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Original Article

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## Evaluation of Genetic Parameters in Agro-physiological Traits of Wheat (*Triticum aestivum* L.) under Irrigated Condition

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### Abstract

Selection of genotypes based on high value of heritability and forecasted genetic conditions would be an effective method for improvement of wheat cultivars. The present investigation was carried out to estimate the genetic variability of agro-physiological characters using biometrical genetic techniques in 20 bread wheat genotypes under irrigated condition. For this purpose an experiment was conducted to estimate the genetic parameters of some agro-physiological traits and their relationship with yield under irrigated conditions. High genetic variability was observed between the genotypes for the characters grain yield (GY), chlorophyll a (Chl a), chlorophyll ab (Chl ab), quantum yield (QY), performance index (PI), relative water loss (RWL) and leaf chlorophyll content (LCC), therefore direct selection is effective for improvement of these traits. Total chlorophyll content (Chl ab), chlorophyll b (Chl b) and PI revealed high heritability and co-heritability with yield. Hence, they can be used as indirect selection for the improvement of yield under irrigated condition.

**Keywords:** Diversity, Genetic parameters, Selection index, wheat.

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### 1. Introduction

Wheat becomes an important cereal which provides calories more and cheaply than any other crops (FAO, 2010). Demand of wheat is increasing by population growth and always be felt new method which can select high yielding varieties fast and accurate. Selection of genotypes based on high value of heritability and forecasted genetic conditions would be an effective method (Ghandorah & Shawaf, 1993). The development of an effective plant breeding program is dependent upon the existence of genetic variability. The efficiency of selection largely depend upon the magnitude of genetic variability present in the plant population. Thus the success of genetic

improvement in any character depends on the nature of variability present in the gene pool for that character. Hence an insight into the magnitude of variability present in the gene pool of a crop species is of utmost importance to a plant breeder for starting a judicious plant breeding program. In earlier years the visual observations used to be the measure of variability in a plant population. Now biometrical methods are available for systematic assessment of variability (Frey, 1966; Singh and Narayanan, 1993). Selection among genotype would be effective only when we have high value of heritability and forecasted genetic conditions for yield and yield components (Ghandorah & Shawaf, 1993). In general, the main goal for all plant breeding programs is achieving high amounts of yield (Ehdaie and Wainies, 1989) and in order to this point, having genetic diversity for the trait under selection with a higher heritability is essential (Falconer and Mackay, 1996). Our understanding about nature of traits and influences of genetic and environmental factors on desire traits also have important effects on breeding programs (Kashif *et al*, 2003; Ali and Awan, 2009; Mohammadi *et al*, 2010). Genetic potential and evaluation of diversity and stability performance are measured by some statistical parameters such as mean, variance, CV%, habitability and genetic gain (Firouzian, 2003; Ali *et al*, 2009). 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 *et al*, 2010). Knowledge of the genetic association between grain yield and physiological traits can help the breeders to improve the efficiency of selection. Therefore, it is important to study the relationships among the characters (Ehdaie & Wainies 1989; Maxwell and Johnson, 2000; Flexas, *et al*, 2007). Quantitative traits with high genetic gain and high heritability are very important in selection of genotype at early stages of breeding programs (Memon *et al*, 2005). Using family selection method may led us to success in the case of selection for traits with low heritability and high interactions between genotypes and environment (Aycicek and Yildirim, 2006). The objectives of the present experiment were to estimate (i) the genetic parameters for the study of genetic diversity in some agro-physiological traits, and (ii) to study the association between the traits investigated and yield under irrigated conditions.

## 2. Materials and methods

Twenty bread wheat genotypes were included in this study (Table 2). This experiment was conducted using a complete randomized block design (20 Genotypes×3 Replications) at Research field of campus of Agriculture and Natural Resources of Razi University, Iran, during 2011 to 2012 growing season. During grain-filling period photochemical efficiency or quantum yield (QY) and performance Index (PI) of the leaves were estimated with portable plant stress meter (PSM; Hansanthech, UK) according to Niari-Khamssi *et al*, (2010) on flag leaves. The measurement was performed at 10:00 am in order to avoid the effects of dew and air humidity. Steady state porometer (SC; Li-1600; LI-COR Inc., Lincoln, NE) was used for measurement of stomatal conductance (SC,  $\text{mmolH}_2\text{O m}^{-2}\text{s}^{-1}$ ). All the measurements were recorded on the flag well-lit leaf around mid day (10:00 am–16:00 pm). Relative water content (RWC) and relative water loss (RWL) were measured based on Barr and Weath erley (1969). Proline content (PC) was estimated based on Bates *et al*, (1973) method and chlorophyll content (Chl a, b, total) was estimated based on Arnon (1949) method. Grain yield per unit area (GY) for each treatment at each replicate was determined based on one  $\text{m}^2$  of middle part of each plot which were hand harvested at maturity stage.

**Table 1**

Analysis of variance for agro-physiological traits in wheat

SOV	df	Mean Square										
		GY	LCC	Chl a	Chl b	Chl ab	QY	PI	PC	SC	RWL	RWC
Rep.	2	1271	11.83	0.57	0.211	2.31	30.23	18.27	0.019	998	4800**	882.81**
Gen.	19	28410**	38.14*	6.58**	1.037**	9.38**	758**	371**	0.0062	1230	357**	164.98
Error	38	11817	20.18	0.40	0.292	0.504	132	50.31	0.0061	1109	127	111.43
CV%		14.12	9.44	10.40	25.59	9.27	22.74	18.73	40.06	25.76	17.73	20.40

GY: Grain yield; LCC: Leaf chlorophyll content; Chl a: Chlorophyll a; Chlorophyll b; Chl ab: Total chlorophyll; QY: Quantum Yield; PI: Performance index; PC: Proline content; SC: Stomatal conductance; RWL: Relative water loss; RWC: Relative water content

**Table 2**

Ranges, means, and LSD5% of the traits investigated in wheat genotypes

Gen	GY	LCC	Chl			QY	PI	PC	SC	RWL	RWC
			Chl a	b	Chl ab						
WC-4537	720.0	48.87	6.69	2.36	7.49	40.91	29.40	0.230	107.0	56.63	69.09
Wc- 4829	726.7	46.00	7.63	2.29	8.27	69.35	49.47	0.152	129.4	63.02	76.35
Wc- 4536	733.3	44.23	5.53	2.14	7.17	78.78	57.67	0.167	116.8	58.50	68.61
Wc-4937	990.0	56.97	6.13	2.59	7.25	29.45	28.80	0.125	127.5	59.52	78.02
WC-4594	763.3	50.03	4.38	2.30	7.09	47.47	36.13	0.239	131.3	63.72	70.22
WC-4924	803.3	49.93	6.73	2.79	6.68	29.73	23.60	0.272	144.5	52.89	74.83
WC-4888	880.0	40.80	5.26	2.79	7.96	21.53	18.73	0.199	114.3	61.74	94.63
WC-4823	900.0	49.90	7.44	2.82	7.64	43.02	38.33	0.228	89.1	61.31	71.10
WC-4827	686.7	47.63	5.68	2.39	6.54	51.76	35.27	0.164	131.4	59.67	62.51
WC-4582	753.3	48.67	3.97	1.24	5.83	53.87	40.73	0.112	144.5	99.88	55.05
WC-4889	773.3	48.20	4.79	1.49	5.56	41.65	32.13	0.246	133.2	63.81	67.27
WC-4515	773.3	47.27	4.65	0.73	5.55	46.10	35.00	0.161	107.5	66.15	54.20
WC-4780	713.3	45.57	4.45	2.62	6.62	83.33	59.33	0.173	115.7	62.68	77.12
WC-4592	620.0	49.73	6.06	1.29	8.36	40.39	24.33	0.137	146.5	63.24	69.20
WC-4610	700.0	46.90	6.08	1.81	9.12	53.04	36.33	0.248	131.3	66.10	60.72
WC-4992	803.3	45.37	4.53	2.07	7.44	44.35	35.53	0.178	131.5	58.69	65.52
WC-4995	790.0	51.97	7.81	2.64	7.55	49.69	38.73	0.227	105.2	48.57	82.07
WC-4573	756.7	47.27	10.08	2.17	7.94	56.99	43.13	0.190	167.0	60.68	67.93
WC-shahryar	920.0	44.40	6.55	2.16	13.75	65.21	56.93	0.234	170.7	84.54	64.43
WC-5047	586.7	42.10	6.54	1.55	9.35	64.14	37.67	0.206	140.7	60.89	67.01
LSD 5%	179.6	7.42	1.04	0.89	1.17	19.00	11.72	0.128	55.1	18.65	23.53
Min	586.7	40.8	4.0	0.7	5.5	21.5	18.7	0.1	89.1	48.6	54.2
Max	990.0	57.0	10.1	2.8	13.7	83.3	59.3	0.3	170.7	99.9	94.6

**2.1. Biometrical genetic analysis**

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 ( $h^2_{bs}$ ), genetic gain and co-heritability were estimated according to (Farshadfar, 2010) from the components of variance and covariance as follows:

$$V_E = MS_e$$

$$V_G = \frac{MS_g - MS_e}{r}$$

$$V_P = V_G + V_E$$

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

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

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

$$h^2_{bs} = \sigma_g^2 / \sigma_p^2$$

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

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

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

$$\sigma_{g_1 g_2} = MSP_v - MSP_e / r$$

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

$$\text{Coheritability} = \frac{Gcov_{X_1 X_2}}{Pcov_{X_1 X_2}} \times 100$$

$$r_p = \frac{PCOV_{XY}}{\sqrt{(PV_X \cdot PV_Y)}}$$

$$r_g = \frac{GCOV_{XY}}{\sqrt{(GV_X \cdot GV_Y)}}$$

$$r_e = \frac{ECOV_{XY}}{\sqrt{EV_X \cdot EV_Y}}$$

Where,  $V_e$  = environmental variation,  $MSE$  = error mean square,  $V_g$  = genotypic variation,  $r$  = number of replication,  $V_p$  = phenotypic variation  $\bar{x}$  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,  $GG$  = genetec 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,  $r_p$  = phenotypic correlation,  $r_g$  = genetic correlation,  $r_e$  = environmental correlation,  $PCOV_{XY}$  = Phenotypic covariation between characters X and Y,  $PV_X$  = Phenotypic variance of X,  $PV_Y$  = Phenotypic variance of Y,  $GCOV_{XY}$  = Genotypic covariation between characters X and Y,  $GV_X$  = Genotypic variance of X,  $GV_Y$  = Genotypic variance of Y,  $ECOV_{XY}$  = Environmental covariation between characters X and Y,  $EV_X$  = Environmental variance of X and  $EV_Y$  = Environmental variance of Y.

### 3. Results and discussion

#### 3.1. Descriptive statistics and variability

Analysis of variance indicated significant differences for GY, Chl a, Chl ab, QY; PI, RWL and leaf chlorophyll content (LCC) (Table 1) indicating the existence of genetic diversity and desirable selection among wheat genotypes for these traits. Several researchers reported phenotypic divergence and extensive variation for physiological traits in wheat germplasems (Spagnoletti and Qualset, 1987; Jaradat, 1991; del Moral *et al*, 2003; Kashif and Khaliq, 2004).

Comparison of means showed that the genotypes Wc-4937, WC-shahryar, WC-4823 and WC-4888 had the highest grain yield, respectively. Range, means and values LSD of the traits for wheat genotypes are shown in Table 2. With regard to the means, it is obvious that genotypes with higher chl a, chl b chl ab, SC, RWC, QY and PI produce high grain yield (Table 2). Reduction of total biomass and subsequently reduced grain yield in irrigated conditions may be due to the considerable decrease in plant growth, photosynthesis and canopy structure (Bhatt and Rao, 2005; Ghobadi *et al*, 2012; Sankar *et al*, 2007). According to Fischer (2007), the rate of photosynthetic activity in plants such as wheat is a very important factor for increasing grain yield potential.

#### 3.2. Genetic variability

Phenotypic and genotypic coefficients of variation, broad sense heritability and genetic gain is presented in Table 3. Generally, GG, PCV and GCV were low for all the traits. The low broad sense heritability estimate indicates

low genetic potentials for the traits under investigation, high effect of the environment in determining measured traits and absence of predominant role of additive gene action. High broad sense heritability seems to be a suitable basis for a reliable selection of wheat genotypes (Kandasamy *et al*, 1989; Thiyagarajan, 1990). PC exhibited very low level of GG indicating high influence of environmental conditions on this trait under irrigated condition. The combination of high heritability and genetic gains are important indicators of the predominant role of additive gene action in characters (Manju and Sreelathakumary, 2002). Predictability of high performance and hence selection of materials based on the above criteria may lead to successful breeding program.

**Table 3**  
Estimation of genetic parameter for the traits under investigation

Traits	Mean	$\sigma^2_G$	$\sigma^2_p$	$\sigma^2_e$	$Cov_{p(GY,i)}$	$Cov_{G(GY,i)}$	$h^2_{bs}$	$c-h^2_{bs}$	PCV	GCV	GG
GY	770	5531	17348	11817	-----	-----	0.32	-----	17.1	9.66	11.2
LCC	47.6	5.99	26.2	20.1	181	81.2	0.23	0.45	10.8	5.14	5.06
Chl a	6.05	2.06	2.46	0.40	11.8	3.67	0.84	0.31	25.9	23.7	44.7
Chl b	2.11	0.249	0.54	0.292	31.3	23	0.46	0.74	34.8	23.6	33.1
Chl ab	7.66	2.96	3.46	0.504	25.6	23.8	0.85	0.93	24.3	22.5	42.8
QY	50.5	209	341	132	-1074	-424	0.61	0.39	36.6	28.6	46.2
PI	37.9	107	157	50.3	-45.7	-94	0.68	2.06	33.1	27.3	46.4
PC	0.194	0.00004	0.006	0.0061	1.1	0.0006	0.01	0.001	39.9	3.26	0.548
SC	129	40.5	1150	1109	128	-417	0.04	-3.26	26.3	4.93	1.91
RWL	63.6	76.8	204	127	-109	187	0.38	-1.72	22.5	13.8	17.4
RWC	69.8	17.8	220	111.43	478	203	0.08	0.43	21.2	6.04	3.54

$\sigma^2_G$ : Genotypic variance;  $\sigma^2_p$ : Phenotypic variance;  $h^2_{bs}$ : Broad sense heritability;  $c-h^2_{bs}$ : Broad sense co-heritability; PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation; GG: genetic gain

### 3.3. P and G-matrices

Evolution by natural selection requires heritable variation. 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. A population will evolve most rapidly along axes that have the most genetic variation, and more slowly in directions with little genetic variance. Because G accounts for genetic covariance as well, G can also help predict 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 4), the highest genetic and phenotypic covariance observed between SC and GY (-417, 128), RWL and GY (187, 109) and QY and GY (-424, -1074) traits, respectively. 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. Also result suggested that selection for low quantity of QY and high value of SC and RWL will increase GY indirectly under irrigated condition.

**Table 4**  
Phenotypic (Lower off-diagonal matrix) and genotypic (Upper off-diagonal matrix) covariance matrix

	GY	LCC	Chl a	Chl b	Chl ab	QY	Pi	PC	SC	RWL	RWC
GY		81.2	3.67	23.0	23.8	-424	-94.1	0.001	-417	187	203
LCC	181		0.807	0.277	-2.11	-22.1	-12.8	-0.036	-7.80	-7.31	-0.592
Chl a	11.8	0.449		0.306	0.976	1.118	1.131	0.012	5.14	-5.84	3.43
Chl b	31.3	0.287	0.281		0.108	-1.314	-0.121	0.008	-1.77	-2.81	3.20
Chl ab	25.6	-1.77	0.852	0.186		6.380	5.91	0.012	15.7	3.99	-0.053
QY	-1074	-21.3	0.311	-0.708	6.18		144	-0.119	72.3	30.1	-48.7
PI	-45.7	-7.73	0.621	0.620	5.72	208		-0.071	37.8	34.3	-32.0
PC	1.100	0.028	0.020	0.010	0.035	-0.148	-0.067		0.046	-0.238	0.031
SC	128	-13.2	5.91	-5.4	17.7	-13.6	5.99	-0.201		96.5	-49.6
RWL	-109	-3.52	-5.74	-3.38	4.04	45.4	33.3	-0.012	85.2		-20.4
RWC	478	-0.285	2.45	5.47	2.89	-23.9	-5.33	0.127	-58.6	-112	



### 3.4. Co-heritability

The lower diagonal of Table 5 has the co-heritability values for pairs of characters. The range of co-heritability was from -3.26 (between SC and GY) to 19.27 (between PC and RWL). The negative co-heritability between SC and GY declared that selection based on lower value of SC will increase grain yield indirectly. High co-heritability was observed between PC and RWL (19.27), PI and SC (6.32) and PI and RWC (6.00). This suggests that selection of either of the characters would simultaneously affect the others positively. Romena and Najaphy (2012) suggested that improving grain yield is related to the balance of SC and RWC in wheat under rain-fed condition. Many researchers reported that low  $\text{CO}_2$  uptake is the consequence of decreasing in relative water content of leaves and stomatal conductance (Chaves *et al*, 2002; Cornic and Massacci, 1996; Fischer, 2007; Krause and Weis, 1991; Lawlor, 1995; Lawlor and Cornic, 2002).

**Table 5**  
co-heritability estimates between the traits under study

	GY	LCC	Chla	Chlb	Chlab	QY	Pi	PC	SC	RWL
LCC	0.449									
Chla	0.310	1.80								
Chlb	0.737	0.967	1.09							
Chlab	0.928	1.20	1.15	0.583						
QY	0.394	1.04	3.60	1.86	1.03					
PI	2.06	1.65	1.82	-0.195	1.03	0.691				
PC	0.001	-1.30	0.590	0.865	0.347	0.808	1.06			
SC	-3.26	0.589	0.871	0.327	0.889	-5.33	6.32	-0.228		
RWL	-1.72	2.08	1.02	0.831	0.987	0.66	1.03	19.27	1.13	
RWC	0.425	2.07	1.40	0.585	-0.018	2.04	6.00	0.244	0.846	0.182

### 4. Conclusion

Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance, and genetic and environmental factors that influence their expression. The genetic variation for the trait under selection and a higher heritability are necessary to have response to selection. The study of components of genetic variance helps in further partitioning of genetic variance into additive, dominance and epistatic components. The magnitude of these components is a measure of the type of gene action involved in the expression of various traits. Information about gene action helps in deciding a breeding procedure for the genetic improvement of a trait.

High genetic variability was observed between the genotypes for the characters GY, Chl a, Chl ab, QY, PI, RWL and LCC, therefore direct selection is effective for improvement of these traits.

Total chlorophyll content (Chlab), Chl b and PI revealed high heritability and co-heritability with yield. Hence, they can be used as indirect selection for the improvement of yield under irrigated condition.

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