Genetic analysis of traits related to grain yield in wheat under drought stress condition by generation mean analysis

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ABSTRACT

In order to study the inheritance of some traits related to grain yield in drought stress conditions in bread wheat (*Triticum aestivum* L.), F_2, F_3 and F_4 generations derived from a Kharchia (tolerant) × Gaspard (susceptible) cross and their parents were used separately in a complete randomized block design with two replications. Stem length, biological yield, main spike straw weight, total spike straw weight, grain yield as well as harvest index were measured in different generations. The results of the analysis of variance showed that generations mean squares were significant for all traits. Therefore, the generations mean analysis was performed for all of the traits. The model of four-parameter including m, [d], [h] and [i] was significantly fitted for the majority of the traits. Although both types of additive and dominance effects were involved in the control of the studied traits but dominant component was more effective than the additive one. Dominance effects and additive × additive epistasis were more important than additive effects and other epistasis components for most traits. Regarding the existence of additive and non-additive effects in controlling studied traits, the recurrent selection followed by pedigree breeding can prove useful in improving drought tolerance in bread wheat.

Keyword: Bread wheat, Gene action, Generation mean analysis, Quantitative traits.

INTRODUCTION

Nowadays in most countries wheat is the major staple food for people, so that it provides more than 20 percent of the needed energy of the population in the world (Anderson and Kempthorns, 1965; Bushuk and Rasper, 1994). Selection of the appropriate breeding method for better exploiting the genetic potential of different traits depends on the type of genes controlling the trait and its inheritance (Akhtar and Chowdhry, 2006). In most crop plants the type of the gene and the genetic effects are studied (Lamkey and Lee, 2005). Increasing yield is the most important aim in any breeding program (Kang, 1994). To determine the genetic parameters, one of the best methods is the generations mean analysis (Kearsey and Pooni, 1998; Singh and Singh, 1992). Generation mean analysis is a simple and useful technique to estimate gene effects such as additive × additive (aa), dominance × dominance (dd) and additive × dominance (ad) effects (Singh and Singh, 1992). Akhtar and Chowdhry (2006) using the generations mean analysis (F_2, F_1, BC_1, BC_2 generations) in wheat indicated that the epistatic effect has a major role in controlling the plant height and the number of grains per spike. Novoselovic *et al.* (2004) stated that, dominance and epistatic effects for grain yield in wheat were more important than additive effects. In another study, Prakash *et al.* (2006) found that the dominance effect to additive effects, dominance × dominance and additive × additive interaction effects had the important role in inheritance of traits. Gamble and Burke (1984) using generation mean analysis and a joint scaling test stud-

ied agronomic traits such as harvest index and concluded that the epistatic action was involved in the inheritance of these traits. Ahmadi *et al.* (2007) reported that the dominance effect had a major role in the heritability of grain yield and plant weight. Selection of the best breeding method and its success depends on the amount of knowledge about genetic control in desired traits and its inheritance (Dixit, 1998). Information about gene action is important in a breeding program. The aim of this study was to identify gene effects on inheritance of quantitative traits through the generation mean analysis. Other objectives of this study were to estimate variance components of generations, broad-sense (h^2_{bs}) and narrow-sense (h^2_{ns}) heritabilities.

MATERIALS AND METHODS

In order to study the inheritance of some traits related to grain yield in drought stress conditions in bread wheat (*Triticume aestivum* L.), different generations including: F_2, F_3, F_4 derived from the Kharchia (tolerant) × Gaspard (susceptible) cross along with their parents were grown in the research field of the International Center for Science, High Technology & Environmental Sciences-Kerman, Iran during the December 2010. The experimental layout was a complete randomized block design with two replications. In each replication there were two rows for the parent, 13 rows for each of the F_2, 150 rows for each F_3 and 100 rows for each F_4 generation with an average of 10 seeds in each row. The distance between rows was 50 cm. All necessary cares were under consideration during the growth period. Stem length, biological yield, main spike straw weight, total spike straw weight, grain yield and harvest index were measured for different generations. First analysis of variance for all traits was done; then generations mean analysis was used according to the Mather and Jinks (1982) method. In this method, the overall average for each trait is shown as follows:

Y = m + α[d] + β[h] + α² [i] + 2αβ[j] + β²[l]

In this formula:

Y: The mean of a generation, m: Average of all generations in a cross, [d]: sum of additive effect, [h]: sum of dominance effect, [i]: sum of interaction effect between additive effects , [j]: sum of interaction effect between the additive and dominance effects, [l]: sum of interaction effect between the effects of dominance and α, β, α², 2αβ, β² are the coefficients of genetic parameters.

The mean values, standard errors and variances of different generations were subjected to weight least squares analysis using the joint scaling test (Mather and Jinks, 1982). Finally, all five generations with two, three, four and five parameters were tested for the most appropriate model that can describe the observed averages. This model was evaluated by chi-square test for the averages. All statistical computations were performed by Minitab software (Mather and Jinks, 1982). The variance values of F_2 plants (V_{F2}), the F_3 family mean variance ($V_{\overline{F3}}$), The F_3 family variance mean ($\overline{V}_{F3}$), environmental variance 1 (E_1), environmental variance 2 (E_2) were estimated as described by Hallauer and Miranda (1981) using the following equations:

$$V_{F_2} = \frac{1}{2}D + \frac{1}{4}H + E_1 \qquad V_{\bar{F}_3} = \frac{1}{2}D + \frac{1}{16}H + E_2$$

$$\overline{V}_{F3} = \frac{1}{4}D + \frac{1}{8}H + E_1$$

Broad sense heritability (h^2_{bs}) , narrow-sense heritability (h^2_{ns}) and degree of dominance were calculated as follows (Mahmud and Kramer,1951):

$$h^2_{bs} = \frac{V_{F_2} - \sqrt{V_{P_1} \times V_{P_2}}}{V_{F_2}} \qquad h^2_{ns} = \frac{\frac{1}{2}D}{V_{F_2}} \qquad \frac{h}{d}$$

RESULTS AND DISCUSSION

Analysis of variance for all the traits showed a significant difference among generations (Table 1). Therefore, the significant difference between generations makes generation mean analysis and surveys of their inheritance possible. The mean values and their standard errors for the analyzed traits were presented in Table 2.

Generation mean analysis results for all traits were presented in Table 3. The results of the generation mean analysis showed that the additive dominance model was not enough to justify all traits. The four parameter model containing m, [d], [h] and [i] for stem length, grain yield, main spike straw weight and total spike straw weight was chosen as the best model. Additive, dominance and additive × additive epistasis effects were involved in controlling the inheritance of

Table 1: Mean squares of traits in Gaspard × Kharchia cross.

Source of variation	DF	Stem length	Biological yield	Main spike straw weight	Total spike straw weight	Grain yield	Harvest index
Replication	1	636.209*	3.01^{ns}	0.0212**	0.412^{ns}	0.791*	32.616^{ns}
Generation	4	352.87^{ns}	8.861*	0.0088*	1.481**	0.333*	32.404*
Error	4	76.506	1.2	0.00074	0.0658	0.0499	5.01

^{ns}, *, **: non-significant, significant at %5 and %1 probabilities level, respectivly.

df: degree of freedom

Table 2: Means and standard deviations for quantitative traits.

Generations	Stem length (cm)	Biological yield (g)	Main spike straw weight (g)	Total spike straw weight (g)	Grain yield (g)	Harvest index
P1	24.3 ± 1.168	7.41 ± 0.77	0.21 ± 0.05	0.65 ± 0.179	0.87 ± 0.12	14.73 ± 3.22
P2	29.48 ± 1.9	13.5 ± 2.03	0.41 ± 0.07	1.2 ± 0.259	1.89 ± 0.27	19.43 ± 3.9
F2	26.22 ± 0.896	8.03 ± 0.67	0.6 ± 0.024	1.98 ± 0.19	1.25 ± 0.162	11.5 ± 0.961
F3	29.34 ± 0.411	10.5 ± 0.36	0.51 ± 0.03	2.52 ± 0.097	1.58 ± 0.08	13.2 ± 0.401
F4	30.045 ± 0.47	10.37 ± 0.412	0.56 ± 0.03	2.67 ± 0.12	1.7 ± 0.102	14.13 ± 0.473

Table 3: The estimates of gene effects on the quantitative traits.

Traits	Mean (m)	Additive [d]	Dominance [h]	Additive × Additive [i]	Dominance × Dominance [l]	X^2
Stem length	31.54 ± 0.668**	2.58 ± 1.117*	-4.79 ± 1.32**	-4.619 ± 1.5**	-	1.234
Biological yield	10.59 ± 0.497**	2.71 ± 0.814**	-3.65 ± 1.91*	-	-	0.519
Main spike straw weight	0.617 ± 0.033**	0.046 ± 0.045^{ns}	-0.209 ± 0.048**	-0.257 ± 0.05**	-	0.044
Total spike straw weight	2.94 ± 0.161**	0.277 ± 0.157*	-0.911 ± 0. 3**	-2.012 ± 0.22**	-	0.323
Grain yield	2.53 ± 0.054**	-0.71 ± 0.177**	-0.4 0 ± 0.121*	-2.46 ± 0.348**	-	0.921
Harvest index	14.29 ± 0.148**	1.81 ± 0.485^{ns}	1.12 ± 0.429**	-	-	1.23

stem length. The results showed that dominance effect was larger than the additive effect. For biological yield, dominance effect was higher than the additive effect which shows the importance of dominance effect in the inheritance of this trait. Degree of dominance for the biological yield was estimated to be over dominance. These results are in accordance with reports published by other authors (e.g Ahmadi *et al.*, 2007). Studies of Munir *et al.* (2002) has shown the role of gene epista-sis effects in controlling plant weight in wheat. In the inheritance of grain yield, additive and dominance ef-fects were significant and additive effects were higher

Table 4: Estimates of variance components for quantitative traits.

Traits	F_2 generation variance (V_{F2})	F_3 generation means variance $(V_{\bar{F3}})$	F_3 generation variances mean $(\bar{V}_{F3})$	Additive variance (D)	Dominance variance (H)	Homogeneous entries generations mean variance (E_1)	Homogneous entries generations variance mean (E_2)
Stem length	84.78	5.919	11.506	110.232	55.08	29.66	52.406
Biological yield	64.86	1.91	7.075	75.98	35.236	26.87	37.097
Main spike straw weight	0.345	0.048	0.286	0.614	3.314	0.038	0.217
Total spike straw weight	2.526	0.134	1.942	3.842	20.003	0.604	2.85
Grain yield	1.65	0.206	1.236	2.356	12.089	0.472	1.748
Harvest index	225.959	2.016	1089.071	210.272	863.112	120.82	43.275

Table 5: Broad-sense (h^2_{bs}) and narrow-sense (h^2_{ns}) heritability and the degrees of dominance.

Traits	Broad-sense heritability (h^2_{bs})	Narrow-sense heritability (h^2_{ns})	Degree of dominance h/d
Stem length	0.71	0.65	-1.85
Biological yield	0.73	0.71	-1.34
Main spike straw weight	0.98	0.88	-4.54
Total spike straw weight	0.8	0.76	-3.28
Grain yield	0.81	0.71	0.56
Harvest index	0.5	0.46	0.618

than dominance effects. Therefore, breeding this trait can be effective with the early generation selection. Estimates of dominance degree showed the partial dominance effect in the control of grain yield. The results of Ahmadi *et al.* (2007) has shown the major role of dominance in the inheritance of this trait. Busch *et al.* (1971) showed that dominance and additive × additive effects were effective in the inheritance of grain yield. Additive × additive epistasis was an important component of the genotypic values in the all traits except in biological yield and harvest index. This epistasis effect was more important than both additive and dominance effects in the grain yield, main spike straw weight and total spike straw weight. Yadava *et al.* (1998) reported that additive × additive epistatic effect had an impact on the inheritance of grain yield. Gambl and Burke (1984)

concluded that epistasis action of genes was involved in the inheritance of grain yield.

The model of the four-parameters was determined as the best model for the main spike straw weight. Additive effect was non-significant for this trait and dominance effect, additive × additive epistasis effects had a major role in the inheritance of this trait. As dominance effect was greater than additive effect and additive effect was non-significant, dominance effect had a major role in controlling the inheritance of this trait.The estimates of the different variance components were presented in Table 4. Generation variance analysis indicated that dominance variance was larger than additive variance for main spike straw weight, total spike straw weight, grain yield and harvest index. According to Table 4, for stem length and biological yield, additive

variance was larger than dominance variance. for the traits that the additive effects were larger than the non-additive, it is suggested that selection in early segregating generations would be effective and for the traits that the non-additive effects were larger than additive, the improvement of the characters needs intensive selection through later generations.

Broad-sense heritability rate was between 0.50 to 0.98 and narrow-sense heritability rate was between 0.46 to 0.88 (Table 5). The degree of negative dominance in some traits indicates that gene effects on traits occur from parent with a lower mean. The heritability estimates showed that Gaspard × Kharchia cross has the greatest chance for genetic improvement in the biological yield, main spike straw weight, total spike straw weight and grain yield (Table 5).

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