Generation Means Analysis for Some Agronomic Characters in Two Crosses of Bread Wheat (*Triticum aestivum* L.) Grown under Saline Soil Conditions

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Abstract: Means of the six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the two wheat crosses , (1) Giza 168 x IG 4198 ICBW 207010 and (2) Gemmeiza 10 x IG 41897 ICBW 201657 were used to estimate type of gene action controlling some agronomic characters. Generation mean analysis revealed that, additive, dominance and epistatic effects seemed to have played role in the inheritance of all the studied characters for two crosses. The magnitude of additive gene effects (d) was small relative to the corresponding dominance effects (h) in most cases. Additive x additive type of gene effects [i] was detected for plant height, number of spikes/ plant and grain yield/plant in the two crosses and heading date and number of kernels/plant in cross 2 and spike length and number of spikelets/spike in cross 1. Additive x dominance epistatic type of gene effects [j] was found to be significant for heading date, spike length, number of kernels/plant, 1000-kernel weight and grain yield/plant in the two crosses under investigations and number of spikelets/spike in cross 2. Concerning the third type of epistatic effect i.e. dominance x dominance [l], was detected for no of spikes/plant, plant height, spike length, number of kernels/plant and 1000-kernel weight in all crosses and heading date and grain yield/plant in cross 2. Spike length in cross 1 and heading date, number of kernels/plant and grain weight/plant in cross 2 showed [i], [j] and [l] type of epistatic effects together which indicated complex inheritance for these characters. When epistasis was absent, the simple genetic model (m, d, and h) was applied. The values of additive (d) were significant or high significant and either positive or negative for all characters except grain yield in the two crosses, number of spikes/plant and number of kernels/plant in cross 1 and 1000-kernel weight in cross 2. The values of dominance (h) were significant or high significant and either positive or negative in all characters, except number of spikelets/spike in the two crosses, heading date and number of kernels/plant in cross 1.

Key words: Gene action · Generation mean analysis · Scaling test · Six generations · Wheat

INTRODUCTION

Bread wheat (*Triticum aestivum* L.), as a nutritive crop, considered the most important cereal crop in Egypt as well as in many parts of the world. The local production of wheat is not sufficient to cover the local consumption in Egypt. Grain yield is a complex character made up of the interaction between different yield components and environmental factors. Due to these complex interaction, it is difficult to improve yield through breeding (especially in the early generation), if yield is the only factor recorded, suggesting that component characters should also be used as selection criteria for yield improvement. This is the reason why it is necessary to know the genetic architecture of yield components [1]. The choice of selection and breeding procedures for genetic improvement of any crop is largely dependent on the knowledge of type and relative amount of genetic component and the presence of non-allelic interaction for different characters in the plant materials under

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investigations. Information of the type of gene action involved in the inheritance of a character is helpful in deciding the breeding procedures to be followed for plant improvement. To form a population with genetic variability for the characters studied, hybridization between genetically diverse parents must be done. Grain yield is a complexly inherited trait of low to moderate heritability and is strongly influenced by environmental conditions. Yield enhancement is often achieved by not only selecting for greater genetic potential for yield *per se* but also by selecting for tolerant to biotic and a biotic stresses that may limit the expression of the cultivar's maximum yield potential. Plant breeders and geneticists frequently use generation mean analysis to obtain information of gene action controlling the economic characters in wheat [2-13].

Therefore, the present study was carried out to obtain information about gene action on yield and its components and available genetic variability for the most important quantitative characters of bread wheat (*Triticum aestivum* L) in the two crosses grown under saline soil conditions.

MATERIALS AND METHODS

Experimental Site Description and Field Trials: This investigation was carried out at the Experimental Farm of the Agronomy Department, Faculty of Agriculture, South Valley University, Qena, Egypt (26°11'N and 32°44'E) during the three growing seasons from 2010/2011 to 2012/2013. Four bread wheat parents i.e. Giza 168 (P_1) and Gemmeiza 10 (P_2) (Egyptian varieties), (low tolerance to salinity with high yielding) and IG 4198 ICBW 207010 (P_3) and IG 41897 ICBW 201657 (P_4) (Introduced lines from International Center for Agricultural Research in the Dry Areas (ICARDA), (high tolerance to salinity with low yielding) were used in this investigation. The name, origin and pedigree of these parental genotypes are presented in Table 1. In the first season (2010-2011), the four parental were intercrossed (by hand emasculation and pollination techniques) to produce two F_1 crosses. The first is Giza 168 x IG 4198 ICBW 207010 and the second is

Gemmeiza 10 x IG 41897 ICBW 201657. In the second season (2011/2012), F_1 plants of each cross were selfed and backcrossed to the two parents to obtain F_2, BC_1 and BC_2 generations, respectively. During the 2012/2013 growing season, parents, F_1, F_2, BC_1 and BC_2 generations for each cross were sown using the randomized complete block design with three replications. Each containing one row of 5 m long for F_1, two rows for each parent and each back cross and three rows for F_2 generation. Each row spaced 20 cm. apart with 10 cm. between plants within rows. All recommended cultural practices of wheat production in the region were applied. The EC of the experimental site and the used irrigation water were 16.71 and 7.90 dS m^{-1}, respectively.

Measurements: Heading date was measured as number of days from sowing to complete emergence of spike on the main stem for 50% of plants. At harvest, ten plants were taken at random from each row to recording , plant height (cm), number of spikes/plant, spike length (cm), number of spikelets/spike, number of kernels/plant, grain yield/plant (g) and thousand kernel weight (TKW) (g.).

Statistical Analysis: The data were subjected in the first to test the differences between parental genotypes by applied "t" test for the studied characters before considering the biometrical analysis, as well as, the scaling test (A, B and C) were applied to detect the presence of epistasis according to Mather and Jinks [14]. Whereas in the presence of non-allelic interaction the analysis was proceeded to estimate the interaction types involved using the six parameters genetic model i.e. (m, d, h, i, j, and l) according to Hayman [15] and Jinks and Jones [16], where m = Mean effect, d = Additive gene effects, h = Dominance gene effects, i = Additive x additive epistatic gene effects, j = Additive x dominance epistatic gene effects and l = Dominance x dominance epistatic gene effects. Joint scaling test proposed by Jinks and Jones [16] was applied to test the adequacy of the genetic model controlling the studied traits. The simple genetic model (m, d, and h) was applied.

Table 1: Pedigree of the studied parental wheat genotypes.

Genotypes	Pedigree	Origin
P_1 (Giza 168)	MRL/BUC//SERI CM93046-8M-OY-OM-2Y-OB-OGZ	Egypt
P_2 (Gemmeiza 10)	Maya74 "S" / On // 1160-147BB/ GALL141CHAT"S" 151 CROW"S" CGM5820-3GM-IGM-2GM-0GM	Egypt
P_3	IG 4198 ICBW 207010	ICARDA (origin country: Jordan)
P_4	IG 41897 ICBW 201657	ICARDA (origin country: Morocco)

Table 2: Means and standard errors of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of the studied characters in the two wheat crosses

Crosses	Generation	Heading date	Plant height (cm.)	Spike length (cm)	No. of spikes/plant	No. of spikelets/spike	No. of kernels/plant	1000-kernel weigh (g.)	Grain weight/ plant (g.)
1	P_1	69.66±0.88	55.20±0.46	9.80±0.11	2.66±0.33	19.00±0.00	38.66±1.45	28.04±0.07	1.15±0.05
	P_2	76.66±0.88	71.4±1.09	10.86±0.20	2.00±0.00	17.00±0.00	38.00±0.57	36.47±0.10	1.06±0.14
	F_1	68.00±0.57	53.06±0.43	9.16±0.08	2.66±0.33	17.00±0.00	46.00±1.73	29.67±0.59	1.37±0.03
	F_2	68.66±0.88	67.60±0.46	11.30±0.28	3.66±0.33	18.66±0.33	36.66±0..33	24.25±0.75	0.95±0.02
	BC_1	69.00±0.00	51.80±0.57	9.20±0.00	1.66±0.33	18.00±0.00	34.00±0.57	26.24±1.15	0.91±0.02
	BC_2	69.00±0.00	59.80±0.57	9.00±0.11	1.66±0.33	18.00±0.00	40.00±0.57	34.83±0.57	1.39±0.02
2	P_1	75.00±0.57	58.60±0.11	6.90±0.05	2.66±0.00	18.00±0.57	60.66±2.60	32.47±2.35	2.39±0.07
	P_2	80.00±0.00	68.10±1.21	10.10±0.05	2.00±0.00	22.00±0.57	68.00±2.30	34.57±0.84	2.30±0.11
	F_1	77.00±0.57	62.30±0.52	9.00±0.46	2.66±0.33	22.00±3.51	76.66±4.33	33.04±0.21	2.50±0.04
	F_2	76.66±0.88	67.06±0.95	10.60±0.11	2.00±0.00	20.00±0.57	68.66±3.18	31.71±2.52	2.35±0.05
	BC_1	73.00±0.00	54.00±1.73	11.80±00	1.33±0.33	19.00±0.57	61.00±2.88	30.38±1.15	1.83±0.05
	BC_2	73.66±0.33	61.90±0.57	9.60±.23	1.66±0.33	19.00±0.57	52.00±2.88	42.67±1.15	2.25±0.08

Table 3: Estimates of six parameter gene effects for yield and yield components of the two wheat crosses for all the studied characters

| Characters | Crosses | Scaling test | | | m | d | h | i | j | l |
		A	B	C						
Heading date	1	0.33	-6.66**	-7.66	68.66**	0.00	-3.83	1.33	3.50**	5.00
	2	-6.00**	-9.66**	-2.33	76.66**	-0.66*	-13.83**	-13.33**	1.83**	29.00**
No. spikes/plant	1	-2.00*	-1.33	4.667**	3.66**	0.00	-7.66**	-8.00**	-0.33	11.33**
	2	-2.66**	-1.33	-2.00**	2.00**	-0.33	-1.66	-2.00*	-0.66	6.00**
Plant height	1	-4.66**	-4.86**	37.66**	67.60**	-8.00**	-57.43**	-47.20**	0.10	56.73**
	2	-12.90**	-6.60**	16.96**	67.06**	-7.90**	-37.51**	-36.46**	-3.15	55.96**
Spike length	1	-0.56**	-2.03**	6.20**	11.30**	0.20	-9.96**	-8.80**	0.73**	11.40**
	2	7.70**	0.10	7.40**	10.60**	2.2**	0.90	0.40	3.80**	-8.20**
No. spikelets/spike	1	0.00	2.00*	4.66**	18.66**	0.00	-3.66**	-2.66*	-1.00	0.66
	2	-2.00	-6.00	-4.00	20.00**	0.00	-2.00	-4.00	2.00*	12.00
No. kernels/plant	1	-16.66**	-4.00	-22.00**	36.66**	-6.00**	9.00**	1.33	-6.33**	19.33**
	2	-15.33**	-40.66**	-7.33	68.66**	9.00*	-36.33**	-48.66**	12.66**	104.66**
1000-kernel weigh	1	-5.24*	3.51**	-26.84**	24.25**	-8.59**	22.53**	25.11**	-4.37**	-23.38**
	2	-4.75	17.73**	-6.28	31.71**	-12.29**	18.78	19.26	-11.24**	-32.24**
Grain yield/plant	1	-0.71**	0.34*	-1.13	0.95**	-0.48**	1.03**	0.77**	-0.52**	-0.41
	2	-1.24**	-0.30	-0.31	2.35**	-0.42**	-1.08**	-1.24**	-0.46**	2.79**

*, ** significant at 0.05 and 0.01 levels of probability, respectively

RESULTS AND DISCUSSION

Mean Performances: Mean performance of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for yield and its components in the two crosses are presented in Table 2. Results revealed that presence of genetic variability for these characters in the studied materials. The F1 population was higher than the respective parents, F_2, BC_1 and BC_2 populations in the two cross for number of kernels/plant and also for grain yield/plant except BC_2 population in cross 1, whereas it came in the first comparing to the others. However, in the other characters studied, the populations have different trends from character to character in the two crosses as shown in Table 2. The mean value of the F_2 population comparing with their parents was higher than the highest parent for number of spikes/plant and spike length in the cross 1 and

spike length in the cross 2 indicating appreciable amount of genetic variability for these characters in the corresponding crosses.

Adequacy of the Genetic Model: The results of scaling test indicated that each of A, B and C were significant or highly significant in the two crosses for most characters (Table 3). Results of the scaling tests (A, B and C) revealed the presence of nonallelic gene interaction for most characters studied in the two crosses except number of spikelets/spike in the cross 2. Mather and Jinks [14] reported that significant results of scaling tests parameters indicate inadequacy of the additive-dominance model to interpret the gene effects involved in their materials i.e. epistatic contributions are important in the inheritance of these characters in the particular materials investigated. These results indicate the adequacy of the

Table 4: Estimates of scaling tests and joint scaling tests for yield and yield components of the two wheat crosses for all the studied characters

Characters	Crosses	Scaling test			Joint scaling test		
		A	B	C	m	d	h
Heading date	1	0.33	-6.66**	-7.66	71.83**	-3.50**	-8.83
	2	-6.00**	-9.66**	-2.33	90.83**	-2.50**	-42.83**
No. spikes/plant	1	-2.00*	-1.33	4.667**	10.33**	0.33	-19.00**
	2	-2.66**	-1.33	-2.00**	4.33**	0.33*	-7.66**
Plant height	1	-4.66**	-4.86**	37.66**	110.50**	-8.10**	-114.16**
	2	-12.90**	-6.60**	16.96**	99.81**	-4.75**	-93.48**
Spike length	1	-0.56**	-2.03**	6.20**	-19.13**	-0.53**	-21.36**
	2	7.70**	0.10	7.40**	8.10**	-1.60**	9.10**
No. spikelets/spike	1	0.00	2.00*	4.66**	20.66**	1.00**	-4.33
	2	-2.00	-6.00	-4.00	24.00**	-2.00**	-14.00
No. kernels/plant	1	-16.66**	-4.00	-22.00**	37.00**	0.33	-10.33
	2	-15.33*	-40.66**	-7.33	113.00**	-3.66*	-141.00**
1000-kernel weigh	1	-5.24*	3.51**	-26.84**	7.14	-4.21**	45.91**
	2	-4.75	17.73**	-6.28	14.26	-1.05	51.02**
Grain weight/plant	1	-0.71**	0.34*	-1.13	0.33*	0.04	1.44**
	2	-1.24**	-0.30	-0.31	3.58**	0.04	-3.87**

*,**significant at 0.05 and 0.01 levels of probability, respectively.

six-parameter model to explain the type of gene action controlling the character in these crosses. These results are in agreement with those obtained by Sharma *et al*. [17], Abd El-Rahman *et al*. [18], Aboshosha and Hammad [19] and Khattab *et al*. [11], who reported that scaling tests were significant for heading date and plant height.

Gene action and Epistasis Effects: Results of types of gene action estimated by generation mean as genetic effects in six parameter model are presented in Table 3. Highly significance for the estimated values of mean effects (m) indicated that all the studied characters were quantitatively inherited. The additive gene effects (d) were significant or high significant and either positive or negative for all characters studied, except number of spikes/plant and number of spikelets/spike in the two crosses and heading date and spike length in cross 1 suggesting the potential for obtaining further improvement of these characters by selection practice of their progenies. The dominance gene effects (h) were found to be highly significant for most studied characters except heading date in cross 1 and plant height, spike length, number of spikelets/spike and 1000-kernel weight in cross 2. The magnitude of additive gene effects (d) were small relative to the corresponding dominance effects (h) in most cases, suggesting that pedigree selection method is a useful breeding program for improving these populations. However, the negative value of (h) observed in most cases indicated that the alleles responsible for less value of the character were dominant over the alleles controlling high value.

These results are in harmony with those obtained by El-Hosary *et al*. [5], Esmail and Khattab [7], Salem [20], Khattab *et al*. [11], Hammad *et al*. [12] and Zaazaa *et al*. [13]. Significant epistatic additive x additive type of gene effects [i] was detected for plant height, number of spikes/plant and grain yield/plant in the two crosses and heading date and number of kernels/plant in crosses 2 and spike length and number of spikelets/spike in cross 1. Additive x dominance epistatic type of gene effects [j] was found to be significant for heading date, spike length, number of kernels/plant, 1000-kernel weight and grain yield/plant in the two crosses under investigations and number of spikelets/spike in cross 2. The negative sign of additive x dominance interaction [j] in most cases also suggested dispersion of genes in the parents.

Concerning the third type of epistatic effect i.e. dominance x dominance [l], highly significant effects were detected for number of spikes /plant , plant height, spike length, no. of kernels / plant and 1000-kernel weight in all crosses and heading date and grain yield/plant in cross 2. These results are in agreement with those obtained by Khattab *et al*. [6], Esmail and Khattab [7], Mahgoub and Hamed [21], Khaled [9], Farag [10] Khattab *et al*. [11] and Zaazaa *et al*. [13]. On the other hand, A, B and C scaling test for number of spikelets/spike in the cross 2 were insignificant, indicating the validity of the three parameter model to explain the type of gene action (Table 4). Mean data on various characters recorded on different generations *viz*., parents, F_1, F_2, BC_1 and BC_2 for two crosses of wheat were subjected to joint scaling test. The weighted least square technique was employed under

three parameter *viz.,* m (mean), d (additive) and h (dominance) .The simple genetic model (m, d, and h) was applied when epistasis was absent. The values of additive (d) were positive or negative significant or highly significant in all characters except grain yield in the two crosses number of spikes plant and number of kernels/plant in cross 1 and 1000-kernel weight in cross 2. The values of dominance (h) were positive or negative significant or highly significant in all characters except number of spikelets/spike in the two crosses, heading date and number of kernels /plant in cross 1. Among the interaction parameters, the component showed the greatest effect for most of the characters in all two crosses where there was evidence of epistasis. The joint scaling test found to be more efficient in detection of epistasis compared to individual scaling tests. Also, Ketata *et al.* [22] concluded superiority of joint scaling test over the simple scaling tests in wheat.

CONCLUSION

It may be concluded that:

- Additive, dominance and epistatic effects seemed to have played role in the inheritance of all the studied characters for two crosses.
- The magnitude of additive gene effects (d) was small relative to the corresponding dominance effects (h) in most cases.
- Spike length in cross 1 and heading date, no. of kernels/plant and grain weight/plant in cross 2 showed [i], [j] and [l] type of epistatic effects together which indicated complex inheritance for these characters.

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