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Estimation of heritability and genetic advance of yield traits in wheat (*Triticum aestivum* L.) under drought condition

Manal H. Eid

Botany Department, Faculty of Agriculture, Suez Canal University, 41522, Ismailia, Egypt.
Email: eid_manl@hotmail.com.

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Four varieties/lines of wheat and their crosses namely, *Sakha8*, *Sids1*, *line 1 Line3* and *Line1x Sakha8*, *Line3x Sakha8*, *Line1x Sids1*, *Line3x Sids1* were evaluated to estimate heritability and genetic advance for yield traits. The experimental material was planted under irrigation as well as drought stress conditions. The mean average for plant height, spike length, number of spikes per plant, number of grains per spike, 50% heading date and 1000 grain-weight revealed highly significant differences among genotypes and crosses under both sowing conditions. Low, medium and high heritability was found in different yield traits under study. High heritability accompanied by high genetic advance was observed for spike length and 1000 grain-weight. Low heritability coupled with low genetic advance was for plant height and number of grains per spike. However, the heritability was generally found to be lower under drought stress conditions. Greater magnitude of heritability coupled with higher genetic advance in some traits under study provided that these parameters were under the control of additive genetic effects. This indicates that selection should lead to fast genetic improvement of the material. Moreover, the genetic correlations in study were high for most of the traits, suggesting a strong inherent association among these traits at the genetic level. These traits therefore deserve better attention in future breeding programs for evolving better wheat in stress environments.

Key words: Wheat, heritability, genetic advance, yield traits.

INTRODUCTION

Wheat is the largest grain crop in the world. It provides food to 36% of the global population, and contributes 20% of food calories. With progressive global climatic change and increasing shortage of water resources and worsening eco-environment, wheat production is influenced greatly (Singh and Chaudhary, 2006). The increasing yield potential has indisputable importance in solving world hunger issue. The grain yield of wheat is determined by three yield components: productive spikes per unit area, kernel per spike and kernel weight. The product of the first two components gives the total kernel numbers per unit area (Collaku, 1994). Its increase is one of the major factors that have contributed to wheat yield improvement, which mainly resulted from increase in kernels per spike or from increase in kernel weight. Yield and its component traits are controlled by polygene, whose expression is greatly affected by environments

(Ahmed et al., 2007). Thus, determination of the number, locations, and effects of this polygene is desired for obtaining optimal genotypes in breeding practice.

However, it is interesting but not surprising that genetic increase in wheat yields in dry areas has not been as great as in more favorable environments or where irrigation is available. A likely reason for this is that those dry environments are characterized by unpredictable and highly variable seasonal rainfall and hence highly variable yields. Since yield has a complex trait and is strongly influenced by the environment, severe losses can be caused by drought, a stress common in most arid and semi arid areas. Accordingly, drought tolerance is one of the main components of yield stability and its improvement is a major challenge to geneticists and breeders.

Therefore, sufficient genetic information regarding the yield traits of wheat under drought is essential and important

important to get progress in plant breeding program. Moreover, understanding of the genetic control of these economic traits through quantitative traits locus analysis allows the identification of discrete chromosome segments controlling complex traits (Frova et al., 1999). Besides, other genetic analysis could determine whether the correlations between the traits are genetics or phonetics, and how its onward transmission from parents to progeny, like heritability takes place. Heritability, a measure of the phenotypic variance attributable to genetic causes, has predictive function of breeding crops (Songsri et al., 2008). It provides an estimate of genetic advance a breeder can expect from selection applied to a population under certain environment. The higher the heritability estimates, the simpler are the selection procedures (Khan et al., 2008). It has been emphasized that heritability alone is not enough to make sufficient improvement through selection generally in advance generations unless accompanied by substantial amount of genetic advance. The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program (Shukla et al., 2004).

Keeping in view, the genetic studies on wheat were undertaken to estimate heritability and genetic advance of yield traits under drought conditions.

MATERIALS AND METHODS

Field experiments were conducted at the Experimental Farm, Faculty of Agriculture Suez Canal University, Ismailia, Egypt during 2006/2007 and 2007/2008 seasons. The experimental material comprised four varieties/lines of wheat namely, Sakha8, Sids1, line 1 and Line3.

During the crop season, 2006/2007, the following cross combinations were made to raise F1 namely: Line1x Sakha8, Line3x Sakha8, Line1x Sids1, and Line3x Sids3. The experimental design used randomized complete block design (RCBD) with three replicates. The experimental plot consisted of 6 rows, 3 m long and 5 cm apart in which grains were drilled by hand. The normal recommended agricultural practices of wheat production were applied at the proper time.

During the next crop season (2007/2008), two experiments, one under irrigation condition and the other under drought stress condition, were done on October 2007. Irrigation water was supplied by sprinklers to provide two water regimes during plant growth. Control regime was watered every 7-10 day throughout the growing season till harvest time. Drought was created in this rain-free environment by withholding irrigation after 30 days from sowing and giving supplementary irrigations every three weeks during 90 days post-sowing. Water application was monitored via a water meter and the control treatment (well-watered) received 420 mm, while the drought experiment (severe stress) received 140 mm.

However, in crop season (2007/2008), ten guarded plants were randomly selected from each plot, genotype and cross for agronomic traits analysis. Date of heading was recorded as the date when 50% of the shoots had reached this stage. At physiological maturity, plant height was measured from the soil surface to the top of the spike on the main shoot. Spike length of the main spike of the selected plant excluding awn was measured

in centimeters: number of spikes per plant. Number of grains per spike was counted from the spikes used for measuring spike length. The total number of grains recorded was divided by the number of spikes, and the average was computed. For 1000 grain-weight, a single sample of 1000 grains was counted in grams from the yield of the selected plants.

Analyses of variance (ANOVA) were carried out on grain yield and its components, using the software Genstat version 6.1 (Lawes Agricultural Trust, Roth Amsted Experimental Station).

Narrow sense heritability (h^2) was estimated from parent offspring regression according to the method of Anderson et al. (1991).

$$Y = a + b x_i + e_i,$$

Where e_i = error and b = the regression coefficient.

$$b = \frac{\sigma_{xy}}{\sigma_x^2}$$

Where σ_{xy} = covariance of parent-offspring and σ_x^2 = total variance of parental measurements.

Genetic correlation between six traits was determined according to the method of Kwon and Torrie (1964):

$$rg = \frac{Cov_{gij}}{(\sigma_{gi}^2 \times \sigma_{gj}^2)}$$

Cov_{gij} and σ_{gi}^2 are the estimates of covariance and variance for traits i and j .

The genetic advance was calculated according to Allard's (1964), and was estimated from the following formula:

$$GA = i h^2 V_p$$

Where i = 1.76 (10 % selection intensity), V_p : phenotypic variances, h^2 : heritability.

RESULTS AND DISCUSSION

Mean performance

The analysis of variance showed that the mean squares for genotypes were significant for all traits studied. This indicates the existence of a high degree of genetic variability in the material to be exploited in breeding program, and that also reflected the broad ranges observed for each trait (Table 1).

Plant height in wheat has been observed to be affected by drought stress to a considerable extent (Table 2). *Line 1* was superior with respect to plant height (69.4 cm), followed by cross *Line3xSakha8* (66.6 cm) and *Line 3xSids1* (65.9 cm), whereas, *Sids1* and *Sakha 8* recorded the lowest plant height under drought condition. However, the varieties that adapted to the water stress environments are generally short in stature, as compared to the ones which adapted to optimal moisture conditions (Foulkes et al., 2004). The height of the culms, size of the leaves, the distance between the veins and the stomata openings are all affected when they are developing under

Table 1. Significance of mean squares due to different sources of variation for evaluating 4 wheat genotypes and crosses.

Source	df	Plant height	Spike-length	No. spike	No. grains/spike	50% heading date	1000-grain weight
Main plots	2	37.5*	12.04**	0.27ns	2.04ns	2.43 ns	78.2*
Blocks	1	47.7**	1.2ns	13.3*	227.6**	1136.1**	1822.1**
Water- reg	15	396.9**	2.4**	0.72*	64.2**	13.06**	19.7**
genotypes	15	3.3**	0.85*	0.66*	31.7**	27.9**	9.8**
genotypes * Water reg	15						

*and ** denote significance at 0.05 and .01 % level of probability.

Table 2. Mean values of various traits of wheat genotypes and crosses under irrigation and drought conditions.

Genotypes/ crosses	Plant height		Spike-length		No. spike		No. grains/spike		50% heading date		1000-grain weight	
	con	stress	con	stress	con	stress	con	stress	con	stress	con	stress
Line1	72.4a	69.4b	9.7ab	9.3b	2bcdef	2bcdef	17.3abc	17.3bc	95ab	89.5d	25.6ab	23.1de
Line3	59e	58.7e	8c	8c	2.8a	2cde	17.2abcd	16.5cdef	94.3bc	94.5abc	25.5abc	23.3de
Sakha8	45.1f	45.0f	8.1c	7.9c	2.2bcde	1.5f	17bcde	16ef	94.2bc	90.8d	24.2cd	19.6f
Sids1	45.3f	45.1f	9.7ab	9.4ab	1.5ef	1.5ef	14.3g	13.4g	95ab	90.5d	24.3abc	20.4f
Line1xSakha8	67.7c	58.5e	8.3c	9.6ab	2.2bcde	2.2bcde	17.3abc	17.3abc	96.7a	94bc	26.2a	20.5f
Line3xSakha8	72a	66.6d	9.8a	8.3c	2.5abc	1.5f	16.2ef	16.5def	94.8ab	93.7bc	26a	21.5ef
Line1xSids1	70.3b	59e	9.7ab	9.5ab	2.3bcd	2def	17.7ab	14.5g	94.7ab	91.5cd	25.9a	23.1de
Line3xSids1	66.6d	65.9d	9.6ab	9.5ab	2.7ab	1.5ef	17.8a	16f	95ab	94bc	25.9	23de
CV	1.4		4.3		21.3		4.8		1.9		4.8	
LSD 0.05%	2.2		1.0		1.2		1.9		3.5		2.3	

Means not sharing a common letter in a column differ significantly at 0.05% level of probability.

limited water supplies. When wheat plants are deprived of water at vegetative and flowering stages, shorter plants are obtained as a result of low moisture absorption, lower soil absorption, lower soil nutrient uptake, reduced cell size and reduced photosynthesis (Ahmed et al., 2007).

Drought caused reduction in spike length and number of spikes per plants. It was observed *Sakha8* was the lowest genotype for spike length (7.9 cm) and number of spike per plant (1.5) under drought conditions.

The number of grains per spike ranged between 13.4 and 17.3 under drought stress condition (Table 2). It is evident from the results that line1 and cross *Line1x Sakha8* produced maximum number of grains per spike (17.3). *Sids1* produced statistically lower number of grains per spike (13.4) than others under drought stress. However, the decreased number of grains per spike in wheat under stress may be attributed to accelerated apex development and reduced number of leaves at the main stem. At the stage of early emergence, water stress affects the reproductive development, grains initiation and hence final number of grains (Riaz and Chwodhry, 2003).

However, compared to well-watered genotypes, drought caused reductions in days to 50% heading. Therefore, genotypes which flowered and matured earlier may have been favored by partial escape from drought and have an ability to complete their life before get ting dehydrated by high summer temperatures 1000 –grain

weight is vital yield component and with similar weight under drought is more or less stable characters of wheat cultivars. Under drought, this trait may be affected to a greater extent and genotypes showing high 1000-grains weight under irrigated conditions may not be able to produce grains with similar weight (Table 2). This is possible due to the shortage of moisture which forces the grains to complete their formation in relatively lesser time. Based on mean performance, comparison of the four crosses under drought condition (Table 2), the highest value with respect to 1000-grain weight (23.1 g) was obtained from the cross *Line1xSids1*, followed by the cross *Line3xSids1* (23 g). It was noted that these two crosses involving genotypes line 1 and line 3 produce higher 1000 grain weights under drought condition as well. The good mean performance in the two crosses reflected that effective selection for this character is possible in appropriate cross combinations and new genotype may evolve, possessing higher 1000 grain weight along with resistance against drought.

Larger estimates of variation coefficients presented in Table 2 number of spike and number of grain and 1000-grain weight and spike length. The magnitude of variation coefficients might indicate that four genotypes and their progenies had exploitable genetic variability for yield characters under investigation. However, these results partially coincided with earlier findings of Riaz and Chwodhry (2003); this is perhaps due to differences in

Table 3. Genetic correlation among the studied traits under irrigation and drought conditions.

Traits	Treatment	Spike length	No. spike	No. grains/spike	50% heading date	1000 grains-weight
Plant height	control	0.545437	0.194535	0.305937	-0.03853	0.423622
	stress	0.195252	0.425327	0.163353	0.29461	0.858464
Spike length	control		-0.10388	-0.02141	-0.08288	0.627319
	stress		0.071888	-0.24338	-0.14403	0.236863
No. spike	control			0.609886	0.213458	0.074922
	stress			0.065956	0.321663	0.529082
No. grains/spike	control				0.424029	0.12229
	stress				0.40878	0.251132
50% heading date	control					-0.14338
	stress					0.380185

breeding material or variation in environment or interaction.

GENETIC CORRELATION AMONG TRAITS UNDER IRRIGATION AND DROUGHT CONDITIONS

Since the correlations have to be made in the light of their genetic behavior, genotypic correlation values are used for further analysis. Genetic relation of traits may result from pleiotropic effects of a gene, linkage of two genes, chromogema and regimental affiliation or due to the environmental influences (Sgro and Hoffmann, 2004).

The relationship of plant height was positive with spike length, number of spikes, and number of grains per spike and 1000-grain weight under control and drought conditions (Table 3).

Also, number of spike per plant and number of grains per spike had positive relationship with the other yield traits under study. These traits might not be independent in their action and are interlinked likely to bring simultaneous change for other characters. They can be effectively used as selection criteria for wheat yield under drought conditions.

Spike length had negative correlation with number of grains per spike and heading date, whereas it was positive with 1000-grain weight under control and drought conditions.

Moreover, spike length had negative correlation with number of spikes under control but positive under drought condition. Similar genetic behavior, with heading date, had negative correlation with 1000 grain weight under control, whereas positive under drought condition. There is evidence that change in conditions can influence genetic interactions among traits as well as genetic variance in traits themselves. Exposure to drought conditions may induce positive correlation among traits

because the expression of new gene will breakdown negative correlations (Sgro and Hoffmann, 2004).

The genetic correlations in general were high for most of the traits, suggesting a strong inherent association among these traits at the genetic level (Table 3).

HERITABILITY AND GENETIC ADVANCE

It has been emphasized that without genetic advance, the heritability values would not be of practical importance in selection based on phenotypic appearance. So, genetic advance should be considered along with heritability in coherent selection breeding program.

In the present investigation, high heritability values coupled with high genetic advance (Table 4) were recorded for spike length under irrigated and drought condition. This indicated the additive nature of genetic variation was transmitted from the parents to the progeny. Also, this trait can easily be fixed in the genotypes by selection in early generations. These results find support from the earlier studies reported (Riaz and Chwodhry, 2003; Hasssan, 2004). However, spike length is a character of considerable importance, as the larger spike is likely to produce more grains and eventually higher yields per plants. Genotypes retaining larger spikes under moisture stress are likely to be more productive under stress environment. Better heritability values recorded point to the possibility of improvement in this parameter (Ahmed et al., 2007; Songsri et al., 2008).

Moderate heritability was accompanied by high genetic advance for number of spike per plant under control, but it had a low value under drought condition.

High heritability accompanied by low genetic advance for days of 50% heading is indicative of non-additive gene actions' predominance which could be exploited through heterosis breeding. Further explanation by Sardana

Table 4. Estimation of heritability and genetic advance for the studied traits under irrigation and drought conditions.

Traits	Heritability	Genetic advance %	Heritability	Genetic advance %
	Control	Control	Stress	Stress
Plant height	0.29249	6.7	0.1631	3.72
Spike length	0.5961	32.8	0.548	15.16
No. spike/ plant	0.339	21.4	0.12	2.02
No. grains /spike	0.2692	1.07	0.25	1.77
50% heading date	0.6269	0.422	0.75	5.3
1000 grain-weight	0.7379	24.07	0.429	6.17

Sardana et al. (2007), suggested that high heritability may not necessarily lead to increased genetic gain, unless sufficient genetic variability existed in the germplasm.

Low heritability with low genetic advance values was found for plant height and number of grains, indicating slow progress through selection for these traits. The reason for the low heritability for these two components is a result of some variances constituting the environment variance.

It is obvious from Table 4 that the heritability estimate for 1000-grain weight was high, coupled with high genetic advance under control condition, whereas its values were low with genetic advance under drought condition. This differential response could be explained by the fact that this study that used genotypes could have different sets of alleles and possibly different loci are being expressed under different environmental conditions. Collaku (1994) reported in his study that low heritability is as a result of drought stress. Nonetheless, Rana et al. (1999) stated that the 1000 grain weight under arid conditions is significant for the phenotypical selection.

However, the comparison of heritability for all the traits was done under drought stress and irrigated conditions. This indicates that except for heading date, heritability increases with better input condition environment. This may be due to influence of environment on genotypes under drought stress condition. Similarly, it was resulted that heritability for yield traits in faba bean was higher in well-watered treatment than drought stress condition (Link et al., 1999; Toker, 2004).

Conclusion

In general, it is considered that if a character is governed by non-additive gene action, it may give heritability but low genetic advance, whereas if the character is governed by additive gene action, both heritability and genetic advance would be high. In the present study expected genetic advance values were based on narrow sense heritability, which incorporates additive portion of the total phenotypic variance. Thus, narrow sense heritability is more useful for measuring the relative

importance of additive portion of genetic variance that can be transmitted to the offspring. The traits under study which had high heritability and also showed high expected genetic advance could be substantially considered or making selections as these traits were mainly influenced by the major effects of additive gene action. With knowledge of inheritance traits it could introduce specific traits into more widely adapted genotypes and thus meet a goal for developing cultivars better adapted to dry land conditions. But the final test for any wheat variety or areas subjected to limited moisture supply will be found in whether it has ability to yield adequate returns under relatively dry conditions over a period of years.

In conclusion, the genetic parameters discussed here are functions of environmental variability, so estimates may differ in other environment. Based on the high heritability and high genetic advance shown by the different characters, especially, spike length, 1000 grain weight, it could conclude that the determinant genetic effects of the phenotypic expression of these characters are fundamentally of the additive type. For this reason, a high response should be achievable after several selection cycles.

The development of varieties adapted to the arid conditions depends on improvement of potential yield and yield evaluation in different environments. However, the inherent understating of the limits of improving potential yield suggested that long range solution of yield improvement cannot be sustained by improving yield potential alone. Many other environmental variables should be controlled and optimized, so as to minimize the relative effect of genotype and environment interaction/ in addition, the most promising genotypes and cross combinations, *Line1* and *Line3* and; *Line1xSids1* and *Line3xSids1*. These genotypes and traits under study therefore deserve better attention in future breeding programs for evolving better wheat for stress environments.

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