The Effect of Drought Stress at the Inheritance of Grain Yield in Wheat Bread

[1]Bahram Mirzamasoumzadeh, [2]Ali Nazirzadeh and [1]Mehran Salaami

[1]Department of Plant Breeding and Agronomy, Ardabil Branch, Islamic Azad University, Ardabil, Iran
[2]Department of Plant Breeding and Agronomy, Kaleybar Branch, Islamic Azad University, Kaleybar, Iran

Abstract: To evaluating the effect of drought stress on Inheritance of grain yield in bread wheat, an experiment in Randomized complete block design at 2010-2011 cropping years was carried out in Ardabil area. To measure the agronomic traits, three plants in each plot were randomly identified and measured and then as the mean of five plants per plot were recorded. Was observed that the mean square rows for The Wr-Vr were not significant. The Wr slope of the regression line on the Vr was a significant difference in stress conditions at 0.01 percentage level. Based on the parental origin of the coordinates Wr on Vr egression can be concluded that in non stress condition, genotypes Gaspard, Saison, Alvand and MV-17 of recessive alleles and genotypes Fangak and Sabalan of alleles are dominant. In stress condition Genotypes Gascoigne and Sabalan had Recessive alleles and Fangak, Pishtaz and Alvand had dominant alleles.

Key words: Bread wheat · Drought stress · Yield · Allele

INTRODUCTION

Wheat production in Mediterranean region is often limited by sub-optimal moisture conditions [1]. Visible syndromes of plant exposure to drought in the vegetative phase are leaf wilting, a decrease in plant height, number and area of leaves and delay in accuracy of buds and flowers [2]. Drought tolerance consists of ability of crop to growth and production under water deficit conditions. A long term drought stress effects on plant metabolic reactions associates with, plant growth stage, water storage capacity of soil and physiological aspects of plant. Drought tolerance in crop plants is different from wild plants. In case crop plant encounters severe water deficit, it dies or seriously loses yield while in wild plants their surviving under this conditions but no yield loss, is taken into consideration. However, because of water deficit in most arid regions, crop plants resistance against drought, has always been of great importance and has taken into account as one of the breeding factors [3]. Achieving a genetic increase in yield under these environments has been recognized to be a difficult challenge for plant breeders while progress in yield grain has been much higher in favorable environments [4]. Thus, drought indices which provide a measure of drought based on yield loss under drought conditions in comparison to normal conditions have been used for screening drought-tolerant genotypes [5]. With regard to these features and increasingly demand for durum

wheat to extend pasta industry in the country, such researchers are important. Drought is one the most important limiting factors of crop plants such as wheat in the world and Iran. This is of great importance especially in the arid and semi arid regions [6]. Over the one fourth of the earth includes dry areas and it has been cleared that nearly one third of the cultivated lands suffer from water deficit [7]. This expriment was done to evaluating the effect of drought stress on wheat yield inheritance.

MATERIALS AND METHODS

To evaluating the effect of drought stress on Inheritance of grain yield in bread wheat, an experiment in Randomized complete block design at 2010-2011 cropping years was carried out in Ardabil area. To measure the agronomic traits, three plants in each plot were randomly identified and measured and then as the mean of five plants per plot were recorded.

Diallel cross progeny from 9 × 9 one-way, including 36 genotypes F1 and 9 parent (Sabalan, Azar 2, Fangkak, Pishtaz, Mv-17, Gascogine, Gaspard, Alvand and Saisonz) used. The operations of land preparation (plowing and disk) on the third row of each cultivar in each plot to grow from 20 cm to 1 m over the planting area of each plot 0.6 square meters. Using genetic components of variance and covariance data for F1 and F2 generations as described in Table 1 was calculated.

Corresponding Author: Bahram Mirzamasoumzadeh, Department of Plant Breeding and Agronomy,
Ardabil Branch, Islamic Azad University, Ardabil, Iran.

According to Table 3 Folmoles, Standard deviation for Genetic components were measured.

Data were analyzed using SPSS16 for analysis of variance and Duncan's multiple range tests was employed for the mean comparisons.

RESULTS AND DISCUSSION

Results of analysis of variance showed non-significant diferance for Wr-Vr (Table 1). But the slope of the regression line of Wr on Vr in stress condition was significant at 0.01 percantage level (Table 2). This indicates that under drought stress model for the inheritance of this incremental partially dominant trait will suffice. In study Tahmasebi *et al*. [8] reported that in non stress condition the additive - dominance was not enough to justify this trait. Significant incremental variance (component a) (Table 3) and component D (Table 4) Indicate the presence of additive effects in controlling this attribute. Dominance genetic effects (changes to source b) were significant. Indicates that the gene controlling this trait is dominant. B1 component of this trait was not significant (Table 3). B2 of the trait number of grains per spike was not statistically significant. Represents that there is symmetry in the distribution of alleles among the parents [9]. Distribution of positive and negative alleles in the parents (H2/4H1) was also performed. The value of this attribute in a minor less than 0.25 respectively.
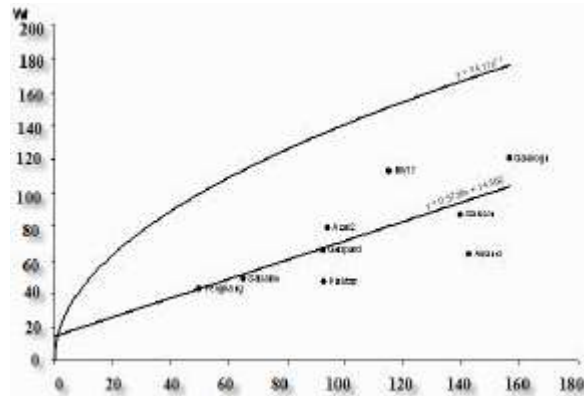

Fig. 1: Regression line of Wr on Vr for Number of seeds in spike in non- stress condition

Indicates that there is slight asymmetry in the distribution of positive and negative alleles for this trait is between the parents. B3 was significant for a number of grains per spike. Genetic component F in the number of grains per spike (only in non-stress conditions) was positive and significant, reflecting the greater frequency dominant alleles among the parents. H2 of the two conditions was significant at 0.01 percentage level. The average degree of dominance in the number of grains per spike was greater than 1 and was controlled by the dominant. In study Mather and Jinks [10], the effects of dominance were controlled by the number of grains per spike. Arshad and Chavdori [11] for the number of grains

Table 1: The formula for calculating Diallel genetic components in generation F1.

Concept	Genetic components
Additive genetic variance	$D = Vp - E$
Dominance variance is not correct	$H_1 = Vp + 4\bar{V}_r - 4\bar{W}_r - \dfrac{5n-4}{n}E$
Dominance variance corrected	$H_2 = 4\bar{V}_r - 4V_{\bar{r}} - \dfrac{4(n-1)}{n}E$
The average covariance between the additive and dominance effects	$F = 2Vp - 4\bar{W}_r - \dfrac{2(n-2)}{n}E$
Dominance effects (sum of all locations where the gene is heterozygous in all).	$h^2 = 4(Ml_1 - Ml_0)^2 - \dfrac{4(n^2-1)}{n^3}E$
Environmental variance of the mean square error divided by the number of iterations is achieved.	$E = \dfrac{MSE}{r}$

Table 2: The standard deviation of the genetic components for the F1 generation in a Diallel crosses

Genetic components	Standard deviation
D	$\sqrt{\dfrac{(n^5 + n^4)}{n^5}}\,S$
H_1	$\sqrt{\dfrac{(n^5 + 41n^4 - 12n^3 + 4n^2)}{n^5}}\,S$
H_2	$\sqrt{\dfrac{(36n^4)}{n^5}}\,S$
h^2	$\sqrt{\dfrac{(16n^4 + 16n^2 - 32n + 16)}{n^5}}\,S$
F	$\sqrt{\dfrac{(4n^5 + 20n^4 - 16n^3 + 16n^2)}{n^5}}\,S$
E	$\sqrt{\dfrac{n^4}{n^5}}\,S$

Table 5: Results of analysis of variance for Wr-Vr

		Number of seeds in spike	
SOV	df	Stress	Non-stress
Rep	1	651.3ns	8417.7 ns
Row	8	737.4 ns	1230.4 ns
Error	8	960.2	2053.6

Ns: Non-significant

Table 6: The incremental test - dominance of the regression slope for Number of seeds in spike

		Number of seeds in spike	
	H0	Stress	Non-stress
b (Wr/Vr)	b=1	0.523±0.147*	0.573±0.203 ns
	b=0	.523±0.147**	0.573±0.203 *

** And * significant at the 0.01 and 0.05 levels, respectively

Table 7: Diallel analysis of variance for the trait number of grains per spike

		Number of seeds in spike	
SOV	df	Stress	Non-stress
Rep	1	55.26ns	146.6ns
A	8	119.15**	340.19**
B	36	134.15**	187.89**
B1	1	152.41*	197.77ns
B2	8	28.73ns	56.43ns
B3	27	164.7**	226.48**
error	77	23.55	53.94

** And * significant at the 0.01 and 0.05 levels, respectively

Table 8: Genetic parameters for agronomic traits in Diallel cross under drought stress and stress-free conditions

Parameter	Number of seeds in spike	
	Stress	Non-stress
D	59.6±3.88**	172.1±4.41**
H_1	154.5±8.57**	198.51±9.74**
H_2	134.88±7.37**	180.8±8.37**
F	1.36±9.06ns	57.8±10.3**
h^2	31.16±4.93**	37.3±5.6**
E	11.77±1.23**	26.97±1.39**
Averag d	1.61	1.07
$H_2/4H_1$	0.218	0.227
KD/KR	1.01	1.37
Hn	0.461	0.477
Hb	0.860	0.805
rYr (Wr+Vr)	0.599**	0.234ns
$\bar{F}_1 - \bar{P}$ %	3.25	-3.7
A	-3.19	14.39

** And * significant at the 0.01 and 0.05 levels, respectively

per spike in non-stress conditions and to stress the dominance incomplete dominance effects were estimated. The average degree of dominance of this trait within the origin of the negative regression line Wr on Vr As can be seen (Fig 1). The total proportion of dominant and recessive alleles in parents (KD / KR) on the number of grains per spike in non-stress conditions was greater than 1. The marker allele frequency is dominant in controlling this trait. The larger the value of a positive value for the ratio F was confirmed. The heritability of grain per spike of 0.461 and 0.477 was different.

Average correlation coefficients between parents and the dominance rVr(Wr+Vr) Number of grains per spike was not significant. This means that there is a relationship between dominance and trait desirability. Sameena *et al*. [12] Dominant genes in trait number of grains per spike were increased. The amount of heterosis in this trait was also low. Based on the parental origin of the coordinates Wr on Vr egression can be concluded that in non stress condition, genotypes Gaspard, Saison, Alvand and MV-17 of recessive alleles and genotypes Fangak and Sabalan of alleles are dominant. In stress condition Genotypes Gascoigne and Sabalan had Recessive alleles and Fangak, Pishtaz and Alvand had dominant alleles.

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