



Estimates of gene action for yield and its components in bread wheat *Triticum aestivum* L.

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Article published on January 12, 2016

Key words: Bread Wheat Cultivars, Narrow Sense Heritability, Broad sense heritability.

Abstract

In order to study gene action for yield and its components using 8×8 diallel crosses excluding reciprocals during 2013/2014 and 2014/2015 growing seasons at Tag El-Ezz Research Station, Dakahlia Governorate, the genotypes were Sides 12, Gemmiza 11, Maser 1, Maser 2, Shandaweel 1, Giza 168, Sakha 93, and Sakha 94. Results revealed that both additive (D) and dominance (H_1 and H_2) genetic variance were significant for the all studied characters, indicating the importance of additive and dominance gene effects in controlling these characters. The dominance genetic variance was higher in the magnitude as compared to additive one, resulting in $(H_1/D)^{0.5}$ exceeding than more unity for all studied characters except spike density and number of tillers/plant. The "F" values which refer to the covariance of additive and dominance gene effects in the parents revealed positive and significant for flag leaf length and flag leaf area, extrusion length, number of tillers/plant number of spikes/plant, number of grains/spike and 1000- grain weight, indicating that dominant alleles were more frequent than the recessive ones in the parents for this character, while negative "F" value for remaining characters indicated excess of recessive alleles among parents. The overall dominance effects of heterozygous loci h^2 , indicated directional dominance for heading date, flag leaf length, flag leaf area, spike length, extrusion length, spike density, grain yield/spike, number of tillers/plant number of spikes/plant, number of grains/ spike and grain yield/plant. Proportion of genes with positive and negative effects in the parent ($H_2/4H_1$) was deviated from 0.25 for all studied characters. Heritability in narrow sense was moderate (0.369) for grain yield/plant.

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Introduction

Wheat *Triticum aestivum* L. is the main food crop for the Egyptian population the amount of wheat needed for human consumption, is for greater than that of the local production. So, intensive efforts have been devoted increasing wheat production by growing high yielding genotypes. The breeding procedure to be followed should be based on a good understanding of the mode of inheritance of economic characters. Among the biometrical approaches which have been developed the diallel analysis technique is considered the one which to provide a detailed genetic information about the nature of gene action controlling the desired characters. Many researchers used diallel technique to obtain genetical information about yield and its attributes. In this respect, Hassaballa *et al.* (1984), Eissa (1989), Al Kaddoussi (1996), Awaad (1996), Ismail *et al.* (2001) and Salama (2002) indicated the importance of additive and dominance gene effects control yield and its component of wheat. The additive gene effects played a great role in the inheritance of spike length, 1000-grain weight (Eissa *et al.*, 1994; Al Kaddoussi *et al.*, 1994; Salama, 2000 a and b), Whereas Eissa ,1989; Al Kaddoussi and Eissa ,1990; Esmail, 2002; Topal, 2004; Awaad, 2005; Adel and Ali, 2013 indicated the importance of dominance gene effects of the inheritance for 1000-grain weight and grain yield/plant. Sultan *et al.* (2006) found that parents Line 1 and Sakha 94 could be used in breeding for drought tolerance. Selection for days to heading, days to maturity, grain filling period, plant height at both conditions may be practiced in early segregating generations to improved bread wheat. Diallel analysis for estimation of genetic parameters in relation to trait of wheat height in normal and drought conditions was used by Shahid *et al.* (2005), Tousei Mojarrad and Ghannadha (2008), Jinbao *et al.* (2014), Naseem *et al.* (2015) and Saddam *et al.* (2015) concluded that the importance of additive and dominance gene effects control yield and its component of wheat, heterosis was height for stress trait. The present investigation was aimed to obtain information about gene action and heritability genetic systems for yield and yield attributes characters in

bread wheat genotypes before starting the breeding program.

Materials and methods

Eight genetically diverse bread wheat genotypes Table 1 were evaluated and crossed in 2013/2014 season, to produce F₁ seeds of diallel cross, excluding reciprocals. In the next season (2014/2015) the parents and their 21 F₁'s crosses were sown in 15th November at Tag El-Ezz research station, Dakhila governorate and evaluated using a randomized complete block design experiment with three replicates. Each plot consisted of 6 rows (2 rows for each parent and F₁). The row length was 2 m, and 20 cm apart. Plant to plant spacing was 10 cm. Description of the studied parental wheat genotypes in Table 1.

Table 1. Description of the studied parental wheat genotypes.

Genotypes	Pedigree
Sides 12	BUC//7C/ALD/5/MAYA74/ON//1160-147/3/BB/GLL /4/CHAT"S"/6/MAYA/VUL//CMH74A.
Gemmiza 11	630/4*SX.SD7096-4SD-1SD-1SD-0SD. BoW"S"/KVZ"S"//7C/SER182/3GIZA168 /SAKHA61.GM7892-2GM---1GM-2GM-1GM-0GM.
Miser 1	OASIS/KAUZ//4*BCN/3/2*PASTOR.C MSSOOYO1881T-050M-030Y-030M-030WGY-33M-0Y-0S
Miser 2	SKAUZ/BAV92.CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S
Shandaweel 1	SITE//MO/4/NAC/TH.AC//3*PVN/3MI RLO/BUC.CMSS93B00567S-72Y-010M-010Y-010M-0HTY-0SH.
Giza 168	MRL/BUC//SERICM93046-8M-0Y-0M-2Y-0B-0GZ.
Sakha 93	SAKHA92/TR810328.S.8871-1S-2S-1S-0S
Sakha 94	OPATA/RAYON // KAUZ.CMBW90 Y3180- 0TOPM-3Y-010M-010M-010Y-10M-015Y-0Y-0AP-0S.

Data were recorded on 10 individual plants for each the parent and F₁ crosses. The study traits were : morphological traits (Heading date (days), Plant height (cm), Flag leaf length (cm), Flag leaf width

(cm) and Flag leaf area (cm²): calculated from the formula: maximum length × maximum width × 0.72.), main spike traits (Spike length (cm), Extrusion length (cm), Number of spikelet's/spike, Spike density: number of spikelet's/spike/spike length (main spike), and Spike grain (g)) and yield and yield components (Number of tailoring/plant, Number of spikes/plant, Number of grain/spike, 1000- grain weight (g) and Grain yield/plant (g)).

The obtained data were subjected to the usual analysis of variance according to Gomez and Gomez (1991). Assessment and quantifying the type of gene action were computed according Hayman (1954) and Mather and Jinks (1982) separate out total genetic variance to its components additive and dominance genetic effects.

The components of En, D, H₁, H₂, h₂ and F were estimated as follows:

$E = (\text{Error SS} + \text{Reps SS}/d.f \text{ (error} + \text{replicates)})/\text{number of replications}$

$$D = V_p - \hat{E}$$

$$H_1 = 4 V_r - V_p - W_r - (3n - 2/n) X \hat{E}$$

$$H_2 = 4 V_r - 4 W_r - 2\hat{E}$$

$$F = 2 V_p - 4 W_r - (3(n - 2)/n) X \hat{E}$$

$$h_2 = 4 (M L_1 - M L_0)^2 - 4 ((n - 1)/n^2) X \hat{E}$$

Where:

\hat{E} = The expected environmental components of variation.

D = Variation due to additive genetic effects.

H₁ = Components of variation due to the dominance effects of the summed over load.

H₂ = The components of variation arising from the (h) increment of segregation genes.

h₂ = Dominance effects as the algebraic sum over all loci heterozygous phase in all crosses.

F = Refers the relative frequencies of dominance vs. recessive genes in the parents.

n = number of parents or number of arrays.

$(H_1/D)^{0.5}$ = Mean degree of dominance at each locus over all loci.

$H_2/4H_1$ = Measures the average frequency of positive (u) versus negative(n) alleles at loci exhibiting dominance. It was maximum value 0.25 when $P_i = q_i = 0.5$

KD/KR = The ratio of total number of dominant to recessive alleles in the parents. It was estimated from the following formula:

$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ The narrow (Tn) and broad sense (Tb) heritability were estimated using the formula of Mather and Jinks (1982) for the F₁ generation as follows:

Narrow sense heritability:

$$(T_n) = \frac{1/2 D + 1/2 H_1 - 1/2 H_2 - 1/2 F}{1/2 D + 1/2 H_1 - 1/4 H_2 - 1/2 F + E}$$

Broad sense heritability:

$$(T_b) = \frac{1/2 D + 1/2 H_1 - 1/4 H_2 - 1/2 F}{1/2 D + 1/2 H_1 - 1/4 H_2 - 1/2 F + E}$$

Results and discussion

Morphological characters

Statistical analysis (Hayman, 1954a and b) are given in Table 2 and indicated that both additive (D) and dominance (H₁ and H₂) genetic variance were significant for the all morphological studied characters and indicating the importance of additive and dominance gene effects in controlling these characters. The dominance genetic variance was higher in the magnitude as camporee to additive one, resulting in $(H_1/D)^{0.5}$ exceeding than more unity for, all morphological characters. In this respect. Over dominance gene effects reported for morphological characters by Jain and Singh (1976), Awaad (1996), Salama (2000 a) and Ahmed *et al* (2015) for number of spikes/plant Dasgupta and Mondal (1988), Al Kaddoussi (1996), Salama (2000 b) and Adel and Ali (2013) for number of grains/spike and 1000-grain weight.

Table 2. Additive [D], dominance (H_1 and H_2) and environmental [E] genetic components together with derived parameters for morphological characters.

Parameters	Days to heading	Plant height (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Flag leaf area (cm ²)
D	1.171**±0.33	2.842**±1.151	0.461**±0.150	0.0012**±0.0002	4.156**±0.314
H ₁	15.162**±2.44	3.471*±1.68	0.513**±0.171	0.0039**±0.0002	5.928**±0.822
H ₂	5.251**±1.62	3.022±1.31	0.326±0.162	0.0023**±0.0003	3.017±0.715
F	-1.616±1.21	0.172±2.611	0.471**±0.133	0.00004±0.0004	4.037**±0.826
h ²	5.620**±1.20	-0.017**±1.55	2.192**±0.017	-0.0013**±0.0001	8.516**±0.366
E	3.192**±0.113	1.291**±0.400	0.193**±0.018	0.0001±0.0001	1.661**±0.200
(H ₁ /D) ^{1/2}	3.598	1.105	1.054	1.802	1.194
H ₂ /4H ₁	0.086	0.217	0.158	0.147	0.127
KD/KR	1.497	1.071	1.628	1.176	4.707
T ⁿ	0.791	0.547	0.315	0.947	0.565
T ^b	0.937	0.812	0.605	0.98	0.846

The ratio of dominance to recessive alleles (K_D / K_R) in the parents which was >1 for; indicated the preponderance of dominance alleles for these characters, Heritability estimates in broad sense were high and ranged from 0.605 (flag leaf length) to 0.980 (flag leaf width) for all the studied characters. Heritability values in narrow sense (T_n) found to be high (>50 %) for days to heading (0.791), plant height (0.547), flag leaf width (0.947) and flag leaf area (0.565). Thus phenotypic selections were effective in improving these characters. Whereas, (T_n) values was moderate and valued flag leaf length (0.315), thus selection on phenotypic base was ineffective.

Spike characters

When using second degree statistics Hayman (1954), various genetic parameters were computed Table (3)

Table 3. Additive [D], dominance (H₁ and H₂) and environmental [E] genetic components together with derived parameters for main spike characters.

	Spike length	Extrusion length (cm)	Number of spikelets/spike	Spike density	Spike grain weight
D	0.248**±0.014	0.426**±0.091	0.091**±0.007	0.051**±0.004	0.067**±0.008
H ₁	0.156**±0.046	0.631**±0.141	0.313**±0.031	0.062**±0.020	0.099**±0.005
H ₂	0.110**±0.035	0.481**±0.021	0.286**±0.021	0.041**±0.020	0.060*±0.013
F	-0.017±0.021	0.361**±0.034	-0.113**±0.011	0.040±0.017	0.006±0.001
h ²	0.092**±0.022	0.036**±0.121	-0.001±0.014	0.015**±0.001	0.716**±0.010
E	0.073**±0.007	0.162**±0.045	0.044**±0.005	0.0036±0.002	0.033**±0.003
(H ₁ /D) ^{1/2}	0.808	1.217	1.854	1.102	1.215
H ₂ /4H ₁	0.205	0.190	0.228	0.165	0.151
KD / KR	0.802	0.442	0.926	2.117	0.076
T _n	0.682	0.397	0.638	0.368	0.601
T _b	0.803	0.843	0.818	0.505	0.783

The " F " values which refer to the covariance of additive and dominance gene effects in the parents revealed positive and significant for extrusion length, indicating that dominant alleles were more frequent than the recessive ones in the parents for this character. The overall dominance effects of heterozygous loci h^2 , indicated directional dominance for all studied characters except number of spikelet's/spike. Proportion of genes with positive and negative effects in the parent ($H_2/4H_1$) was deviated from 0.25 in the main spike characters. The ratio of dominance to recessive alleles (K_D/K_R) in the parents which was < 1 for the main spike characters except spike density; showed an excess of decreasing alleles among parental genotypes. Heritability in broad sense ranged from 0.505 (spike density) to 0.843(extrusion length) for all the studied characters. Heritability values in narrow sense (T_n) found to be high (>50 %) for spike length (0.682), number of spikelets/spike (0.638), and spike grain weight (0.601), Thus phenotypic selections was effective in improving these character.

Yield and yield components

When using second degree statistics Hayman (1954), various genetic parameters were computed Table (4)

and indicated that both additive (D) and dominance (H_1 and H_2) genetic variance were significant for the all studied characters, indicating the importance of additive and dominance gene effects in controlling these characters. The dominance genetic variance was higher in the magnitude as compared to additive one, resulting in $(H_1/D)^{0.5}$ exceeding than more unity for, all studied characters except number of tillers/plant. Using The diallel crosses among nine bread wheat cultivars in two sowing dates for grain yield/plant and yield components i.e. number of spikes/plant, number of grains/pike as well as 1000-grain weight. Resulted showed that the importance of additive gene effects in controlling these characters. The dominance gene effects were significant for number of grains/spike in both sowing dates and pooled data as well as 1000-grain weight in late sowing. But, additive gene effects were significant in pooled data for 1000-grain weight. (Jain and Singh (1976), Awaad (1996) and Salama (2000 a), for number of spikes/plant, Dasgupta and Mondal (1988), Al Kaddoussi (1996), Salama (2000a), Jinbao *et al.* (2014), Naseem *et al.* (2015) and Ahmed *et al.* (2015) for number of grains/spike and 1000-grain weight).

Table 4. Genetic components together with derived parameters for Yield and yield components.

	Number of tillers/plant	Number of spikes/plant	Number of grains/spikes	1000-grain weight	Grain yield/plant
D	0.216**±0.029	0.107**±0.028	0.982**±0.007	0.916**±0.141	0.310**±0.114
H ₁	0.152*±0.073	0.341**±0.071	3.156**±1.851	3.988**±1.00	7.852**±0.636
H ₂	0.138**±0.043	0.272**±0.036	2.981*±1.432	2.532**±0.491	4.814**±1.431
F	0.160**±0.068	0.162**±0.056	1.063**±1.025	1.410**±0.151	1.521±1.528
h^2	1.021**±0.041	1.750**±0.022	0.416±1.731	3.061**±0.245	8.173**±0.151
E	0.130**±0.015	0.141**±0.010	1.568**±0.231	1.853**±0.126	1.991**±0.542
$(H_1 / D)^{1/2}$	0.839	1.785	1.792	2.086	5.033
$H_2 / 4H_1$	0.226	0.199	0.236	0.158	0.2077
K_D / K_R	2.584	2.473	3.3511	2.169	1.972
T_n	0.729	0.472	0.259	0.206	0.369
T_b	0.801	0.932	0.611	0.477	0.750

The " F " values which refer to the covariance of additive and dominance gene effects in the parents revealed positive and significant for all studied characters except grain yield / plant, indicating that dominant alleles were more frequent than the

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recessive ones in the parents for this character. The overall dominance effects of heterozygous loci h^2 , indicated directional dominance for all yield characters except number of grains/spike. The value of ($H_2/4H_1$) was deviated from 0.25 in yield

characters. The ratio of dominance to recessive alleles (K_D / K_R) in the parents which was >1 for yield and yield characters; indicated the preponderance of dominance alleles for these characters.

Heritability estimates in broad sense ranged from 0.477(1000-grain weight) to 0.932 (number of spikes / plant) for all the studied characters. Heritability values in narrow sense (T_n) found to be high ($>50\%$) for number of tillers/plant (0.729), Whereas, (T_n) values was moderate and valued (0.472) for number of spikes/plant as well as (0.369) for grain yield/plant, thus selection on phenotypic base was ineffective.

Conclusion

Generally, it could be concluded from results of the diallel analysis of these study, the dominance gene effects were the predominant components and accounted for the major part in the total variation for yield and its attributes. The presence of considerable amount of non-additive gene effects for most the studied characters could be explained on the basis of past history of selection which had been imposed on population from which the studied local wheat cultivars had been derived.

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