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Genetic Variability of Some Morpho-Physiological Traits in Durum Wheat (*Triticum turgidum* var. *Durum*)

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Abstract: The present investigation was carried out to (i) study some agro-physiologic traits and (ii) to estimate genetic variability parameters for the studied traits in 12 advanced durum wheat genotypes along with the two local checks (Zardak and Sardari). Statistical analysis showed significantly differences among the genotypes based on the studied traits. Genotypic and phenotypic coefficients of variations were high for number of tiller (NT), Leaf Dry Weight (LDW), Stem Dry Weight (STW), Spike Length (SL) and Leaf Area Duration (LAD). Heritability estimates were high for Plant Height (PH), LDW and SL. High genetic gain was observed for grain yield, NT, Peduncle Length (PL), LDW, STW, Spike Dry Weight (SPW), SL and LAD. Correlation analysis showed the grain yield was significantly correlated with traits LP, SPW, SL and Relative Growth Rate (RGR). High heritability estimates associated with high genetic advance as percent mean (GG) were obtained in characters i.e., LDW, PH, SL and LAD, whereas low heritability and high genetic advance was observed for the grain yield.

Key words: Genetic variability parameters, genetic advance, genetic gain, heritability, durum wheat

INTRODUCTION

Durum wheat (*Triticum durum* Desf.) is one of the most widely cultivated and important food crop in the world and is mainly (>90%) cultivated in the Mediterranean basin, Europe and India (Abaye *et al.*, 1997; Nachit *et al.*, 1998). The development of high yielding wheat cultivars is the main objective of any breeding programs in the world (Ehdaie and Waines, 1989). The genetic variation for the trait under selection and a higher heritability are necessary to have response to selection (Falconer and Mackay, 1996; Moghaddam *et al.*, 1997; Shukla *et al.*, 2006). Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance and genetic and environmental factors that influence their expression. To plan an efficient development program, it is necessary to have an understanding of the breeding systems coupled with statistical analysis of inheritance data (Srivastava and Dhamania, 1989; Yap and Harvey, 1972).

Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to yield of a crop would be great importance in planning a successful breeding programme

(Mary and Gopalan, 2006). Development of high-yielding varieties requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value between generations (Shukla *et al.*, 2006). Success in crop improvement generally depends on the magnitude of genetic variability and the extent to which the desirable characters are heritable. However, variability studies for different crops already have been done (Ehdaie and Waines, 1989; Moghaddam *et al.*, 1997; Sumathi *et al.*, 2005; Baye and Becker, 2005; Vanaja and Babu, 2006; Mary and Gopalan, 2006; Shukla *et al.*, 2006; Kaushik *et al.*, 2007) but very limited on durum wheat. Knowledge of the genetic association between grain yield and its components can help the breeders to improve the efficiency of selection. Therefore, it is important to study the relationships among the characters (Ehdaie and Waines, 1989). However, the objective of this research was to study genetic variability of some agro-physiological characters in durum wheat.

MATERIALS AND METHODS

This study was carried out with 14 genotypes based on Randomized Complete Blocks Design (RCBD) with four replications at the research farm of the Agricultural college, Razi University, Kermanshah, Iran, in 2004-2005 cropping season. The genotypes used in this study are given in Table 1. The plot sizes were 7.0×1.2 m. Standard cultural practices were followed for raising the crop. The characters studied were Plant Height (PH), number of tiller (NT), Peduncle Length (PL), Flag Length (FL), Spike Number (SN), Leaf Dry Weight (LDW), Stem Dry Weight (STW), Spike Dry Weight (SDW), Spike Length (SL), Leaf Area Index (LAI), Crop Growth Rate (CGR), Relative Growth Rate (RGR), Leaf Area Ratio (LAR), Net

Assimilation Rate (NAR) and Leaf Area Duration (LAD). Data were statistically analyzed for each character separately. Plant growth analysis was done based on Bullock *et al.* (1993).

The analysis of variance for different characters were measured followed by Duncan's New Multiple Range Test (DMRT) (Steel and Torrie, 1960), to test the significance difference between means. The mean squares were used to estimate genotypic and phenotypic variance according to Johnson *et al.* (1955). The coefficient of variation was calculated based on the formula suggested by Burton (1952). The genotypic and phenotypic coefficient of variation and heritability were calculated as suggested the formula used by Singh and Choudhury (1985) and genetic advance by Allard (1960) as well as correlation coefficient by Zaman *et al.* (1982). The goal of this research was to study some agro-physiologic traits of durum wheat genotypes (ii) to estimate genetic variability parameters for the studied traits.

RESULTS AND DISCUSSION

The genotypes showed significant differences for grain yield, PH, NT, PL, FLL, SN, LDW, STW, SPW, SL and LAD, indicating the presence of adequate variability among the genotypes (Table 2).

Genotype D-009 showed the highest mean yield performance and the local bread wheat, Saradari, as well as local durum wheat, Zardak, out yielded by this genotype (Table 3).

Table 1: The genotypes used in this study

Genotype	Descriptive	Source and origin
D-001	Advanced durum wheat lines	*DARI, Kermanshah, Iran
D-002	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-003	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-004	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-005	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-006	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-007	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-008	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-009	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-010	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-011	Advanced durum wheat lines	DARI, Kermanshah, Iran
D-012	Advanced durum wheat lines	DARI, Kermanshah, Iran
Zardak	Local durum wheat cultivar	DARI, Kermanshah, Iran
Sardari	Local bread wheat cultivar	DARI, Kermanshah, Iran

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Table 2: Mean squares for different characters of 14 genotypes of *Triticum durum*

Sources	df	Mean square													
		Yield	PH	NT	PL	FLL	LDW	STW	SPW	SL	CGR	RGR	LAR	NAR	LAD
Block	3	1.01	29.74	0.48	3.93	0.65	0.25	2.93	1.01	0.65	0.019	0.005	0.001	95.99	0.000
Genotypes	13	13182**	435.12**	11.52**	24.63**	8.94*	1.03**	20.92**	3.12**	17.14**	0.009 ^{ns}	0.001 ^{ns}	0.001 ^{ns}	59.89 ^{ns}	0.006* ^{ns}
Error	39	3802	19.22	1.37	3.24	5.127	0.11	4.77	0.89	0.51	0.009	0.001	0.001	53.50	0.001

**Significant at 1% level of probability, *Significant at 5% level of probability, ^{ns}Non-significant probability

Table 3: Mean performance of 14 genotypes of *Triticum durum* for different characters

Genotypes	Characters									
	Yield (g m ⁻²)	PH (cm)	NT	PL (cm)	FLL (cm)	LDW (g)	STW (g)	SPW (g)	SL (cm)	LAD
D-001	286.23 ^{ab}	71.05 ^{bcd}	4.00 ^{cde}	13.30 ^{abcd}	14.93 ^{ab}	0.77 ^{de}	6.45 ^{bcd}	4.37 ^{ab}	6.10 ^f	0.068 ^{bc}
D-002	222.70 ^{bcd}	77.85 ^b	3.75 ^{cde}	15.73 ^a	15.13 ^{ab}	1.02 ^{cde}	8.40 ^{abcd}	3.40 ^{bcd}	6.60 ^{def}	0.067 ^{bc}
D-003	260.03 ^{abc}	71.35 ^{bcd}	7.50 ^a	11.75 ^{bcd}	15.85 ^{ab}	1.07 ^{cde}	5.15 ^{cd}	3.97 ^{abc}	6.47 ^{ef}	0.065 ^{bc}
D-004	245.62 ^{abcde}	62.28 ^f	6.00 ^{abc}	9.92 ^{cdefg}	14.25 ^{ab}	0.90 ^{de}	5.40 ^{bcd}	3.75 ^{abcde}	8.12 ^{cd}	0.071 ^{bc}
D-005	160.47 ^{cde}	64.93 ^{def}	3.25 ^{de}	7.17 ^g	14.80 ^{ab}	0.52 ^e	3.65 ^d	3.45 ^{cde}	7.72 ^{cde}	0.009 ^e
D-006	158.51 ^{cde}	87.18 ^a	2.75 ^e	14.83 ^{ab}	18.17 ^{ab}	0.70 ^{de}	6.47 ^{bcd}	2.42 ^{cde}	9.10 ^e	0.067 ^{bc}
D-007	256.76 ^{abcd}	60.67 ^f	6.75 ^a	9.65 ^{cdefg}	19.02 ^a	1.07 ^{cde}	7.75 ^{bcd}	3.92 ^{abcd}	6.47 ^{ef}	0.042 ^c
D-008	147.37 ^e	88.53 ^a	5.5 ^{abcd}	8.57 ^g	15.85 ^{ab}	1.15 ^{cd}	7.10 ^{bcd}	2.25 ^e	7.12 ^{def}	0.052 ^{bc}
D-009	330.77 ^a	72.18 ^{bc}	3.75 ^{cde}	13.65 ^{abc}	16.02 ^{ab}	0.85 ^{de}	9.50 ^{abc}	5.05 ^a	6.75 ^{def}	0.045 ^c
D-010	225.97 ^{bcd}	90.47 ^a	7.75 ^a	10.45 ^{cdefg}	15.65 ^{ab}	1.70 ^b	12.70 ^a	3.45 ^{bcd}	10.55 ^b	0.052 ^{bc}
D-011	250.21 ^{abcde}	84.75 ^a	7.25 ^a	9.97 ^{cdefg}	17.33 ^{ab}	1.05 ^{cde}	6.67 ^{bcd}	3.82 ^{abcde}	7.77 ^{cde}	0.167 ^a
D-012	147.37 ^e	75.25 ^b	4.25 ^{bcd}	10.93 ^{cdefg}	13.93 ^b	1.52 ^{bc}	6.57 ^{bcd}	2.25 ^e	6.72 ^{def}	0.065 ^{bc}
Zardak	232.52 ^{abcde}	89.07 ^a	6.50 ^{ab}	12.73 ^{abcde}	17.10 ^{ab}	2.45 ^a	10.15 ^{ab}	3.55 ^{abcde}	7.30 ^{def}	0.042 ^c
Sardari	155.23 ^{de}	67.97 ^{cde}	6.00 ^{abc}	9.15 ^{efg}	14.80 ^{ab}	0.57 ^e	6.55 ^{bcd}	2.37 ^{de}	13.77 ^a	0.120 ^{ab}

D: Durum

In case of PH, genotypes ranged from 60.67-90.47 cm and the mean was 75.97 (Table 4). Moderate genotypic and phenotypic co-efficient of variations were observed for PH (Table 5). This trait showed a significant and positive correlation with LDW and STW and had a significant and negative correlation with SPW and NAR (Table 6).

The number of tillage per plant (NT) varied from 2.75 to 7.75 with mean value 5.36 (Table 4). The high heritability and genetic gain was observed for the NT, indicating the major part of phenotypic variations is belonging to genotypic variations (Table 5). The NT was significantly and negatively correlated with LP, CGR and RGR and positively correlated with LDW and LAD.

The range and mean values for Peduncle Length (PL) were 7.17-15.73 and 11.27 and high genotypic and phenotypic coefficient of variation (GCV and PCV) were

also observed (Table 4, 5) showing little environment effect on the expression of PL. This trait was significantly and positively correlated with STW.

Low heritability and genetic gain were observed for Flag Leaf Length (FLL) (Table 5), suggesting selection for this character would not be effective due to predominant effects of non additive gene in this population.

Mean range in the genotypes for Spike Height (SL) was 6.10-13.77 cm. The difference between GCV and PCV for SL was little, showing the minimum effect of the environment on its expression. The high values of heritability (89.13%) and genetic gain (50.02%) was observed for SL (Table 5) showed this character was governed by additive genes in studied durum wheat genotypes. Similar results were also observed by Ehdai and Waines (1989). The traits intercorrelated with grain yield like SL had comparatively high PCV, GCV,

Table 4: Range, mean, standard error of mean and co-efficient of different characters of 14 genotypes of *Triticum durum*

Characters	Range	Mean	SE (±)	Coefficient of variation (%)
Yield	147.37-330.77	219.98	15.45	28.02
PH	60.67-90.47	75.97	2.79	5.77
NT	2.75-7.75	5.36	0.45	21.83
PL	7.17-15.73	11.27	0.66	15.97
FLL	13.93-19.02	15.92	0.40	14.22
LDW	0.52-2.45	1.09	0.14	1.80
STW	3.65-12.70	7.32	0.61	34.56
SPW	2.25-6.05	3.43	0.84	27.50
SL	6.10-13.77	7.90	2.07	9.03
LAD	0.009-0.167	0.07	0.01	4.50

Table 5: Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance in percentage of mean for different characters of 14 genotypes of *Triticum durum*

Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (%)	Genetic gain (%)
Yield	22.01	35.64	38.15	61.62	28.00
PH	13.42	14.61	84.40	19.29	25.40
NT	29.73	36.88	64.96	2.64	49.36
PL	20.52	26.00	62.29	3.75	33.35
FLL	6.12	15.48	15.62	0.79	4.98
LDW	44.00	53.49	67.65	0.81	74.55
STW	27.42	40.52	45.75	2.79	38.04
SPW	21.82	35.11	38.69	0.96	27.98
SL	25.81	27.35	89.13	3.97	50.02
LAD	50.51	67.76	55.56	0.05	78.17

Table 6: Correlation coefficient among different morpho-physiological characters of *Triticum durum*

Characters	Yield	PH	NT	PL	FLL	LDW	STW	SPW	SL	CGR	RGR	LAR	NAR
PH	-0.27												
NT	0.22	0.12											
PL	0.37*	0.28	-0.38*										
FLL	0.19	0.25	0.21	0.160									
LDW	0.05	0.55**	0.45**	0.120	0.15								
STW	0.29	0.55**	0.13	0.330*	0.23	0.64**							
SPW	0.95**	-0.32*	0.12	0.240	0.13	-0.05	0.16						
SL	-0.42**	0.09	0.20	-0.280	-0.12	-0.16	0.14	-0.45**					
CGR	-0.21	-0.27	-0.77**	0.030	-0.14	-0.23	-0.21	-0.03	-0.33*				
RGR	-0.34*	-0.08	-0.45**	0.050	-0.07	-0.07	0.03	-0.28	-0.08	0.67**			
LAR	-0.15	0.01	0.05	-0.180	-0.11	0.41**	0.19	-0.05	0.14	0.08	0.39*		
NAR	-0.20	-0.41**	-0.68**	-0.060	-0.20	-0.24	-0.34*	0.02	-0.30	0.91**	0.63**	0.27	
LAD	0.02	0.15	0.34*	0.003	-0.05	-0.15	-0.09	-0.12	0.36*	-0.74**	-0.76**	-0.40*	-0.64**

heritability and genetic advance as per cent of mean (GG), so more emphasis on these characters can be given during the selection process to increase yield.

The range of variation for Leaf Dry Weight (LDW) was 0.52-2.45 with mean value 1.09. Genotypic and phenotypic co-efficient of variations were 44.00-53.49 (Table 5). Similar result was observed by Pathak and Nema (1985). The range of Spike Dry Weight (SPW) varied from 2.25-6.05 g suggesting that durum wheat produced heavier spikes. Genotypic and phenotypic co-efficient of variation were high (21.82-35.11). In some studies genotypic and phenotypic co-efficient of variation were reported to be moderate (Das and Rahman, 1984).

The progress of a breeding program is conditioned by the magnitude and the nature of the genotypic and non-genotypic variation in the various characters. Since, most of the economic characters (e.g., yield) are complex in inheritance and are greatly influenced by various environmental conditions, the study of heritability and genetic advance is very useful in order to estimate the scope for improvement by selection. Heritability magnitude indicates the reliability with which the genotype will be recognized by its phenotype expression (Chandrababu and Sharma, 1999).

The heritability estimates were high (>60%) for characters PH, NT, PL, LDW and SL. The characters STW and LAD showed heritability values ranging that are, between 40 to 60%. A comparatively low value of heritability was observed for the character yield, FLL and SPW (<40%) (Table 5). Earlier, in durum found high heritability values for characters such as PH and NT (Paul *et al.*, 2006). The heritability estimates for different characters depend upon the genetic make up of the breeding materials studied. Therefore, knowledge about these values in the materials in which breeders are interested is of great significance. High heritability estimates indicate that the selection for these characters will be effective being less influenced by environmental effects. Heritability estimates have been found to be useful in indicating the relative value of selection based on phenotypic expression of different characters. Johnson *et al.* (1955) impressed that heritability values along with estimates of Genetic Gain (GG) were more useful than heritability alone in predicting the effect of selection. High heritability estimates associated with high genetic advance as percent mean (GG) were obtained in the characters i.e., LDW, PH and LAD, which indicated that selection for these characters would be more effective because these characters have high heritability and genetic advance. High heritability values followed by high genetic advance indicated the presence of additive gene action (Johnson *et al.*, 1955; Kashif *et al.*, 2003).

Grain yield among durum wheat genotypes ranges from 147.37-330.77 g plot⁻¹ with mean value 219.98 g plot⁻¹. Low heritability and high genetic advance was observed for the grain yield as has been already reported by Paul *et al.* (2006). The results of correlation coefficient analysis showed that the PH, SPW, SL and RGR contributed significantly towards grain yield (Table 6). It can be concluded on the basis of the results obtained in the present investigation that the range of variability was quite appreciable for almost all the characters studied among different genotypes.

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