. The third group includes accessions with a very long awn and an awn longer than the ear. The fourth group assembles accessions that have medium brush hair in dorsal view.

CONCLUSION

Tunisian durum wheat germplasm studied in this paper presented a diversity index of about 0.63 showing a relatively important phenotypic diversity of this collection. The estimates of the Shannon-Weaver diversity index, *H'* for the three regions (Toujene, Matmata and Soukra) showed that Matmata and Toujene presented the best *H'*, 0.75 and 0.61, respectively. The high diversity observed showed that Tunisia is one of the centres of diversity of tetraploid wheat. This genetic diversity can be exploited in improvement programs.

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