Heritability of Drought Tolerance in Wheat

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Abstract: Drought tolerance of wheat (*Triticum aestivum* L.) is related to many morphological and physiological traits that are under strong environmental influences, often their genetic control is confounded by environmental stress. The objectives of this study are to estimate narrow-sense heritability for grain yield and yield components under naturally water deficient conditions and to provide selection criteria for drought tolerance in early generations. In this work 60 families derived from three wheat populations in the F2 generation were studied. The experiment was conducted under the effect of naturally drought stress. The Restricted Maximum Likelihood (REML) method was used to estimate genetic variance components. Kernel per spike had the lowest heritability ($h2 = 0.23$). The highest heritability estimates were found for heading date (0.58), 10000-kernel weight (0.45) and plant height (0.43). Strong genetic correlations were observed between grain yield and heading date ($r = 0.89$) andbetween grain yield and 1000-kernel weight ($r = 0.53$). Selection for a relatively highly heritable trait, such as heading date would be an effective way to improve drought tolerance in early generations, as grain yield has a low heritability.

Key words: *Triticum dicoccoides* · Droughttolerance · heritability

INTRODUCTION

Drought imposes major limits on crop production and food security in many countries. In Iran, drought constraints on yields have increased in importance as climate change leads to increasingly hotter and drier summers. As a result crop growth rate is reduced and yield is lowered. In spite of greet difficulties in breeding for high yield under drought stress genetic improvement for yield is possible and has been accomplished in many drought prone areas of the world [1]. However, it still needs further improvement. Thus, it is desirable to screen the genotypes under stress conditions to identify better adaptive ones to utilize in future breeding programs. Genotypic variation for tolerance to stress conditions in wheat has been reported in several studies [2-7]. The objectives of this study are to estimate heritability of drought tolerance for grain yield and other quantitative traits of wheat in early generations and to provide selection criteria for drought tolerance in wheat breeding programs.

MATERIALS AND METHODS

The genetic material consisted of 60 families derived from four related segregation F_2 populations: Population 1: TA1055/Chinese Spring; population 2: TA1150/Chinese Spring; population 3: TA1131/Chinese Spring and Population 4: TA1395/Chinese Spring. *T. dicoccoides* accessions are tolerance to drought conditions and Chinese Spring was included in crosses as a sensitive variety to drought conditions. In 2003, seed from all four crosses was separately planted 7.5 cm pots. Two weeks after germination, plants were transplanted in the field at Agricultural Faculty of Lorestan University, Khorramabad, Iran. Plots were 5.0 × 2.0m. Plants that had disease incidence were eliminated from the study. About 120 to 150 plants were grown for each population. From these, 20 plants per population were randomly chosen and hand harvested separately to produce $F_{2:3}$ families. In total, 60 plants were chosen from the four populations.

The 60 families in 2004-2005 were $F_{2:3}$, i.e., F_2-derived F_3 families, as no selection was applied to the base population of 120 to 150 F_2 plants per population. In the

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2005-2006 season, the 60 families were $F_{2.4}$. Variation among F_2-derived lines possesses the same amount of additive variance as subsequent generations, regardless of generation (i.e., F_3 and F_4) when the measurements were taken, since no selection was applied during 3 years of the study [8,9]. The 60 families from the four populations were studied in a Randomized Complete Block Design with three replications under the effect of naturally drought stress. Plots consisted of three 22-cm-row spacing × one meter. Soil type was silt loam.

Plant measurements were taken on the mid-row of each plot. Measurements for height andkernel number were taken on three randomly selected plants in plants in each plot. Heading date was recorded as number of days from planting to the date when the main spike of each plant was fully emerged from the flag leaf. Three to four readings were taken for each plant andthe mean was used for the data analysis. Measurements for height and kernel number were taken at harvest time. Tiller number was measured by counting the number of heads in a 20-cm-row length. Kernel weight was determined from a 100 seed sample for each plot. Grain yield was measured by hand harvesting and threshing the mid-row in each plot.

Traditional mating designs used to estimate genetic variance components are applicable only when parental components are unrelated, but as in our study families from different population have a degree of relationship by using REML to estimate genetic variance components in a mixed model approach [10,7] it is possible to account for the relationship among derived families. The mixed model [5] applied to estimate genetic variance components from 60 families studied in three years (environments), was:

$$y = X\beta + Z_1\alpha + Z_2\gamma + Z_3\delta + \varepsilon$$

where y is the vector of n observations for each family; X and β are the design matrix and the vector of trial effects (including environments and replications within environments), respectively; β is the vector of fixed effects b, where b = 1×r, and $1 \le I \le 3$ is the number of environments *and* $1 \le r \le 3$ is the number of replications within environments; Z_1 and α are design matrix and vector of additive effects α ($1 \le d \le 4$), where d is number of populations; Z_2 and γ are design matrix and vector of

dominance effects, $d(1 \le d \le 4)$, where d is number of populations; Z_3 and δ are design matrix and vector of genotype × environment (GE) interaction effects g as a result of cross combination of entries with environments ($1 \le g \le 225$); and å is the vector of experimental error effects.

The following assumptions have been made for the random effects [7]: the additive effects are normally distributed (N), with mean 0 and variance σ^2_A, dominance effects are N (0, σ^2_D), GE interaction effects are independently identically distributed (iid) N(0, σ^2_{GE}) anderrors are iid N(0, $\sigma^2_å$). Random effects have the following variance-covariance matrix:

$$Var\begin{pmatrix} \alpha \\ \gamma \\ \delta \\ \varepsilon \end{pmatrix} = \begin{pmatrix} A\sigma^2_A & 0 & 0 & 0 \\ 0 & D\sigma^2_D & 0 & 0 \\ 0 & 0 & I\sigma^2_{GE} & 0 \\ 0 & 0 & 0 & I\sigma^2_\varepsilon \end{pmatrix}$$

The additive matrix A has dimensions 60 × 60 with diagonal elements equal to 1 and off-diagonal elements equal to 2 times coancestry coefficient ($2r_{xy}$) between 60 families in the study [11]. They have a value of between full-sib families, i.e., between families 1 to 15, 16 to 30, 31 to 45 and 46 to 60 and smaller values as the relationship between families becomes weaker. Elements of the covariance matrix D represent double coancestry coefficients (u). Diagonal elements are 0.25 as double coancestry coefficients among full-sib families, while off-diagonal elements are 0 or greater than 0, depending on the relationship among different groups of families. Elements of matrix A and D were obtained by using "Proc Inbreeding of SAS" and then appended in the "Proc Mixed of SAS" to estimate additive and dominance variance based on the mixed model approach [5]. I is the identity matrix. The vector of observations y is assumed to be multivariate normal with mean E(y) = Xβ andvariance-covariance Var(y) = $Z_1\hat{R}_1Z'_1 + Z_2\hat{R}_2Z'_2 + Z_3\hat{R}_3Z'_3 + R$ [12]. The estimates of α, β, γ were described by Collaku and Harrison [5] and δ can be obtained by solving the following system of mixed model equations:

$$\begin{pmatrix} X'\hat{R}^{-1}X & X'\hat{R}^{-1}Z_1 & X'\hat{R}^{-1}Z_2 & X'\hat{R}^{-1}Z_3 \\ Z'_1\hat{R}^{-1}X & Z'_1\hat{R}^{-1}Z_1 + G_1^{-1} & Z'_1\hat{R}^{-1}Z_2 & Z'_1\hat{R}^{-1}Z_3 \\ Z'_2\hat{R}^{-1}X & Z'_2\hat{R}^{-1}Z_1 & Z'_2\hat{R}^{-1}Z_2 + G_2^{-1} & Z'_2\hat{R}^{-1}Z_3 \\ Z'_3\hat{R}^{-1}X & Z'_3\hat{R}^{-1}Z_1 & Z'_3\hat{R}^{-1}Z_2 & Z'_3\hat{R}^{-1}Z_3 + G_3^{-1} \end{pmatrix} \begin{pmatrix} \hat{\beta} \\ \hat{\alpha} \\ \hat{\gamma} \\ \hat{\delta} \end{pmatrix} = \begin{pmatrix} X'\hat{R}^{-1}y \\ Z'_1\hat{R}^{-1}y \\ Z'_2\hat{R}^{-1}y \\ Z'_3\hat{R}^{-1}y \end{pmatrix}$$

The REML method was used to estimate additive and dominance genetics variance components and non-genetic variance components.

Narrow sense heritability [13] was estimated on a plot basis, as:

$$h^2 = \hat{\sigma}_A^2 / \hat{\sigma}_P^2$$

where: $\hat{\sigma}_P^2 = \left(\hat{\sigma}_A^2 + \hat{\sigma}_D^2 + \hat{\sigma}_{GE}^2/l + \hat{\sigma}_\varepsilon^2/rl\right)$, $r = 3$ is the number of replications and $l = 3$ is the number of years. Standard error of heritability was calculated according to Knapp *et al.* [14].
Genetic correlation coefficient was calculated as:

$$r = \frac{Cov_{XY}}{\sqrt{\hat{\sigma}_{A(X)}^2 \hat{\sigma}_{A(Y)}^2}}$$

Where Cov_{xy} is the additive covariance between two traits X and Y.

RESULTS AND DISCUSSION

The populations under present study were in the F_2 generation, therefore the presence of both additive and dominance variance for all characters studies was anticipated. The absolute value of the additive variance component was greater than the dominance variance component for heading date, 1000-kernel weight and plant height (Table 1). For some other characters, in particular for grain yield, kernel per spike and tiller number the additive variance component was considerably smaller than the dominance components, showing that these traits are under a stronger control of dominance effects.

Among the traits studied, the highest heritability estimate of 0.58 and 0.45 were found for heading date and 1000-kernel weight, respectively (Table 2). However, heritability for heading date had a high standard error (0.29), however, the standard error for 1000-kernel weight heritability was low (0.07). These findings are in accordance with those of Ansari *et al.* [15] and Gupta and Verma [16]. Heritability of kernel per spike (0.21) was the lowest among the traits studies. Previously, kernel number has been found to be highly heritable [6,7]. The low heritability estimates reported in this study were probably attributed to drought stress.

Strong genetic correlations were observed between grain yield and heading date ($r = 0.89$) and between grain yield and 1000-kernel weight ($r = 0.53$) (Table 3). Heading

Table 1: REML estimates of additive and dominance variance from 60 families derived under drought conditions

Trait	$\hat{\sigma}_A^2$	SE of $\hat{\sigma}_A^2$	$\hat{\sigma}_D^2$	$\hat{\sigma}_{GE}^2$	$\hat{\sigma}_\varepsilon^2$
Grain yield	150.16	8.21	224.71	496.51	127.16
Heading date	46.27	0.25	21.3	32.14	16.23
Plant height	5.06	0.42	2.4	10.9	4.99
1000-Kernel weight	0.31	0.09	0.27	0.25	0.19
Kernel per spike	7.32	0.73	22.55	15.05	4.34
Tiller number	5.11	0.68	6.98	6.07	12.76

Table 2: Heritability estimates for grain yield, heading date, plant height,1000- kernel weight kernel per spike and tiller number of 60 soft winter wheat families under drought stress

Traits	h^2	SE of h^2
Grain yield	0.27	0.38
Heading date	0.58	0.29
Plant height	0.43	0.44
1000-Kernel weight	0.45	0.07
Kernel per spike	0.21	0.09
Tiller number	0.23	0.31

Table 3: Genetic correlation among grain yield and other traits from 60 families under drought stress

Trait	Plant height	1000-Kernel weight	Kernel per spike	Tiller number	Grain yield
Heading date	0.13	0.33*	0.41**	0.34*	0.89**
Plant height		0.37**	0.38**	0.13	0.06
1000-Kernel weight			0.39**	0.46**	0.53**
Kernel per spike				0.17	0.31*
Tiller number					0.49**

* Significant at P = 0.05   ** Significant at P = 0.01

date had a significant genetic correlation with most of the traits, showing that selecting for this trait would notably improve other important traits associated with grain yield. Genetic correlation among plant height and other traits were generally low. Although plant height has a high heritability, it seems to have little effect on grain yield or other traits. Selection for a relatively highly heritable trait, such as heading date and 1000-kernel weight would be an effective way to improve drought tolerance in early generations, as grain yield has a low heritability.

Heritability of grain yield under drought conditions was low. Other traits with high heritability and strong correlation with grain yield, such as heading date, represent useful selection alternatives for introducing drought tolerance in early generations, in other hand selecting in early generations for grain yield or kernel number would not be as effective as selecting for traits as heading date and 1000-kernel weight.

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