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Estimation of genetic architecture for agro-morphological characters in common wheat

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Abstract

In order to estimate genetic parameters and variability of agro-morphological characters in bread wheat an experiment was conductetd in the frame of randomized complete block design with three replications under water stress conditions in the experimental greenhouse of the College of Agriculture, Razi University, Kermanshah, Iran. The analysis of variance showed highly significant differences among the genotypes for stress yield (Ys), biomass (BI), harvest index (HI), thousand seed weight (TSW), number of seed per spike (NSPS), spike length (SL), awn length (AL), plant height (PH), spike weight (SW) and peduncle length (PL) suggesting the presence of considerable amount of variability among the genotypes of wheat according to the characters evaluated in the present study. Mean comparisons classified the genotypes in different groups for all the characters under study indicating the presence of genetic variability found in the analysis of variance. The phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variati (GCV) for all the characters. The highest values were shown by AL, Ys and TSW. GCV was higher than environmental coefficient of variation (ECV) for all the characters except for SL indicating that the traits studied are more genetic. High heritability estimates (> 0.5) were observed for all the characters investigated except SL. High heritability estimates associated with high genetic gain for Ys, TSW and AL reflecting the involvement of additive gene action.According to the results, the highest genotypic and phenotypic covariance observed between Ys and SW indicating significant contribution of these traits to increase grain yield in wheat under raifed condition (correlated response). High co-heritability was observed between BI and AL (4.195) and SL and PH (4.097). Positive coheritability estimate was observed between Ys and all the agro-morphological traits. This suggests that selection of either of the characters would simultaneously affect the Ys positively.

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Introduction

Bread wheat (*TriticumaestivumL.*) is the most important widely adapted consumed food cereal in Iran. Therefore, wheat breeders are concentrating their efforts to improve the yield potential of wheat to meet the future goals by developing new cultivars with desirable genetic makeup (Magda andAbd El-Rahman, 2013).Cultivated land and crop yield of wheat are respectively 6.6 million hectares and 13.4 million tonnes in Iran and 225.4 million hectares and 681.9 million tonnes in the planet Earth (Aharizad*et al.,* 2012). Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production (Khodadadi *et al.*, 2011).

To make the heritable improvement in characters, estimation of genetic parameters and index of their transmissibility is required. Heritability estimates provide information about the extent to which a particular character can be transmitted to the successive generations. Knowledge of heritability of a trait thus guides a plant breeder to predict behavior of succeeding generations and helps in making desirable selections. Conventional analysis of variance and statistical parameters like phenotypic and genotypic coefficients of variability, heritability and genetic advance have been used to assess the nature and magnitude of variation in wheat breeding material (Muhammad Cheema*et al.,* 2006).

Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance, genetic and environmental factors that influence their expression (Kashif*et al.,* 2003; Ali and Awan, 2009; Mohammadi*et al.,* 2010). The study of statistical parameters like mean, variance, CV%, habitability and genetic advance is a measure to evaluate genetic potential, diversity and stability performance of any genotype for effective selection of particular traits in that genotype (Firouzian, 2003; Ali *et al.,* 2009).

Genetic gain (GG) is usually estimated in field crops as the collective contribution of several breeding programmes. For the individual breeder, however, the genetic gain realized within a single programme is critical (Khalil *et al.,* 1995). Knowledge of the changes associated with advances in crop productivity is essential for understanding yield-limiting factors and developing strategies for future improvement (Donmez*et al.,* 2001).

In light of this therefore, easily measurable characters with high heritability and having useful relationship with grain yield are of paramount importance to practice indirect selection for high yield (Falconer and Mackey, 1996). Grain yield is a complex multi component character and is greatly influenced by various environmental conditions. Various morphological and physiological characters contribute to grain yield. Each of these component characters has its own genetic systems. Further these yield components are influenced by environmental fluctuations. Therefore, it is necessary to separate the total variation into heritable and nonheritable components with the help of genetic parameters i.e. genotypic and phenotypic co-efficient of variation, heritability and genetic gain (Kahrizi & Mohammadi 2009, Maniee *et al.*, 2009).

Chowdhry*et at.*(1997) found moderate heritability with high genetic advance for number of tillers/plant whereas high heritability coupled with high genetic advance was reported for this trait by Ghimiray and Sarkar (2000), Gupta and Verma (2000), and Firouzian*et at.* (2003). Low to moderate heritability and genetic advance (Firouzian*et et.,*2003; Safeer-ul-Hassan, 2003) and moderate heritability with high genetic advance (Chowdhry*et al.,* 1997) was reported for spike length. Muhammad *et al.* (2001) and Safeer-ul- Hassan (2003) observed low to moderate heritability and genetic advance for spikelets/spike. Moderate heritability (Muhammad *et al.,* 2001), low to moderate heritability and genetic advance (Safeer-ul-Hassan, 2003), moderate heritability and high genetic advance (Chowdhry*et al.,* 1997) and high heritability with high genetic advance (Deswal*et al.,* 1996; Ghimiray and Sarkar, 2000; Gupta and Verma, 2000; Firouzian*et al.,*2003; Salim*et al.,* 2003) was observed for number of grains/spike. Low to moderate heritability and genetic advance (Safeer-ul-Hassan, 2003), high heritability (Muhammad *et al.,* 2001) while high heritability with high genetic advance (Deswal*et al.,* 1996; Shukla*etal.,* 2000) was reported for 1000-grain weight.Safeerul- Hassan (2003) observed low to moderate heritability with high genetic advance for grain yield/plant whereas Ozkan*et at.* (1997), Shukla*et al.* (2000), Firouzian*etal.*(2003) and Salim*et al.* (2003) reported high heritability with high genetic advance for this trait.

The present study was carried out to evaluate the genetic variability and inheritance of yield and some related plant traits to develop desirable wheat genotypes for the rainfed areas.

Materials and methods

Plant genetic materials and experimental layout

Eight genotypes of bread wheat (*TriticumaestivumL.*) including: Bahar (G1), Pishtaz (G2), Vrinak (G3), Yavaros (G4), S-80-18 (G5), Crasalborz (G6), Santor (G7) and D-79-15 (G8)were assessed in a randomized complete block design with three replications under and water stress conditions in the experimental greenhouse of the College of Agriculture, Razi University, Kermanshah, Iran (47° 9_ N, 34° 21_ E and 1319m above sea level). The seed samples were planted in the plastic pots with 15 cm diameter and 20 cm height and filled with 3kg soil containing sand and animal fertilizer, as 1: 1: 1. In the 3 leaves stage, there were 5 bushes in each pot. The pots were kept in the planting capacity area through regular watering (irrigation), the damp of the pots were maintained about 40 percent of the farm capacity in the stress environment.

Measurement of characters

At harvest time, stress yield (Ys) was measured from 5 spikes per pot. The following agro-morphological characters were also measured in the stress condition. Biomass (BI), harvest index (HI=Ys/BI), Thousand . seed weight (TSW), number of seed per spike (NSPS), spike length (SL), awn length (AL), plant height (PH), spike weight (SW) and peduncle length (PL).

Biometrical genetic analysi

The recorded data were subjected to analysis of variance using SAS V9.1 software to ascertain existence of variability among the genotypes. The phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability (h^2bs), genetic gain and co-heritability were estimated according to (Farshadfar, 2010) from the components of variance and covariance as follows

$$V_E = MS_e$$

$$V_G = \left(MS_{g\_}MS_e\right)/r$$

$$V_p = V_G + V_E$$

$$PCV = 100\ \sqrt{\sigma_p^2/\bar{x}}$$

$$\mathbf{G}CV = 100\ \sqrt{\sigma_g^2/\bar{x}}$$

$$ECV = 100\ \sqrt{\sigma_E^2/\bar{x}}$$

$$h_{bs}^2 = \sigma_g^2/\sigma_p^2$$

$$GG = \left(i.\sigma_g^2/\sqrt{\sigma_p^2}\right)100/\bar{x}$$

$$E(MSP_V)\sigma e_1e_2 + r\sigma g_1g_2$$

$$E(MSP_e) = \sigma e_1e_2$$

$$\sigma g_1g_2 = (MSP_V - MSP_E)/r$$

$$\sigma p_1p_2 = \sigma g_1g_2 + \sigma e_1e_2$$

$$Coheritability = (Gcov\ X_1X_2/PcovX_1X_2) \times 100$$

$$SI = K \times (V_P)^{0.5}$$

Where, Ve = environmental variation, MSE = error mean square, Vg = genotypic variation, r = number of replication, Vp = phenotypic variation is the mean, σ^2g is genetic variance, σ^2p is phenotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, ECV = environmental coefficient of variation, h^2bs = broadsense heritability, GG = genetic gain, the standard selection differential (i) for 5% selection intensity was 2.06, $\sigma^2g(1,2)$ = genetic covariance of characters 1 and 2, $\sigma^2p(1,2)$ is phenotypic covariance for characters 1 and 2, σ_{e1e2}= environment covariance of character 1 and 2, PCOV XY = Phenotypic covariation between characters X and Y, PVX = Phenotypic variance of X, PVY = Phenotypic variance of Y, GCOV XY = Genotypic covariation between characters X and Y, GVX = Genotypic variance of X, GVY = Genotypic variance of Y, ECOV XY =

Environmental covariation between characters X and Y, EVX = Environmental variance of X and EVY = Environmental variance of Y and SI = value of selection index for each character and K = 2.06 at 5% selection intensity (Kang *et al.,*1983).

Expected response to selection (Re) was determined using 20% selection intensity according to the procedure outlined by Falconer and Mackay (1996):

$Re = i_x(Vp\times h2)^{0.5}$

Where i_x = 20% selection intensity (=1.40) for trait x, Vp= phenotypic variance for the trait x and h2= heritability for the trait x.

Results and discussion

Analysis of variance and mean comparisons

The analysis of variance showed highly significant differences among the genotypes for all the characters studied (Table1), thereby suggesting the presence of considerable amount of variability among the genotypes of wheat evaluated in present study, similar findings were also reported by Narwal*et al.*, (1999), Tazeen*et al.*, (2009) and Kumar *et al.* (2013). Mean comparisons (Table 2) classified the genotypes in different groups for all the characters under study indicating the presence of genetic variability found in the analysis of variance. Maximum Ys, HI, TSW, AL and PL was attributed to G8, while maximum BI, NSPS and SL was related to G7. G6 revealed the longest plant height.

Table 1. Analysis of variance for the agro-morphological characters investigated.

S.O.V	D.F	Ys	BI	HI	TSW	NSPS	SL	AL	PH	PL
Replications	2	0.001^{ns}	0.002 ^{ns}	23.95ns	0.527 ^{ns}	8.0 ^{ns}	1.33 ^{ns}	13.15*	18.5 ^{ns}	13.15*
Genotypes	7	0.092**	0.001 ^{ns}	128.5**	52.75**	71.52**	5.22**	19.92**	134.7ns	19.92**
Error	14	0.001	0.001	16.62	0.466	4.10	1.69	2.82	65.21	2.82
CV%	-	3.53	6.74	9.23	0.35	5.54	15.11	4.49	10.89	4.49

*; **: Significant at 5% and 1% level of probability; ns=non-significant.

Estimation of genetic parameters

The phenotypic and genotypic coefficient of variation (PCV and GCV) estimates of the component of variance, heritability and genetic advance are shown in Table 3. The PCV was generally higher than the GCV for all the characters. The highest values were shown by AL, Ys and TSW. GCV was higher than ECV for all the characters except for SL indicating that the traits studied are more genetic.Present study are broadly in conformity with previous reports in wheat (Kumar *et al.,* 2003).

Table 2. Mean comparisons of agro-morphological traits

Codes	Ys	BI	HI	TSW	NSPS	SL	AL	PH	PL
G1	0.540 e	1.486 cd	36.3 c	15.1 f	35.7 bc	9.4 a	10.5bc	78.7 ab	37.3 ab
G2	0.557 e	1.421 cd	39.2 bc	15.7 f	35.3 bc	7.7 ab	9.0c	68.3 b	35.2 bc
G3	0.820 c	1.773 b	46.7 b	21.1 c	39.0 b	9.0 a	7.7c	69.0 b	32.5 c
G4	0.840 c	1.814 b	46.6 b	24.2 b	34.7 c	8.1 ab	13.0b	68.7 b	39.7 a
G5	0.653 d	1.614 bc	40.6 bc	23.7 b	27.7 d	9.6 a	10.0bc	73.3 ab	39.7 a
G6	0.610 d	1.382 d	44.7 b	16.9 e	36.0 bc	9.1 a	7.8c	87.0 a	36.9 ab
G7	0.890 b	2.134 a	41.7 bc	19.8 d	45.0 a	9.9 a	7.5c	78.3 ab	37.8 ab
G8	1.017 a	1.764 b	57.7 a	26.3 a	38.7 b	5.9 b	16.8a	69.7 b	40.0 a

*: Mean with common letters have no significant difference.

High heritability estimates (> 0.5; Stanfield, 2005) were observed for all the characters investigated except SL. The heritability value alone provides no indication of the amount of genetic progress that would result in selecting the best individual, but heritability estimates alongwith the genetic advance is considered more useful (Ajmal*et al.,* 2009).

High heritability estimates associated with high genetic advance for Ys, TSW and AL reflecting the involvement of additive gene action. Similar results have been reported by Atta *et al.* (2008), Bhoite*et al.* (2008), Ajmal*et al.* (2009) and Bharat *et al.* (2013). Such estimates of genetic advance indicated that moderate gains could be achieved with strengthening the selection. The heritability is a parameter extremely importantfor plant breeding programs. This is the proportion of phenotypic variation in a population that is due to genetic variation between individuals. Thus, it can be perpetuated via selection and has been object of study by many authors (Londero*et al.,* 2006, Dawson *et al.,* 2008).

Table 3. Genetic parameters estimated for agro-morphological traits under rainfed condition.

Traits	Mean	σ^2_G	σ^2_p	σ^2_e	$Cov_{p(GY,i)}$	$Cov_{G(GY,i)}$	h^2_{bs}	c-h^2_{bs}	PCV	GCV	ECV	GG
YS	0.741	0.030	0.031	0.001	-----	-----	0.978	-----	23.748	23.484	3.530	47.839
BI	1.673	0.058	0.071	0.013	0.034	0.035	0.819	0.968	15.924	14.411	6.773	26.868
HI	44.188	36.875	53.907	17.032	0.983	0.903	0.684	1.089	16.616	13.743	9.340	23.414
TSW	20.371	17.219	17.894	0.674	0.576	0.578	0.962	0.996	20.765	20.370	4.031	41.165
NSPS	36.500	22.478	26.571	4.094	0.474	0.428	0.846	1.109	14.123	12.989	5.543	24.610
SL	8.592	1.178	2.863	1.685	-0.105	-0.102	0.411	1.029	19.693	12.630	15.109	16.687
AL	10.292	9.379	12.378	2.999	0.282	0.286	0.758	0.988	34.185	29.758	16.826	53.361
PH	37.383	5.699	8.520	2.821	0.137	0.127	0.669	1.078	7.808	6.386	4.493	10.759
SW	773.917	17735.738	20076.036	2340.298	21.155	21.249	0.883	0.996	18.308	17.208	6.251	33.318
PL	348.125	3723.169	4174.554	451.384	3.208	3.032	0.892	1.058	18.560	17.528	6.103	34.099
Traits	Ys	BI	HI	TSW	NSPS	SL	AL	PH	SW	PL		
RE	0.25	0.34	8.5	5.8	6.64	1.92	4.3	3.34	186	85		
SI	0.36	0.55	15	8.7	10.6	3.5	7.25	6.0	292	133		

Characters like HI, BI, NSPS, SW and PL showed high heritability coupled with moderate genetic advance indicating the chance of effective selection of these traits for improvement of grain yield. SL and PH displayed low and high heritability with low genetic advance. Non-additive (dominance/epistasis) gene effects were more important for these traits.Expected response to selection (Re) ranged from 0.25 for Ys to 186 for SW. The same pattern was observed for value of selection index(SI) (Table 3).

Table 4. Co-heritability estimates betweenagro-morphological traits under rain-fed condition.

	Ys	BI	HI	TSW	NSPS	SL	AL	PH	SW	PL
BI	1.033									
HI	0.918	2.905								
TSW	1.004	0.987	0.996							
NSPS	0.902	1.078	0.582	0.692						
SL	0.972	0.118	0.785	1.058	0.535					
AL	1.012	4.195	0.918	0.948	0.706	0.779				
PH	0.928	1.319	0.587	0.927	1.092	4.097	1.207			
SW	1.004	0.979	1.068	1.023	0.935	0.718	1.040	1.069		
PL	0.945	0.970	1.069	0.983	0.846	0.582	0.919	0.749	1.040	

Phenotypic and genotypic matrix

The most common way to represent the pattern and magnitude of the genetic basis of a series of traits is the genetic variance–covariance matrix, also known as the G-matrix. G -matrix is extremely useful for predicting the response to selection over the short term. Genetic variance–covariance matrix accounts for genetic covariance as well as predicting the indirect response to selection on one character from selection on another trait. If the genetic covariance between two traits is different from zero, selection on one trait will affect response to selection on the other (Guillaume and Whitlock, 2007). According to the results (Table 3), the highest genotypic and phenotypic covariance observed between Ys and SW indicating significant contribution of these traits to increase grain yield in wheat under raifed condition (correlated response). High values of genetic and/or phenotypic covariance between two traits may represent a high level of variation (genetic, phenotypic or both) between two traits. High values of genetic variation in breeding programs can be very useful (Farshadfar*et al.,* 2013).

Co-heritability

The lower diagonal of Table 4 has the co-heritability values for pairs of characters. The range of co-heritability was from 0.535 (between NSPS and SL) to 4.195 (between BI and AL). High co-heritability was observed between BI and AL (4.195) and SL and PH (4.097). Positive coheritability estimate was observed between Ys and all the agro-morphological traits. This suggests that selection of either of the characters would simultaneously affect the Ys positively. The same situation was indicated for the rest of the characters.

References

Aharizad S, KarimiFard A, Mohammadi SA, Sedaghat S. 2012. Evaluation of Bread Wheat Recombinant Inbred Lines under drought conditions. Annals of Biological Research **3(12),** 5744-5747.

Ajmal SU, Zakir N, Mujahid MY. 2009. Estimation of genetic parameters and character association in wheat. Journal of Agriculture and Biological Science **1(1),** 5-18.

Ali MA, Abbas A, Niaz S, Zulkiffal M, Ali S. 2009. Morpho-physiological criteria for drought tolerance in sorghum (*Sorghum bicolor*) at seedling and post-anthesis stages. International Journal of Agriculture and Biology **11,** 674-680.

Ali MA, Awan SI. 2009. Inheritance pattern of seed and lint traits in *Gossypiumhirsutum*L. International Journal of Agriculture and Biology **11,** 44-48.

Atta YA, Akhter BMJ, Lateef PZ. 2008. Genetic variability, association and diversity studies in wheat (*Triticumaestivum*L.) germplasm. Pakistan Journal of Botany **40(5),** 2087-2097.

Bharat B, Bharti S, Ojha A, Pandey M, Singh Gourav SH, Singh Tyagi BH, Singh G. 2013. Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. Journal of WheatResearch **5(1),** 24-29.

Bhoite KD, Rasal RN, Gadekar DA. 2008. Genetic variability, heritability and genetic advance in durum wheat (*Triticum durum* L.). Journal of Maharashtra Agricultural Universities **33(1),** 102-103.

Chowdhry MA, Iqbal S, Subhai GM, Khaliq I. 1997. Heritability for some quantitative characters in bread wheat. Journal of Applied Sience7 **(1-2),** 27-28.

Dawson JC, Murphy KM, Jones SS. 2008. Decentralized selection and participatory approaches in plant breeding for low-input systems.Euphytica **160,** 143-154.
http://dx.doi.org/10.1007/s10.681-007-9533-0

Deswal RK, Grakh SS, Berwal KK. 1996. Genetic variability and character association between grain yield and its components in wheat. Annals of Biology **12(2),** 221-224.

Donmez E, Sears RG, Shroyer JP, Paulsen GM. 2001. Genetic gain in yield attributes of winter wheat in the Great Plains. Crop Science **41,** 1412–1419.
http://dx.doi.org/102135/cropsci2001.4151412x

Falconer DS, Mackay TFC. 1996. Introduction to quantitative genetics. 4th Ed. Longman Scientific and

Tech. England.

Farshadfar E, Romena H, Shabani A. 2013. Evaluation of genetic parameters in agro-physiological traits of wheat(*TriticumaestivumL.*) under irrigated condition. International journal of Advanced Biological and Biomedical Research **1(4),** 331-340.

Farshadfar E. 2010. New discussions in biometrical genetics vol 1.Islamic Azad University of Kermanshah press (in Farsi).

Firouzian A. 2003. Heritability and genetic advance of grain yield and its related traits in spring wheat. Pakistan Journal of Biological Science **6(24),** 2020-2032.
http://dx.doi.org/10.3923/pjbs.20032020.2023

Firouzian A, Khan AS, Ali Z. 2003. Genetic variability and inheritance of grain yield and its components in wheat. Pakistan Journal of Agricultural Science **40(3-4),** 176-179.

Ghimiray TS, Sarkar KK. 2000. Estimation of genetic parameters of some quantitative traits in wheat (*Triticumaestivum* L.) grown in Terai soils of West Bengal. Environment and Ecology **18(2),** 338-340.

Guillaume F, Whitlock MC. 2007. Effects of migration on the genetic covariance matrix. Evolution **61(10),** 2398-2409.
http://dx.doi.org/10.1111/j.1558-5646.2007.00193x

Gupta SK, Verma SR. 2000.Variability, heritability and genetic advance under normal and rainfed conditions in durum wheat (*TriticumdurumDesf.*).Indian Journal of Agricultural Research **34(2),** 122-125.

Kahrizi D, Mohammadi R. 2009. Study of Androgenesis and Spontaneous Chromosome Doubling in Barley (*Hordeum vulgare* L.) genotypes using Isolated Microspore Culture. Acta Agronomica Hungarica **57(2),** 155–164.

Kang MS, Mille JD, Tai PYP. 1983. Genetic and phenotypic path analysis and heritability in sugarcane. Crop Sci**23,** 643-647.
http://dx.doi.org/10.2135/cropsci19830011183X002300040010x

Kashif M, Ahmad J, Chowdhry MA, Perveen K. 2003. Study of genetic architecture of some important agronomic traits in Durum Wheat (*Triticum durum* Desf.). Asian Journal of Plant Science **2(9),** 708-712.
http://dx.doi.org/10.3923/ajps.2003.708712

Khalil IH, Carver BF, Smith EL. 1995. Genetic gains in two selection phases of a wheat breeding program. Plant Breeding **114,** 117–120.
http://dx.doi.org/10.1111/j.14390523.1995.tb00774x

Khodadadi M, Fotokian MH, Miransari M. 2011. Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. Australian Journal of Crop Science **5(1),** 17-24.

Kumar R, Singh Gaurav SH, Bharat B, Pal R. 2013.Study of genetic parameters and genetic divergence for yield and yield components of bread wheat (*TriticumaestivumL.*).Journal of Wheat Research **5 (2),** 39-42.

Kumar S, Dwivedi VK, Tyagi NK. 2003. Genetic variability in some metric traits and it contribution to yield in wheat (*TriticumaestivumL.*). Progressive Agriculture **3(1-2),** 152-153.

Londero PMG, Ribeiro ND, CargneluttiFilho A, Rodrigues JA, Antunes IF. 2006. Herdabilidade dos teores de fibraalimentar e rendimento de grãosempopulações de feijoeiro. PesquisaAgropecuáriaBrasileira **41,** 51-58.

Magda E, El-Rahman AB. 2013. Estimation of some genetic parameters through generation mean analysis in three bread wheat crosses.Alex Journal of Agricultural Research **58(3),** 183-195.

Maniee M, Kahrizi D, Mohammadi R. 2009. Genetic variability of some morpho-physiological traits in durum wheat (*Triticum durum* Desf.). Journal of Applied Sciences **9(7),** 1383-1387.

Mohammadi R, Armion M, Kahrizi D, Amri A. 2010. Efficiency of screening techniques for evaluating durum wheat genotypes under mild drought conditions. International Journal of Plant Production **4(1),** 11-24.

Muhammad Cheema N, Muhammad Ashraf M, Muhammad I, Ghulam R, Abid M. 2006. Studies on variability and some genetic parameters in spring wheat**.**Pakistan Journal of Agricultural Science **43(1-2),** 32-35.

Muhammad F, Deniel H, Shahzad K, Khan H. 2001. Heritability estimates for yield and its components in wheat. Sarhad Journal of Agriculture **17 (2),** 227- 234.

Narwal NK, Verma PK, Narwal MS. 1999. Genetic variability, correlation and path-coefficient analysis in bread wheat in two climatic zones of Haryana. Agriculture Science Digest, Karnal **19,** 73-76.

Ozkan H, Yaghasanlar T, Gene I. 1997. Genetic analysis of yield components, harvest index and biological yield in bread wheat under Mediterranean climatic conditions. RACHIS **18(1- 2),** 49-52.

Safeer-ul-Hassan M. 2003. Genetic analysis of some biometric characters in bread wheat *(Triticumaestivum).*M.Sc. (Hons) Thesis. Univ. Arid Agric.,Rawalpindi, Pakistan.

Salim I, Khan AS, Ali A. 2003. Estimates of heritability and genetic advance for grain yield traits in *Triticumaestivum* L. Journal of Animal and Plant Science **13(1),** 52-54.

Shukla RS, Mishra Y, Singh CB. 2000. Variability of some agro-physiological traits in wheat. Journal of Applied Biology **9(1),** 25-27.

Stansfield WD. 2005. Genetics, Theory and problems.3rd ed. McGraw-Hill, New York, USA.

Tazeen M, Naqvi FN. 2009. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. Journal of Food Agriculture and Environment **7(3-4),** 278-282.