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## Estimation of genotypic and phenotypic parameters for agro-physiological indicators of drought tolerance in wheat

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### Abstract

The present investigation was carried out to determine genetic variability and the estimate of genetic parameters for agro-physiological characteristics in bread wheat genotypes. The results of analysis of variance (ANOVA) showed significant difference ( $p < 0.01$ ) for flag leaf area (FLA), relative water content (RWC), evaporate transpiration efficiency (ETE), water use efficiency (WUE), chlorophyll a (Chl<sub>a</sub>), chlorophyll b (Chl<sub>b</sub>), total chlorophyll (Chl<sub>t</sub>) and grain yield per spike (GY/S). The highest estimate of broad sense heritability was recorded for GY/S, WUE, Chl a, Chl<sub>a</sub>/b, Chl b, RWC, and ETE (>80%). The characters GY/S and WUE exhibited high broadsense heritability ( $h^2_{bs}$ ) coupled with high genetic gain indicating that these traits can be further improved through individual plant selection. High positive co-heritability was observed between stomatal conductance (SC) and ETE (714.3), whereas high negative co-heritability was observed between relative water loss (RWL) and Chl<sub>a</sub>/b (-466.7).

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## Introduction

Wheat (*Triticum aestivum* L.) represents about 30% of the world's cereal area, with over 220 million ha cultivated worldwide, often under abiotic stress (Mariano Cossani and Reynolds, 2012). Drought stress is a pervasive feature of wheat production in world's major cereal growing regions. To improve the productivity in these areas, the importance of traits associated with tolerance to drought needs to be quantified (Jatoi *et al.*, 2012).

The presence and magnitude of genetic variability in a gene pool is the pre-requisite of a breeding program. The knowledge of certain genetic parameters is essential for proper understanding and their manipulation in any crop improvement program. Genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are useful biometrical tools for determination of genetic variability. There is a direct relationship between heritability and response to selection, which is referred to as genetic progress. The expected response to selection is also called as genetic advance (GA). High genetic advance coupled with high heritability estimates offers the most effective condition for selection. The genetic variation for the traits under selection process, higher heritability and genetic advance are necessary to approach the best cultivars in breeding program (Falconer and Maccay, 1996; Ulloa, 2006).

The grain yield is a complex character, quantitative in nature and an integrated function of a number of component traits. Therefore, selection for yield per se may not be much rewarding unless other yield attributing traits are taken into consideration. Selection efficiency could be increased if specific physiological and/or morphological attributes related to yield under specific environments could be identified and used as selection criteria for complementing traditional plant breeding (Acevedo, 1991).

The objectives of this study were i) to determine genetic variability and the estimate of genetic and environmental variances and covariances for agro-physiological characters in bread wheat genotypes, ii) to calculate broadsense heritability and response to selection for these traits, and iii) to obtain coheritability estimate for all pairs of characteristics.

## Materials and methods

### Experimental protocol

This study was conducted at greenhouse and environmental stress laboratory of Agricultural Science and Natural Resources of Razi University, Kermanshah, Iran, during 2012-2013. Eight wheat genotypes i.e., Bahar, Pishtaz, Vrinak, Yavaros, S-80-18, Cras alborz, Santor and D-79-15, were used in the experiment under water regime treatment. Pots were prepared with a mixture of sandy, loam and manure and arranged in a completely randomized design with three replications. These genotypes exposed to water stress treatment to 40% field capacity. In each plot, five plants were randomly selected to record data of flag leaf area (FLA), other leaf area (OLA), assimilation rate (AR), stomatal conductance (SC), excised leaf water retention (ELWR), relative water content (RWC), relative water loss (RWL), evaporate transpiration efficiency (ETE), water use efficiency (WUE), SPAD chlorophyll meter reading (SCMR), chlorophyll a (Chla), chlorophyllb (Chlb), chlorophylla/b (chla/b), total chlorophyll (Chlt), and grain yield per spike (GY/S).

### Statistical background

Separate analyses of variance and covariance for all traits and pairs of characters selected for this study were carried out. Some of genetic parameters estimated based on formula as follows (Falconer and Mackay, 1996, Farshadfar *et al.*, 2013):

$$V_E = MS_e$$

$$V_G = (MS_g - MS_e)/r$$

$$V_p = V_G + V_E$$

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

$$GCV = 100 \sqrt{\sigma_g^2 / \bar{x}}$$

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

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

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

$$E(MSP_V) = \sigma_{e_1 e_2} + r \sigma_{g_1 g_2}$$

$$E(MSP_e) = \sigma_{e_1 e_2}$$

$$\sigma_{g_1 g_2} = (MSP_V - MSP_e) / r$$

$$\sigma_{p_1 p_2} = \sigma_{g_1 g_2} + \sigma_{e_1 e_2}$$

$$\text{Coheritability} = (Gcov X_1 X_2 / Pcov X_1 X_2) \times 100$$

Where,  $V_e$  - environmental variation,  $MSE$  = error mean square,  $V_g$  = genotypic variation,  $r$  = number of replication,  $V_p$  = phenotypic variation is the mean,  $\sigma_g^2$  is genetic variance,  $\sigma_p^2$  is phenotypic variance,  $PCV$  = phenotypic coefficient of variation,  $GCV$  = genotypic coefficient of variation,  $ECV$  = environmental coefficient of variation,  $h^2_{bs}$  = broadsense heritability,  $GG$  = genetic gain, the standard selection differential ( $i$ ) for 5% selection intensity was 2.06,  $\sigma^2_{g(1,2)}$  = genetic covariance of characters 1 and 2,  $\sigma^2_{p(1,2)}$  is phenotypic covariance for characters 1 and 2,  $\sigma_{e_1 e_2}$  = 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  $Y$ .

## Results and discussion

### Analysis of variance and mean comparisons

Analysis of variance for various agro-physiological traits indicated highly significant differences ( $P \leq 0.01$ ) among cultivars for GY/S, FLA, RWC, ETE, WUE, Chl a, Chl b, and Chl t (Table 1). The genetic variability of a metric trait can be studied through the use of various statistical parameters like genotypic mean,

range, variance components and coefficients of variation (Tables 2, 3). The variation among cultivars for all the traits showed promise for their improvement through breeding. The GY/S ranged from 0.54 gr (Bahar) to 1.02 gr (D-79-15), and mean yield of all genotypes was 0.54 gr per spike (Table 3). Genotypes Pishtaz, Crossalborz, Bahar, and Santor had the highest and genotypes Vrinak, S-80-18, and D-79-15 had the lowest flag leaf area, respectively. Comparison of means also exhibited that genotype Sanator had the maximum ETE, and genotype D-79-15 had the maximum WUE, chl a, chl b, and chl t.

### Estimation of genetic parameters

Table 3 also represented various genetic parameters including phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability ( $h^2_{bs}$ ) and genetic gain (GG). Generally the PCV and GCV were low for all the traits with very high genetic proportion in GY/S, WUE, Chl a, Chl t, Chl b, RWC, and ETE (>90%).

The high broad sense heritability estimate suggested that the traits exhibited high genetic potentials, low environmental effect and additive gene action could play predominant role on their expression (Adewale *et al.*, 2010). Maximum estimates of broad sense heritability ( $h^2_{bs}$ ) was recorded for GY/S, WUE, Chl a, Chl t, Chl b, RWC, and ETE (>80%) (Table 3). These high estimates of heritability revealed the feasibility of selection for these traits under drought stress. Very low estimates of broad-sense heritability was observed for GS, Chl a/b, ELWR, OLA, AR, and SCMR (<35%) displaying that these traits could not be considered as basis for selection. Heritability magnitude indicates the reliability with which the genotype will be recognized by its phenotype expression (Chandraba and Sharma, 1999). Reliable selection of genetic materials can be made on the basis of high broadsense heritability estimates in wheat (Farshadfar *et al.*, 2013; Kianersi *et al.*, 2013; Kahrizi *et al.*, 2010; Mohsin *et al.*, 2009).

**Table 1.** Analysis of variance of various agro-physiological characteristics of bread wheat genotypes under moisture stress conditions.

Geno- types	GY/S	FLA	OLA	AR	GS	SCMR	RWC	ELWR	RWL	ETE	WUE	Chl a	Chl b	Chl t	Chl a/b
Block	0.001 <sup>ns</sup>	18867 <sup>ns</sup>	2276706 <sup>ns</sup>	28.9 <sup>ns</sup>	1.82 <sup>**</sup>	3.12 <sup>ns</sup>	690.95 <sup>**</sup>	210.6 <sup>ns</sup>	95.8 <sup>ns</sup>	1010.4 <sup>ns</sup>	103.5 <sup>ns</sup>	0.007 <sup>ns</sup>	0.004 <sup>ns</sup>	0.017 <sup>ns</sup>	0.002 <sup>ns</sup>
Geno- types	0.092 <sup>**</sup>	169715 <sup>**</sup>	1441784 <sup>ns</sup>	24.5 <sup>ns</sup>	0.001 <sup>ns</sup>	4.80 <sup>ns</sup>	88.7 <sup>**</sup>	150.5 <sup>ns</sup>	211.75 <sup>ns</sup>	13812.5 <sup>**</sup>	6732.4 <sup>**</sup>	0.18 <sup>**</sup>	0.306 <sup>**</sup>	0.95 <sup>**</sup>	0.001 <sup>ns</sup>
Error	0.001	21508.3	1009479	11.20	0.004	1.98	5.68	130.95	222.2	935.3	50.21	0.005	0.02	0.04	0.001
CV%	3.53	8.28	14.08	24.73	14.91	4.14	5.06	25.85	24.34	6.74	3.53	3.84	6.39	4.99	4.06

**Table 2.** Mean performance of bread wheat genotypes for various agro-physiological characteristics under moisture stress conditions.

Genotypes	Genotypic Mean														
	GY/S	FLA	OLA	AR	GS	SCMR	RWC	ELWR	RWL	ETE	WUE	Chl a	Chl b	Chl t	Chl a/b
<b>Bahar</b>	0.54e	1951.4ab	6164.2a	10.3b	0.38a	34.7ab	46.6cd	37.1a	63.6a	403.2cd	146.5e	1.77c	2.09b	3.86 b	0.85a
<b>Pishtaz</b>	0.56e	2064.2a	7114.3a	15.5ab	0.38a	34.3ab	43.9de	42.1a	69.8a	385.4cd	151.0e	2.10ab	2.50a	4.61 a	0.84a
<b>Vrinak</b>	0.82c	1468.7e	6126.5a	14.7ab	0.40a	33.0b	40.9e	47.2a	62.3a	480.9b	222.5c	2.10ab	2.57a	4.67 a	0.82a
<b>Yavaros</b>	0.84c	1750.9bcd	7767.7a	10.7b	0.38a	33.8b	48.0bcd	34.8a	59.2a	492.1b	227.9c	1.75c	2.01bc	3.76 bc	0.88a
<b>S-80-18</b>	0.65d	1520.7de	7248.1a	16.5ab	0.40a	36.8a	40.5e	41.9a	66.6a	437.8bc	177.2d	1.53d	1.77c	3.30 d	0.87a
<b>Crossalborz</b>	0.61d	2047.0a	7003.4a	17.3a	0.43a	32.8b	51.5b	53.8a	47.1a	374.8d	165.5d	1.99b	2.35a	4.34 a	0.85a
<b>Santor</b>	0.89b	1810.0abc	7945.7a	11.6ab	0.40a	33.3b	56.7a	43.0a	51.1a	579.0a	241.5b	1.62d	1.85bc	3.47 cd	0.88a
<b>D-79-15</b>	1.02a	1557.9cde	7697.6a	10.9ab	0.41a	33.6b	48.8bc	54.2a	70.2a	478.6b	275.8a	2.19a	2.52a	4.71 a	0.87a
<b>Mean</b>	0.74	1771.4	7133.4	13.4	0.40	34.0	47.1	44.3	61.2	454.0	201.0	1.88	2.21	4.09	0.85
<b>Min.</b>	0.54	1468.7	6126.5	10.3	0.38	33.0	40.5	34.8	47.1	374.8	151.0	1.53	1.77	3.30	0.82
<b>Max.</b>	1.02	2064.2	7945.7	17.3	0.43	36.8	56.7	54.2	70.2	579.0	275.8	2.19	2.57	4.71	0.88

**GY/S:** grain yield per spike (gr); **FLA:** flag leaf area (cm<sup>2</sup>); **OLA:** other leaf area (cm<sup>2</sup>); **AR:** assimilation rate (umol(CO<sub>2</sub>)/m<sup>2</sup>.s); **GS:** stomatal conductance (mol/m<sup>2</sup>.s); **ELWR:** excised leaf water retention (%); **RWC:** relative water content (%); **RWL:** relative water loss (%); **ETE:** evaporate transpiration efficiency (%); **WUE:** water use efficiency (gr/mil); **SCMR:** SPAD chlorophyll meter reading; **Chla:** chlorophyll a (mil gr/mil lit); **Chl b:** chlorophyllb (mil gr/mil lit); **chl a/b:** chlorophylla/b; **Chl t:** total chlorophyll (mil gr/mil lit).

**Table 3.** Estimates of components of variance, coefficients of variation, heritability and genetic gain for various agro-physiologic traits in wheat genotypes.

Traits	Mean	Genetic	Phenotypic	Environmental	Coefficient of variation (%)			Broadsense	Genetic
		variance	variance	variance	Phenotypic	Genetic	Environmental	Heritability	Gain
		(σ <sup>2</sup> <sub>e</sub> )	(σ <sup>2</sup> <sub>p</sub> )	(σ <sup>2</sup> <sub>e</sub> )	(PCV)	(GCV)	(ECV)	(h <sup>2</sup> <sub>bs</sub> )	(GG)
GY/S	0.74	0.03	0.031	0.001	23.79	23.41	3.53	0.97	47.43
FLA	1771.35	49402.23	70910.53	21508.3	15.03	12.55	8.3	0.70	21.58
OLA	7133.45	144101.67	1153580.67	1009479	15.06	5.32	14.09	0.12	3.87
AR	13.43	4.433	15.63	11.20	29.44	15.68	24.83	0.28	17.20
GS	0.40	0.00	0.003	0.004	13.69	0.00	13.11	0.00	0.00
SCMR	34.05	0.94	2.920	1.98	5.02	2.85	4.81	0.32	3.33
RWC	47.10	27.673	33.35	5.68	12.26	11.17	5.54	0.83	20.96
ELWR	44.27	6.517	137.467	130.95	26.48	5.77	25.76	0.05	2.59
RWL	61.23	0.00	218.717	222.2	24.15	0.00	24.15	0.00	0.00
ETE	453.99	4292.4	5227.70	935.3	15.93	14.43	6.75	0.82	26.94
WUE	200.99	2227.40	2277.61	50.21	23.74	23.48	3.56	0.98	47.84
Chl a	1.88	0.058	0.063	0.005	13.35	12.81	2.76	0.92	25.32
Chl b	2.21	0.095	0.115	0.02	15.34	13.95	5.81	0.83	26.11
Chl t	4.09	0.303	0.343	0.04	14.32	13.46	5.08	0.88	26.06
Chla/b	0.85	0.00	0.001	0.001	3.72	0.00	0.00	0.00	0.00

The expected genetic gain (GG) is a gain or a change produced by selection and is of main interest to the plant breeder since it changes the population mean. Higher values of GG for GY/S, WUE exhibited effectiveness of the selection for these traits and this parameter was under the control of additive genes. They equally had high broad sense heritability. In general, it is believed that if a character is governed by non-additive gene action, may give higher heritability but low genetic advance, whereas if the character is governed by additive gene action, both heritability and genetic advance would be high (Manal, 2009). Mohsin *et al.* (2009) reported that heritability estimate obtained for flag leaf area was moderate (67.22) with a low genetic advance (7.16) in synthetic elite lines of wheat.

*Genetic variance – covariance 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 and improvement of the efficiency of selection over a short period. As G-matrix includes genetic covariance as well, it can also help to predict the indirect response to selection of 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; Kearsy and Pooni, 2004). According to the results (Table 4), the highest genetic covariance observed for OLA with ETE, WUE, RWL, RWC (26675, 17172, -4503, 2315, respectively) , FLA with ETE and WUE (-7290 and -6829, respectively), between OLA and FLA (-7265), and between ETE and WUE (2499). Gupta *et al.* (2001) observed positive correlations of leaf water potential, plant height, leaf area, tillers, and shoot dry weight with grain yield at both boot and anthesis stages, while negative correlations among the leaf diffusive and leaf canopy temperature and also with grain yield.

**Table 4.** Phenotypic (Lower off-diagonal matrix) and Genetic (Upper off-diagonal matrix) covariance matrix of agro-physiological characteristics at moisture stress conditions.

	GY/S	FLA	OLA	AR	GS	SCMR	RWC	ELWR	RWL	ETE	WUE	Chl a	Chl b	Chl t	Chl b/a
GY/S		-25.17	63.31	-0.22	0.000	-0.08	0.30	0.31	0.01	9.21	8.40	0.01	0.004	0.01	0.001
FLA	-26.71		-7265.12	88.76	-1.14	-88.60	489.83	-446.15	-517.76	-7289.81	-828.82	1.15	-0.58	0.63	0.34
OLA	66.65	-5992.60		-97.89	-1.92	14.09	2314.61	386.24	-4502.71	26674.67	17172.23	-23.59	-38.08	-59.98	2.19
AR	-0.24	68.67	-440.18		0.038	0.33	-5.83	-1.93	-8.63	-100.83	-60.22	0.11	0.18	0.29	-0.02
GS	0.001	-0.42	1.26	0.02		0.01	0.07	0.17	-0.20	-0.50	0.14	0.001	0.001	0.002	0.0001
SCMR	-0.09	-64.81	-17.32	0.56	-0.01		-4.17	-6.55	11.98	-33.78	-21.77	-0.18	-0.25	-0.42	0.02
RWC	0.32	529.46	2112.51	-5.79	0.03	-3.78		11.18	-33.23	160.93	80.77	-0.14	-0.36	-0.50	0.07
ELWR	0.38	-223.89	156.24	7.76	0.11	-3.98	6.59		-27.45	-79.16	84.20	1.04	1.46	2.48	-0.10
RWL	0.03	-698.99	-791.51	-3.59	-0.07	5.58	-30.96	-8.38		-178.92	1.183	0.43	0.11	0.54	0.14
ETE	9.41	-8049.58	24497.36	-100.01	-0.07	-19.76	158.96	-57.11	-110.05		2499.41	-5.16	-7.62	-12.77	0.73
WUE	8.30	-7104.74	18025.17	-64.69	0.18	-23.19	85.00	102.42	6.46	2557.37		1.77	1.19	2.98	0.39
Chl a	0.007	3.22	-41.76	0.07	0.001	-0.18	-0.19	1.07	0.59	-5.21	1.90		0.08	0.15	-0.004
Chl b	0.005	3.89	-80.68	0.15	0.001	-0.23	-0.38	1.30	0.73	-7.58	1.22	0.08		0.20	-0.01
Chl t	0.01	7.53	-122.47	0.22	0.002	-0.41	-0.58	2.36	1.32	-12.89	3.05	0.14	0.18		-0.01
Chl a/b	0.002	-0.37	12.48	-0.03	0.000	0.007	0.06	-0.03	-0.03	0.71	0.41	-0.003	-0.005	-0.008	

*Coheritability estimate*

Coheritability is another effective genetic parameter for enhancing the efficiency of plant selection since it enables to study the changes in pairs of characters. The lower diagonal of table 5 has the co-heritability values for pairs of characters. The range of co-

heritability was from -466.67 (between RWL and Chl a/b) to 714.29 (between GS and ETE). High positive co-heritability was observed between GS and ETE (714.3), OLA and RWL (568.9), and ELWR with Chl a/b and RWL (333.3 and 327.6), indicating that selection of either of the characters would

simultaneously affect the others positively. The high negative co-heritability Chl a/b in combination with RWL and GS (-466.7 and -135.4, respectively), and GS with OLA and SCMR (-152.4 and -100.0, respectively), declared that selection based on lower value of either of the characters will increase the others indirectly. Coheritability estimates was the highest between grain yield per spike and Chl a (142.86), followed by WUE and Chl t (101.20 and

100.0, respectively). These estimates of grain yield with GS, RWL and Chl a/b was low. Farshadfar *et al.* (2014) reported that co-heritability of seed per spike, harvest index, earliness and relative water content (RWC) with grain yield of wheat-agropyron disomic addition lines is high, indicating that selection of either of the characters would simultaneously affect the others positively.

**Table 5.** Co-heritability estimates between agro-physiological characteristics at moisture stress conditions.

	GY/S	FLA	OLA	AR	GS	SCMR	RWC	ELWR	RWL	ETE	WUE	Chl a	Chlb	Chl t
<b>FLA</b>	94.2													
<b>OLA</b>	95.0	121.2												
<b>AR</b>	91.7	129.3	22.2											
<b>GS</b>	50.5	271.4	-152.4	190.0										
<b>SCMR</b>	88.9	136.7	-81.4	58.9	-100.0									
<b>RWC</b>	93.8	92.5	109.6	100.7	233.3	110.3								
<b>ELWR</b>	81.6	199.3	247.2	-24.9	154.6	164.6	169.7							
<b>RWL</b>	33.3	74.1	568.9	240.4	285.7	214.7	107.3	327.6						
<b>ETE</b>	97.9	90.6	108.9	100.8	714.3	171.0	101.2	138.6	162.6					
<b>WUE</b>	101.2	96.1	95.3	93.1	77.8	93.9	95.0	82.2	18.3	97.7				
<b>Chl a</b>	142.9	35.7	56.5	157.1	100.0	100.0	73.7	97.2	72.9	99.0	93.2			
<b>Chl b</b>	80.0	-14.9	47.2	120.0	100.0	108.7	94.7	112.3	15.1	100.5	97.5	100.0		
<b>Chl t</b>	100.0	8.4	49.0	131.8	100.0	102.4	86.2	105.1	40.9	99.1	97.7	107.1	111.1	
<b>Chl a/b</b>	50.0	-91.9	17.6	66.7	-135.4	285.7	116.7	333.3	-466.7	102.8	95.1	133.3	200.0	125.0

**Conclusion**

The potential of a crop to favorably respond to breeding/selection and bioengineering programs depends upon the nature and magnitude of genetic variability (Akhtar *et al.*, 2007). The characters GY/S and WUE showed high heritability ( $h^2_{bs}$ ) coupled with high genetic gain indicating that these traits can be further improved through individual plant selection. The very high values of broad sense heritability with the high genetic gain indicated that traits are mostly under the control of additive type of gene action and improvement of these traits could be productive for development of high yielding elite genetic material (Bugarcic *et al.*, 1997). Several workers (Farshadfar *et al.*, 2014; Kianersi *et al.*, 2013; Degewione *et al.*, 2013; Kahrizi *et al.*, 2010, Mohsen *et al.*, 2009) have calculated Genotypic and different components of variance, and heritability for different yield characters in wheat and have revealed that selection was

effective for a population with broad genetic variability and character with high heritability.

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