



Genetic Analysis of Grain Yield and Its Components in Bread Wheat (*Triticum aestivum* L.)

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Authors' contributions

This work was carried out in collaboration between all authors. All authors read and approved the final manuscript.

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ABSTRACT

Aims: Increasing yield is the most important aim in any breeding program. Since yield is a complex trait with low inheritance and involves several quantitative components, its direct study is not usually sufficient and therefore it is suggested that its components be investigated instead. Awareness of gene action of traits is very important in plant breeding methods.

Study Design: The experiment was conducted using a randomized complete block design with two replications for each generation.

Place and Duration of Study: P₁, P₂, F₂, F₃ and F₄ generations of a Gaspard (sensitive) × Kharchia (tolerant) cross were used as genetic materials. The parents and F₂, F₃ and F₄ populations were grown in 2010-2011 growing season in the research farm of international center for sciences, High Technology & Environmental Science-Kerman Iran.

Methodology: Generation mean analysis using parents (Gaspard & Kharchia) and their progenies (F₂, F₃, F₄) was used to study the type of gene action and the best genetically

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model of traits under drought stress condition.

Results: Generation mean analysis was performed by scaling test. Meanwhile, the three parameter model the additive-dominance was adequate to demonstrate the genetic variation and it is important in the inheritance of spike length with awn, flag leaf length and flag leaf width. Generation means analysis revealed all types of gene action (additive, dominance and epistatic) were involved in the inheritance of grain yield, plant height, spike length and total spike weight of plant. In inheritance the peduncle length, number of grain per plant were effective additive effect and additive \times additive epistatic effect. Dominance effects were more important than additive effects in most traits.

Conclusion: Therefore to improve these traits hybridization and using of hybrid vigor would be much efficient than the selection strategies.

Keywords: Bread wheat; gene action; generation mean analysis; yield.

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important cereal crop of the world [1]. Drought is the most significant environmental stress in agriculture worldwide and improving yield under drought is a major goal of plant breeding [2]. Wheat grain yield can be improved through indirect selection on the basis of yield components [1]. Sufficient understanding of the inheritance of quantitative traits and information about heritability of grain yield and their components is essential to develop an efficient breeding strategy [1]. To increase the yield attention to the it's related characteristics could be important in reaching to this purpose. For this purpose the studying of each one of the traits related to the yield of and determining the method of the inheritance in each of them is very important in the selection of the suitable breeding methods [3]. Generation mean analysis is a simple but useful technique is to estimating gene effects such as additive \times additive (aa), dominance \times dominance (dd) and additive \times dominance (ad) effects [4]. Therefore heritability and gene action of yield and yield components were estimated in a Kharchia (tolerant) \times Gaspard (sensitive) cross using generations mean analysis. The research reported in this paper was carried out to provide information about gene effects and available genetic variability for the most important quantitative traits of wheat (*Triticum aestivum* L.). 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 [5]. Gene effects have been examined in wheat by several researchers [6,7]. They found that additive, dominance and epistatic gene effects were involved in the expression of yield and yield components. Novoselovic [6] reported that additive, dominance and epistatic gene effects were involved in the expression of yield and additive-dominance model is adequate for plant height. Yadava et al [8] conducted a study on two populations of wheat through generation mean analysis concluded that in grain weight, plant height and peduncle length is involved additive \times additive epistatic effects. Panhank and Sharma [9] using generations mean analysis and Five-and six-parameter model Hayman studied the nature of gene action for yield and its components in wheat and reported that epistatic action of genes involved in control of all parameters studied. The purpose of this study was to provide information about gene effects and available genetic variability and also determine the potential of yield trait and its component for drought tolerance of bread wheat.

2. MATERIALS AND METHODS

P₁, P₂, F₂, F₃ and F₄ generations of a Gaspard (French cultivar & salt sensitive) × Kharchia (It is the most salt tolerant wheat genotype found in India. Kharchia is red grained and is highly susceptible to rust) cross were used as genetic materials. The parents and F₂, F₃ and F₄ populations were grown in 2010-2011 growing season in the research farm of international center for sciences, High Technology & Environmental Science-Kerman Iran. Soil in the test was sandy loam. Electrical Conductivity (EC) and pH of this soil were 4.04 dS and 7.82 respectively. The experimental layout was a Randomized Complete Block Design with two replications. In each replication there were two rows for each of the parents, 13 rows for each of the F₂, 150 rows for each of the F₃ and 100 rows for each F₄ generation. The length each of row was 1m. In each row, twenty seeds were planted. The distance between rows was 50 cm. All necessary cares were under consideration during the growth period. Analysis of variance and expected value of mean squares of parents, F₃ and F₄ entries tested in one environment (Table 1). The mean values, standard errors and variances of different generations were subjected to weight least squares analysis using the joint scaling test [10] to fit models of increasing complexity until an adequate description of the observed means was found as non-significant χ^2 test.

$$y = m + \alpha[d] + \beta[b] + \alpha^2[i] + 2\alpha\beta[j] + \beta^2[l]$$

where y, m, d, h, i, l and j represent mean for one generation, mean of all generations, sum of additive effects, sum of dominance effects, sum of additive × additive, sum of additive × dominant and sum of dominant × dominant interactions, respectively. α , β , $2\alpha\beta$, α^2 , β^2 are the coefficients for the additive, dominant effects and their interactions in the model, respectively.

The significance of gene effects was tested by t-test. On the established population, grain yield, plant height, spike length, total spike weight of plant, peduncle length and number of grain per plant were measured. The genetic parameters such as heritability and gene effects were estimated for the investigated characters.

Variance components (additive, dominance and environment) were estimated as described using the following equations:

$$V_{F_2} = \frac{1}{2}D + \frac{1}{4}H + E_1$$

$$V_{F_3} = \frac{1}{2}D + \frac{1}{16}H + E_2$$

$$\bar{V}_{F_3} = \frac{1}{4}D + \frac{1}{8}H + E_1$$

$$E_1 = M_2/r$$

$$E_2 = M_{11}$$

Table 1. Analysis of variance and expected value of mean squares of parents, F₃ and F₄ entries tested in one environment

Source of variation	Mean squares	Expected mean quares
Replication		
Entries	M ₃	
Among generation	M ₃₁	$\sigma^2 + r\sigma^2_g$
Among F ₃ progenies	M ₃₂	$\sigma^2 + r\sigma^2_{F_3}$
Error	M ₂	σ^2
Total		
Within	M ₁	
F ₃ entries	M ₁₂	$\sigma^2_{wg} + \sigma^2_{we}$
Homogeneous entries	M ₁₁	σ^2_{we}

Broad sense heritability (h^2_b) and narrow-sense heritability (h^2_n) were calculated as follows:

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

3. RESULTS AND DISCUSSION

The results showed that generations mean squares were significant for all the traits. Significant differences among generations for different traits indicated the presence of genetic variability between the parent varieties. Therefore, the generations mean analysis was performed for all of traits. Mean squares are presented in Table 2. Mean values and their standard errors for the analyzed traits are presented in Table 3. The estimates of genetics of variation in grain yield and its component are given in Table 4. The model four parameters contain m , d , h and i determined the best fit for grain yield. The higher amount of "h" than "d" showed the important of dominance to additive in the inheritance of this trait. Also Kamboj et al. [11] reported that the additive genetic effects were important for grain yield. But Willa et al. [7], Chowdhry et al. [12], and Akhtar and Chowdhry [13] showed that dominance genetics effects were the most important than additive gene action for grain yield per plant in wheat. About plant height the model four parameters including m , d , h and i was recognized as the best fit model. All components of this model were significant expect additive effect in the level %1. Novoselovic et al. [6] disclosed that plant height was governed by additive \times additive $[i]$ gene interaction. For plant height components of this model are significant in the level %1 expect additive effect. Estimate the degree of dominance showed the over dominance effect in controlling plant height. Although in Akhtar and Chowdhry [13], Mostafavi et al. [14], Yadava et al. [8] studies epistatic effects had an important role in controlling inheritance this trait. Sheikh et al [15] showed that plant height be controlled by genes with additive effects. Therefore according to the results obtained there will possible to improve this trait by selection in early generations. Dominance effects were negative and significant for grain yield, plant height, spike length, total spike weight of plant and number of grain per plant. The three-parameter model with parameters m , d and i was sufficient to explain genetic variation for peduncle length and number of grain per plant that additive effects and additive \times additive epistatic effects are involved in controlling the inheritance of these traits. Yadava et al. [8] reported additive \times additive epistatic effect had an impact in the inheritance peduncle length. Mean and additive components were

significant for peduncle length and number of grain per plant and indicated that selection in early generation is effective. For spike length should be considered epistatic effects of genes in controlling this trait that additive effect was non-significant and observed more roles the dominant effect. The degree of dominance for this trait was determined over dominance. Chowdhry et al. [16] reported that spike length inheritance is controlling with partial dominance. Although Mostafavi et al. [14] additive and dominance effects reported for spike length. For spike length with awn, flag leaf length, flag leaf width three parameters of the genetic model [m], additive [d] and dominance [h] were shown to be the best fit of the observed to the expected generation means. It means that for these traits epistatic was not making a significant contribution to the differences among the generations mean. Dominant effect has major role in controlling the inheritance of length of flag leaf. Degree of dominance for this trait was estimated of over dominance and in flag leaf width and the Additive effect was of non-significant. Mean and additive components were significant for spike length with awn, peduncle length, number of grain per plant and indicated that selection in early generations is effective. Dominance effects were positive and significant for flag leaf width. The additive gene effects (d) were significant and either positive or negative for spike length with awn, grain yield, total spike weight of plant, peduncle length and number of grain per plant studied and non-significant for other traits.

From generation of variance analysis is used to estimate variance components and heritability of traits associated with drought tolerance in wheat. According to Table 5, grain yield, spike length, total spike weight of plant, number of grain per plant and peduncle length except plant height, dominance variance (D) is larger than additive variance, that obtained results in generations mean analysis are almost according to [d] and [h] component and other results that are not according to, could be possibly due to neutralize the gene positive and negative effect of dominance responsible in more loci [17]. It is noted that using of hybrid vigor through crossing is better than selection in initial generation, while selection strategies would be an efficient method for traits with higher additive variance.

Heritability estimates in both of broad and narrow sense were generally found to be high in magnitudes for studied traits (Table 6). Broad-sense heritability rate was between 0.56 to 0.93 and narrow-sense heritability rate was between 0.51 to 0.86. The degree of dominance negative in some traits indicates that gene effects on traits happen of parent with lower mean. The degree of dominance indicated partial dominance for grain yield. Spike length trait was controlled by over-dominance type of gene action. So it can be concluded that selection in early segregating generations will not be fruitful for spike length. Partial dominance with additive type of gene action for peduncle length was found. The presence of over-dominance type of gene action for plant height trait showed that transgressive segregates should be searched out in later filial generations. Amount of degree of dominance Larger than one is shows existence the over dominance in most traits such as plant height, spike length, spike length with awn, flag leaf length, flag leaf width, total spike weight of plant and number of grain per plant and in fact is showing greater share of non-additive effects of genes controlling these traits. Also phenomenon of over dominance in these traits may be due accumulation effects a large number of genes of with partial or complete dominance and linkage favorable dominance genes and unfavorable dominance [18].

Table 2. Mean squares of traits in Gaspard × Kharchia cross

Source	Degree of freedom	Grain yield	Plant height	Spike length	flag leaf length	Flag leaf width	Spike length with awn	Total spike weight of plant	Peduncle length	Number of grain per plant
Replication	1	0.791*	19.45 ^{ns}	27.65 ^{ns}	0.058 ^{ns}	0.045 ^{ns}	1.223 ^{ns}	2.408*	155.1 ^{ns}	3165.14*
Generation	4	0.333*	25.16*	37.28*	4.52*	1.36*	12.239**	2.517*	85.83*	2066.06*
Error	4	0.0499	3.57	0.665	0.665	0.211	0.442	0.23	28.36	301.253

ns, *, **: non-significant, significant in the level %5 and %1 respectively

Table 3. Mean and standard error for different traits in Gaspard × Kharchia cross

Generation	Grain yield	Plant height	Spike length	Flag leaf width	Flag leaf length	Total spike weight of plant	Number of grain per plant	Peduncle length	Spike length with awn
P ₁	0.87 ± 0.12	32.17 ± 1.46	0.5 ± 0.076	7.1 ± 0.341	10.13 ± 0.918	1.52 ± 0.19	22.54 ± 1.79	7 ± 1.009	2 ± 0.233
P ₂	1.89 ± 0.27	39.2 ± 3.9	0.75 ± 0.12	7.55 ± 0.46	14.53 ± 1.24	3.1 ± 0.356	46.81 ± 9.47	8.54 ± 1.12	2.36 ± 0.36
F ₂	1.25 ± 0.162	35.61 ± 1.07	1.22 ± 0.06	9.47 ± 0.23	11.97 ± 0.403	3.2 ± 0.338	78.17 ± 9.34	6.22 ± 0.44	1.19 ± 0.14
F ₃	1.58 ± 0.08	40 ± 0.498	0.82 ± 0.05	7.7 ± 0.106	14.3 ± 0.175	4.18 ± 0.18	93.48 ± 4.55	7.11 ± 0.18	1.57 ± 0.07
F ₄	1.7 ± 0.102	40.61 ± 0.36	0.7 ± 0.06	8.1 ± 0.134	13.5 ± 0.181	4.32 ± 0.21	98.9 ± 6.045	7.37 ± 0.23	1.53 ± 0.08

Table 4. Estimates of genetic components for some traits in Gaspard × Kharchya cross

The traits of Genetic components	Mean (m)	additive [d]	Dominance [h]	additive × additive [i]	dominance × dominance [j]	χ^2
Grain Yield	2.53 ± 0.054 **	-0.71 ± 0.177**	-0.4 ± 0.121*	-2.46 ± 0.348**	-	0.921
Plant height	42.64 ± 0.839 **	3.51 ± 2.085 ^{ns}	-6.268 ± 1.65 **	-6.95 ± 2.24 **	-	2.063
Spike Length	8.251 ± 0.184 **	0.327 ± 0.284 ^{ns}	-0.879 ± 0.35 *	-0.92 ± 0.339 **	-	0.807
Flag Leaf Length	14.76 ± 0.274**	0.725 ± 0.343 ^{ns}	-3.27 ± 1.115**	-	-	1.76
Flag Leaf Width	0.708 ± 0.06**	0.13 ± 0.068 ^{ns}	0.502 ± 0.348 **	-	-	0.88
Spike length with awn	11.331 ± 0.24 **	2.7 ± 0.498 **	-2.88 ± 0.937 **	-	-	1.06
Total Spike weight of plant	4.77 ± 0.283 **	0.786 ± 0.202**	-1.401 ± 0.53**	-2.46 ± 0.348**	-	0.793
Peduncle length	14.63 ± 0.182 **	3.01 ± 0.885 **	-	-1.701 ± 0.87**	-	5.5
Number of grain per plant	93.17 ± 3.38 **	12.136 ± 4.18**	-	-58.49 ± 5.89**	-	3.47

Table 5. Estimates of variance components for some quantitative traits of the Gaspard x Kharchiya cross

Traits	F2 generation variance (V_{F_2})	F3 generation means variance ($V_{\bar{F}_3}$)	F3 Generation variances mean (\bar{V}_{F_3})	Additive Variance (D)	Dominance Variance (H)	Homogeneous entries generations mean Variance (E_1)	Homogeneous entries generations Variance mean (E_2)
Grain yield	1.65	0.206	1.236	2.356	12.089	0.472	1.748
Plant height	217.195	0.747	42.63	224.232	88.356	104.83	73.979
Spike length	4.25	0.682	1.618	5.004	13.62	1.75	2.75
Flag leaf length	28.565	0.068	3.053	30.822	32.93	13.153	7.26
Flag leaf width	0.802	0.257	0.3009	1.382	4.58	0.11	1.64
Spike length with awn	4.49	2.84	5.196	4.846	40.239	2.067	4.99
Total spike weight of plant	4.611	1.84	7.257	7.308	67.56	0.956	7.82
Peduncle length	98.94	0.082	5.269	52.264	55.765	17.047	16.09
Number of grain per plant	2703.2	148.87	5611.65	4594.46	51916.95	405.97	5240.79

Table 6. Broad-sense (h^2_{bs}) and narrow-sense (h^2_{ns}) heritability, degree of dominance

Traits	Broad-sense heritability (h^2_{bs})	Narrow-sense heritability (h^2_{ns})	Degree of dominance $\frac{h}{d}$
Grain yield	0.81	0.71	0.56
Plant height	0.71	0.51	-1.78
Spike length	0.63	0.58	-2.68
Spike length with awn	0.62	0.53	-1.06
Flag leaf length	0.56	0.53	4.51
Flag leaf width	0.88	0.86	3.86
Total spike weight of plant	0.84	0.79	-1.78
Peduncle length	0.68	0.6	-0.214
Number of grain per plant	0.93	0.84	4.06

4. CONCLUSION

Generation mean analysis of the data revealed additive and non-additive types of gene effects in traits. The magnitude of additive gene effects (d) were small than dominance effects (h) in plant height, spike length, flag leaf length, flag leaf width, spike length with awn and total spike weight of plant expect grain yield. The magnitude and significance of the estimates for [i], [I] indicated that epistatic genes are important in the basic mechanism of traits involved in drought tolerance inheritance in the wheat cross studied. In traits such as grain yield, peduncle and number of grain per plant the additive effects were larger than the non-additive, it is suggested that selection in early segregating generations would be effective and about the traits such as plant height, spike length, flag leaf length, flag leaf width and spike length with awn that the non-additive portion were larger than additive, the improvement of the characters needs intensive selection through later generation. Traits the plant height, spike length, flag leaf length, flag leaf width, total spike weight of plant, and spike length with awn are with most the gene dominance effects, that determine appropriate breeding method selection to improve these traits. Additive \times additive interaction that was significant for some traits is stabilized genetic component. Positive or negative sign of the additive effect of genes depends on which parent as P_1 and which parent as P_2 is considered [19]. The opposite signs of the additive effect and additive \times additive effect in traits the plant height, spike length, total spike weight of plant, peduncle length and number of grain per plant is represents opposite nature for these traits. So we can consider for drought tolerance methods of recurrent selection and pedigree and or cross of two parents with a choice of methods.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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