

INHERITANCE OF YIELD AND YIELD COMPONENTS IN A BREAD WHEAT (*Triticum aestivum* L.) CROSS

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ABSTRACT

Heritability and gene action of yield and yield components were estimated in a Golia x Cumhuriyet 75 cross using generation mean analysis. The additive-dominance model was valid for spike length, number of spikelets per spike, thousand kernel weight, fertile tiller number, and grain yield. On the other hand, the six-parameter model was fitted for explaining genetic variation for number of kernels per spike, number of kernels per spikelet, and single spike yield. Heritability estimates and genetic advances were low for number of kernels per spike, thousand kernel weight and grain yield; medium for spike length, number of kernels per spikelet; high for number of spikelet per spike, spike yield and fertile tiller number. It could be possible that selection in advanced generations might be effective for number of spikelets per spike, number of kernels per spike, number of kernels per spikelet, single spike yield, thousand kernel weight, fertile tiller number, grain yield.

Key words: Generation mean analysis, gene effects, heritability, additive-dominance model

INTRODUCTION

Wheat is a major crop in Turkey where bread wheat production constitutes about 70 of the total wheat production. The wheat breeders are concentrating to improve the yield potential of wheat by developing new varieties with desirable genetic make up in order to overcome the consumption pressure of ever increasing population (Memon et al., 2007). High grain yield has been the main aim in wheat breeding. The inheritance of grain yield in wheat has been the subject of intensive studies (Sharma et al., 2002; Heidari et al., 2005; Rebetzke et al., 2006). Grain yield in wheat is a complex character determined by several traits. Reported heritability estimates indicate that certain morphological traits that influence grain yield in wheat are more heritable than yield itself (Fethi and Mohamed, 2010).

The high heritability resulting to high genetic advance for yield components in wheat offer better scope of selection of genotypes in early segregating generations (Singh & Chatrath 1992; Memon et al., 2005). In this regard heritability estimates plays an important role for planning the breeding strategy. The heritability of a character determines the extent to which it is transmitted from one generation to the next and it is a valuable tool when used in conjunction with other parameters in predicting genetic gain that follows in the selection for that characters (Afiah et al, 2000; Baloch et al, 2003; Ansari et al, 2004, 2005). The heritability values become a measure of the genetic relationship between parents and progeny; hence considerable research work has been carried out to incorporate the desirable genes in present wheat varieties to increase the productivity of the crop (Memon et al., 2007).

There are different analysis methods to estimate genetic basis of quantitative variability of selected plant characters. Among these, generation mean analysis allows breeders to predict epistasis. It has been reported that epistatic gene action is a nontrivial factor in the inheritance of investigated plant characters (Goldringer et al., 1997). In different crosses, dominance-epistatic effects and only epistatic effects were found predominant for grain yield. To utilize non-fixable gene effects (non-additive) which were higher in magnitude than fixable (additive), breeding methods involving reciprocal recurrent selection or biparental mating were suggested for further improvement in grain yield and tillers per plant in wheat (Shekhawat et al., 2006). In the study on durum wheat by Fethi and Mohamed (2010), dominance effects and dominance x dominance epistasis were found to be more important than additive effects and other epistatic components for the number of heads per plant, spikelets per spike and grains per spike.

Heritability estimate is a valuable parameter for determining the magnitude of genetic gain from selection. Low, medium, and high narrow-sense heritability estimates have been reported for yield and yield components in wheat (Anwar and Chowdhry, 1969; Bhatt 1972; Ketata et al., 1976b; Tosun et al., 1995; Toklu 2001).

Gene effects have been examined in wheat by several researchers (Chapman and McNeal 1971; Bhatt 1972; Sun et al., 1972; Ketata et al., 1976b; Carvalho and Qualset 1978; Kanbertay 1984; Walia et al., 1995; Altınbaş and Bilgen 1996; Toklu 2001; Novoselovic 2004). They found that

additive, dominance and epistatic gene effects were involved in the expression of yield and yield components.

The purpose of the this study was to estimate the gene effects and heritabilities in a specific bread wheat cross in order to use in the approval of efficient breeding strategies in wheat breeding.

MATERIALS AND METHODS

P₁, P₂, F₁, F₂, B₁, and B₂ generations of a Golia x Cumhuriyet 75 cross were used as genetic materials. Golia has short plant height, medium ear density and excellent fertilizer response while Cumhuriyet 75 has high plant height and high thousand kernel weight. The parents and F₁, F₂, B₁, and B₂ populations were grown in the 2002-2003 growing season at Adnan Menderes University, experimental field of Agricultural Faculty. The experimental layout was a Randomized Complete Block Design with three replications. The plots consisted of two rows 2.25 m long and 140 seeds placed in each row. Fertilization (18 kg/da N, 9 kg/da P₂O₅ and 9 kg/da K₂O), irrigation and other standart cultural practices were carried out.

On the established population, spike length, number of spikelets per spike, number of kernels per spike, number of kernels per spikelet, single spike yield, thousand kernel weight, fertile tiller number, and grain yield were measured. Measurements were taken on 30 plants for non-segregating

populations and 90 plants for segregating populations. The genetic parameters such as heritability, genetic advance and gene effects were estimated for the investigated characters. Heritability in the narrow sense (h^2) was estimated using formula given by Warner (1952). Standard errors of heritabilities and expected gain from selection were calculated using the methods described by Ketata et al. (1976b). Generation mean analysis of the six generations (P₁, P₂, F₁, F₂, B₁ and B₂) were conducted using a joint scaling test (three-parameter model) based on an additive-dominance model (Cavalli 1952; Mather and Jinks 1971; Singh and Chaudhary 1979; Hill et al., 1998). The validity of the additive-dominance model was examined using chi-square analysis. When the three-parameter model was not adequate to explain genetic variation, six-parameter model (Hayman 1958; Singh and Chaudhary 1979) was used.

RESULTS AND DISCUSSION

Generation means and their standard errors, heritability values, genetic advance, three and six-parameter model in a Golia x Cumhuriyet 75 cross related to yield and yield components are presented in Table 1 and in Table 2. Heritability estimates and genetic advances were low for number of kernels per spike, thousand kernel weight, and grain yield, were medium for spike length, number of kernels per spikelet, were high for number of spikelets per spike, single spike yield, and fertile tiller number.

Table 1. Generation means, standard errors, heritability, and expected genetic advance in a Golia x Cumhuriyet 75 cross related to yield and yield components

Generation	Spike lenght	Spikelets/ spike	Kernels/ spike	Kernels/ spikelet	Single spike yield	Thousand kernel weight	Fertile tiller number	Grain yield
P ₁	9.08 ± 0.84	20.70±1.03	62.97±7.42	3.04±0.32	1.98±0.33	31.34±3.06	2.29±0.03	551.33±14.0
P ₂	11.98±0.89	17.10±0.95	51.47±6.32	3.01±0.28	2.06±0.34	40.06±3.55	1.99±0.26	514.00±15.7
F ₁	11.52±0.73	18.93±1.03	55.30±7.46	2.92±0.32	2.38±0.33	43.18±3.08	2.19±0.08	590.67±16.9
F ₂	10.55±1.42	18.51±1.63	55.51±8.80	3.00±0.40	2.21±0.41	39.91±5.37	2.62±0.38	519.33±27.2
B ₁	10.31±1.20	19.59±1.24	53.87±8.16	2.75±0.36	1.99±0.29	37.39±5.25	2.41±0.36	566.67±26.0
B ₂	11.02±1.32	17.29±1.45	46.90±8.79	2.70±0.37	2.01±0.36	43.18±4.95	2.32±0.26	530.33±27.0
h^2	0.41 ± 0.29	0.62* ± 0.25	0.14 ± 0.34	0.32 ± 0.31	0.71***±0.23	0.19 ± 0.33	0.59 ± 1.75	0.09 ± 2.34
GA	11.42	11.18	4.68	8.65	26.99	5.36	17.40	0.97

The three-parameter model was sufficient to explain genetic variation for spike length, number of spikelets per spike, thousand kernel weight, fertile tiller number, and grain yield. On the other hand, the six-parameter model was fitted for explaining genetic variation for number of kernels per spike, number of kernels per spikelet, and single spike yield. For spike length, additive and dominance effects were significant whereas additive effects relatively higher than dominance effects. This agrees with results explained by Walia et al. (1995).

Additive and dominance effects made the major contributions to the inheritance of spikelets per spike but dominance effects were negative and higher than additive effects. Toklu (2001) also found that both additive and dominance gene action were significant in the inheritance of this yield component. Sharma et al. (2002) explained that epistatic effects were also present in the inheritance of spikelets per spike.

Additive, dominance, additive x additive, dominance x dominance effects contributed significantly to the inheritance

of kernels per spike in this cross. Duplicate type of epistasis was detected since [d] and [dd] parameters which were significant and in opposite sign. Success of the selection would be affected negatively by these interactions. No epistasis were involved in the inheritance of kernels per spike reported by Ketata et al. (1976b) and Amawate and Behl (1995). Nevertheless, Carvalho and Qualset (1978) declared that significant additive variation was present in the inheritance of same character.

Dominance, additive x additive, dominance x dominance effects were found to be significant in the inheritance of kernels per spikelet; which is in agreement with results of Ketata et al. (1976a). And also duplicate interactions were detected in the inheritance of this character.

Additive-dominance-epistatic model was valid for explaining genetic variation for single spike yield. Dominance x dominance effects were significant in the inheritance of single spike yield. Altınbaş and Bilgen (1996)

Table 2. Three and six parameter model in a Golia x Cumhuriyet 75 cross related to yield and yield components

Genetic model	Spike length	Spikelets/spike	Kernels/spike	Kernels/spikelet	Single spike yield	Thousand kernel weight	Fertile tiller number	Grain yield
3 parameter								
M	10.33 ± 0.216	18.69 ± 0.378	55.04 ± 1.454	2.94 ± 0.047	1.99 ± 0.093	36.14 ± 1.501	2.21 ± 0.116	528.86 ± 10.083
A	1.26** ± 0.216	1.99** ± 0.361	8.73 ± 1.429	-0.04 ± 0.044	0.004 ± 0.082	4.93** ± 1.450	0.09 ± 0.116	20.31* ± 10.133
d	0.92* ± 0.414	-25.00** ± 0.645	-2.46 ± 2.276	-0.26 ± 0.097	0.06 ± 0.137	7.88** ± 2.614	0.003 ± 0.1460	52.39** ± 19.303
X ² (3)	2.95	2.81	25.54	20.53	8.41	0.68	2.10	2.48
P	0.40	0.42	< 0.001	< 0.001	< 0.05	0.88	0.55	0.48
6 parameter								
m	10.55 ± 0.184	18.51 ± 0.2400	55.51 ± 0.620	3.00 ± 0.053	2.21 ± 0.104	39.913 ± 1.449	2.62 ± 0.219	519.33 ± 15.677
a	-0.71 ± 0.315	-2.30 ± 0.409	-6.97** ± 1.619	-0.04 ± 0.036	-0.02 ± 0.062	-5.790 ± 1.933	-0.08 ± 0.257	-36.33 ± 21.662
d	1.43 ± 1.001	-0.25 ± 1.319	-22.44** ± 4.306	-1.20** ± 0.234	-0.47 ± 0.447	8.96 ± 7.135	-0.99 ± 1.018	174.67 ± 77.078
aa	0.44 ± 0.968	-0.28 ± 1.261	-20.53** ± 4.079	-1.09** ± 0.224	-0.83 ± 0.433	1.47 ± 6.968	-1.03 ± 1.014	116.67 ± 76.219
ad	0.75 ± 0.345	-0.50 ± 0.482	-1.22 ± 1.966	-0.02 ± 0.057	0.02 ± 0.100	-1.43 ± 2.165	0.07 ± 0.268	-17.67 ± 22.498
dd	1.00 ± 1.546	2.19 ± 2.047	44.03** ± 7.465	2.06** ± 0.291	1.66** ± 0.533	-4.85 ± 10.140	0.23 ± 1.361	-64.00 ± 109.393

noted that additive, dominance and epistatic effects were important in the inheritance of this yield component. Similarly, Fethi and Mohamed (2010) reported that dominance effects and dominance x dominance epistasis were more important than additive effects and other epistatic components for grains per spike.

Joint scaling test results indicated that no epistasis found in the inheritance of thousand kernel weight. Both additive and dominance effects were significant in genetic control of thousand kernel weight. For this character, significant additive effects were stated by Bhatt (1972), Ketata et al. (1976b), Awaad (1996); importance of additive, and dominance effects were reported by Chapman and McNeal (1971), Sun et al. (1972); importance of epistatic effects were noted by Ketata et al. (1976a), Amawate and Behl (1995), Toklu (2001), Sharma and Sain (2003). Selection in advanced generations were suggested by Toklu (2001); whereas early generation selection were recommended by Ketata et al. (1976b) for thousand kernel weight.

However, additive-dominance model was sufficient to explaining genetic variation for fertile tiller number; additive and dominance effects were not significant. Significant epistatic effects were reported by Ketata et al. (1976b), Shekhawat et al. (2000). For fertile tiller number, Van Sanford and Utomo (1995) suggested that early generation testing might be effective; on the other hand, Ketata et al. (1976b) recommended that selection in advanced generations might be useful due to epistasis.

In the inheritance of grain yield, additive and dominance effects were significant and dominance effects were higher than additive effects. For the genetic variation of grain yield, significance of dominance and additive x additive effects were reported by Busch et al. (1971); significance of epistatic effects were noted by Chapman and McNeal (1971), Ketata et al. (1976a), Ketata et al. (1976b), Goldringer et al. (1997), Shekhawat et al., 2006).

The genetic advance should be considered along with heritability in coherent selection breeding program (Eid, 2009). In our study, high heritability values coupled with

high genetic advance (Table 1) were recorded for single spike yield, fertile tiller number and spikelets per spike. It could be concluded that additive effect of genetic variation was transmitted from the parents to the progeny. Low heritability with low genetic advance value was determined for grain yield, indicating slow progress through selection for grain yield. Especially, the reason for grain yield (kg/da) is a result of some variances constituting the environment variance. It is clear that grain yield (kg/da) as a complex character cannot be used a selection criteria in a breeding program.

CONCLUSION

Based on the genetic parameters evaluated; selection in the advanced generations might be effective for number of spikelets per spike, number of kernels per spike, number of kernels per spikelet, single spike yield, thousand kernel weight, fertile tiller number, grain yield, due to dominance and epistatic effects. On the other hand, early generation testing and selection might be recommended for spike length. This objective could be achieved by restricted recurrent selection (Joshi, 1979) and/or diallele selective mating (Jensen, 1978) methods for the number of kernels per spike, number of kernels per spikelet, single spike yield.

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