

## HERITABILITY OF YIELD AND SOME YIELD COMPONENTS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES

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### Abstract

Estimation of heritability of yield and yield components for 20 bread wheat genotypes showed low for the characters such as grain yield, spike number per square meter, plant height, grain number per spike, grain weight per spike, 1000 kernel weight and time to heading.

### Introduction

As for many field crops, the studies regarding the new cultivars for wheat are being conducted and the selection continues to be the basic method. The effectiveness of the selections of both yield, which is a quantitative character, and the yield components depend on the genetic variability and heritability. It is necessary to specify the components that establish the phenotypical variation in order to predict the genetic variation and heritability based on the variation.

The simplest way for the prediction of the variance components is the experimentation of a large number of genotypes for two or more years and at two or more locations (Mayo 1980). The purpose of this study was to predict the yield of bread wheat.

### Materials and Method

The experiments were conducted for two consecutive growing years (1999 - 2000 and 2000 - 2001) at the research plots at Pasinler and Ilca locations of Erzurum Province Center in Turkey (39° 55' North, 41° 16' East), with 1680 m and 1812 m above sea levels, respectively. Precipitation during the growing period for 1999 - 2000 and 2000 - 2001 was 238.8 and 364.5 mm in Ilca and 279.8 and 330.9 mm in Pasinler, respectively.

Five soft winter wheat lines (BVDB-1, BVDB-2, BVDB-3, BVDB-4 and BVDB-5), eight red winter wheat lines (BVVK-1, BVVK-2, BVVK-3, BVVK-4, BVVK-5, BVVK-6, BVVK-7 and BVVK-8), two local (TIR and KIRIK) and five commercial cultivars (DOGU-88, PALANDO-KEN087, GEREK-79, KARASU-90 and HAWK) were used as genetic materials in the trials. The experiments were designed in a randomized complete block design with three replications. The plot size was 6 m length with 6 rows and row spacing was 20 cm. Genotypes were sown at the seed rate of 500 seed m<sup>-2</sup> in November and harvested in the first half of August. Mineral fertilizer was applied at the rate of 60 kg N and 60 kg P<sub>2</sub>O<sub>5</sub> per hectare.

Data were recorded on spike number per square meter, plant height, grain number per spike, grain weight per spike, 1000 kernel weight, heading date and grain yield.

The phenotypical variance ( $\sigma^2_P$ ) will be constituted basically by three components. (Poehlman and Sleper 1995):

$$\sigma^2_P = \sigma^2_G + \sigma^2_E + \sigma^2_{GE}$$

Here,  $\sigma_G^2$  = the variance of genetic effects (the genotypical variance),  $\sigma_E^2$  = the environmental variance and  $\sigma_{GE}^2$  = the variance of the genotype  $\times$  environmental interaction effects.

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Two types of genetic degree as explained by Gordon *et al.* (1972) have been predicted in this study, which has been carried out for a period of two years and at two locations:

(a) The heritability with full phenotypical variance definition:

$$h_1^2 = \sigma_G^2 / \sigma_P^2 = \sigma_G^2 / (\sigma_R^2 + \sigma_S^2 + \sigma_Y^2 + \sigma_{SY}^2 + \sigma_G^2 + \sigma_{GY}^2 + \sigma_{GS}^2 + \sigma_{GSY}^2 + \sigma^2)$$

(b) The heritability with limited phenotypical variance definition:

$$h_2^2 = \sigma_G^2 / \sigma_P^2 = \sigma_G^2 / (\sigma_G^2 + \sigma_{GY}^2 + \sigma_{GS}^2 + \sigma_{GSY}^2 + \sigma^2).$$

Here,  $\sigma_G^2$  is the genotypical variance,  $\sigma_P^2$  is the phenotypical variance,  $\sigma_R^2$  is the variance belonging to repetitions,  $\sigma_S^2$  is the variance of the locations,  $\sigma_Y^2$  is the variance of the years,  $\sigma_{SY}^2$  is the location  $\times$  interaction variance,  $\sigma_{GY}^2$  is the genotypical  $\times$  year interaction variance,  $\sigma_{GS}^2$  is the genotypical  $\times$  location variance,  $\sigma_{GSY}^2$  is the genotypical  $\times$  location  $\times$  year interaction variance and  $\sigma^2$  is the error variance.

## Result and Discussion

*The phenotypical variance and the components that constitute the phenotypical variance:* Data on the yield components and the results of the variance analysis related to the yield and yield components as well as the predictions of the variance components ( $\sigma^2$ ,  $\sigma_R^2$ ,  $\sigma_S^2$ ,  $\sigma_Y^2$ ,  $\sigma_{SY}^2$ ,  $\sigma_G^2$ ,  $\sigma_{GY}^2$ ,  $\sigma_{GS}^2$ ,  $\sigma_{GSY}^2$ ,  $\sigma^2$ ) are shown in the Tables 1, 2 and 3, respectively. The F-tests have been used at the significance tests of the components.

**Table 1. Data belong to yield components and the yield by the average of locations, years and genotypes.**

Traits	Range	Mean
Spike number per M <sup>2</sup>	344 - 1613	719
Plant height (cm)	50,0 - 120,0	83,6
Grain number per spike	35,0 - 44,0	40,2
Grain weight per spike (g)	0,75 - 1,39	1,15
1000 kernel weight (g)	33,0 - 43,1	38,3
Time to heading (days)	152 - 168	162
Grain yield per decacre	103 - 756	303

The genotypical ( $\sigma_G^2$ ) variance from among the variance components that have been examined has been specified as the significant component with respect to all components that have been dealt with in the study. This significance has been established at 5 % level of with respect to the spike number per square meters and at 1 % level of with respect to the other components. The statistical significance of the genotypical variance establishes the existence of the genetic variance. This shows that a selection in the direction of increase or decrease can be carried out with respect to the components that have been dealt with in the research.

*The heritability:* The value of the components with negative sign has been accepted as zero in order to prevent the unnecessary reduction of the phenotypical variance value at the prediction of the genetic degree (Allard 1960, İkiz 1976, Göksoy *et al.* 2003).

The heritability with full and limited phenotypical definition that have been taken into consideration in the research are exhibited in Table 4. Since the predictions of the heritability with full phenotypical variance definition are exhaustive, they are more realistic than the other one. Therefore, the priority will be given to this heritability (Turan 1989, Göksoy *et al.* 2003).

As can be seen from the examination of the Table 3, the highest heritability has been achieved at the grain number per spike from among all characters that have been dealt with ( $h^2 = 0.2218$ ). Although low values such as 0.42 (Zaheer and Ahmad 1991) and 0.35 (Fida *et al.* 2001) have been obtained for the grain number per spike in some studies that were conducted previously, Udin *et al.* (1997) obtained middle, Awaad (1996) and Singh *et al.* (1999) got high heritability in the studies they conducted. Collaku (1994) states in his study that he has obtained a low heritability as a result of the drought stress but Rana *et al.* (1999) state in their study that they have conducted under wet and dry conditions that the grain number per spike is a significant property for the phenotypical selection.

**Table 2. The results of analysis of variance of yield and yield-related traits of the bread wheat genotypes.**

Source of variation	D.F	Components						
		Spike no./ M <sup>2</sup>	Plant height	Grain no./spike	Grain wt./spike	1000 ker- nels wt.	Time to heading	Grain yield
Years (Y)	1	3114709.5**	15424.0**	15.5**	0.047*	160.8**	3096.0**	4113139.8**
Locations (L)	1	1458444.5**	53521.0**	3.5	0.929**	41.5**	633.7**	2574874.5**
Y × L	1	512358.0**	340.8**	17.6**	0.157**	2.0	395.2**	750513.5**
Blocs	8	6291.4	64.1*	1.5	0.008	2.3	1.1	261.4
Genotypes (G)	19	27862.6*	337.9**	9.7**	0.027**	8.3**	9.4**	8781.0**
Y × G	19	19044.3	92.1**	2.8**	0.014 *	5.5**	0.9	4927.5**
L × G	19	21368.9	38.9	2.1*	0.008	1.6	1.3	6618.0**
Y × L × G	19	19371.9	111.1**	1.7	0.010	3.8**	0.9	3599.1**
Error	152	14783.6	29.5	1.1	0.008	1.6	0.8	1157.1

The value of the heritability obtained for the 1000 kernel weight was 0.0881. This value can be considered to be low matches with the values obtained by Al-Marakby *et al.* (1994). However, there are other studies, in which middle (Chaturvedi and Gupta 1995) and high (Pawas *et al.* 1989, Awaad 1996, Mehta *et al.* 1997, Udin *et al.* 1997, Fida *et al.* 2001)] values for the heritability regarding the 1000 kernel weight have been obtained. Nonetheless, Rana *et al.* (1999) have stated that the 1000 kernel weight under arid conditions is significant for the phenotypical selection.

The value of the heritability with full phenotypical definition for grain weight per spike has been obtained as 0.049 in the study. Low values of heritability for the grain weight per spike have been obtained in the studies conducted by Pawas *et al.* (1989) and Al-Marakby *et al.* (1994). Contrary to this, Chaturvedi and Gupta (1995) have obtained middle values while Singh *et al.* (1999) have obtained high values for the grain weight per spike in the studies they have

conducted. Rana *et al.* (1999) have stated that the phenotypical selection is a significant property with regard to the grain weight per spike under both wet and arid conditions.

We have obtained a low value for the heritability in the comprehensive meaning with regard to the plant height in our study ( $h^2 = 0.0402$ ). Middle (Mehta *et al.* 1997) and mostly high values had been obtained for the plant height in the studies that have been previously conducted (Pawas *et al.* 1989, Mosaad *et al.* 1990, Mladenov 1993, Chaturvedi and Gupta 1995, Awaad 1996, Dhonde *et al.* 2000, Fida *et al.* 2001).

A low value of heritability corresponding to 0.0207 has been obtained from the time to heading whereas middle (Chaturvedi and Gupta 1995, Mehta *et al.* 1997, Fida *et al.* 2001) and high (Pawas *et al.* 1989, Mosaad *et al.* 1990, Moghaddam *et al.* 1997, Udin *et al.* 1997) values for the heritability related to time to heading were obtained in the studies that were conducted previously. Dhonde *et al.* (2000) have achieved high genetic improvement with high values of heritability.

The heritability for the plant density has been specified as 0.0101. This value is considered to be low matches the results of the study conducted by Pawas *et al.* (1989). Contrary to this, Dhonde *et al.* (2000) have specified high heritability with regard to the plant density and Rana *et al.* (1999) have stated that the heritability for the density was high under both wet and arid conditions.

The value of the heritability related to the grain yield that can be considered to be a function of the components dealt with in the study has also been found to be low ( $h^2 = 0.0012$ ). The values obtained in the other studies for the yield that is a quantitative character were generally middle (Moghaddam *et al.* 1997) and low values (Pawas *et al.* 1989, Zaheer and Ahmad 1991, Fida *et al.* 2001).

An important issue that draws the attention in this study is that there is large difference between genetic degrees with limited and full phenotypical variance definitions particularly for the plant height and the time to heading. The reason for the low heritability in the limited meaning for these two components is a result of some variances constituting the environmental variance. The high variance for the years and locations with regard to the plant height and the high variance for the time to heading with regard to the years  $\times$  location interaction and the increase in the value of the phenotypical variance constitute the reason for the very low value of heritability in the comprehensive meaning (with phenotypical variance definition).

All traits observed in the study are quantitative characters. Those are called complex characters also but because they are controlled by many genes. The variation within quantitative characters is due to its complex inheritance and to the influence of the environment (Fehr 1978). The genotype  $\times$  environment ( $G \times E$ ) variance components were the most important source of phenotypic variance for all traits observed. Thus, the heritability estimates for all characters found were low levels.

As a results, the low heritabilities and high  $G \times E$  interactions indicated that yield and yield components are inherited quantitatively in wheat. Therefore, pure line selection for improved yield and yield components has a low achievement chance. Using family selection method one may increase success in breeding for improvement in the seed yield.

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