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Genetic Studies on Some Earliness and Agronomic Characters in Advanced Generations in Bread Wheat (*Triticum aestivum* L.)

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Authors' contributions

This work was carried out in collaboration between all authors. Author MAA designed and carried out the study. Author WZEF managed the literature searches, analyses of the study wrote the first draft of the manuscript. All authors read and approved the final manuscript.

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ABSTRACT

The early generation (F_3 families) analysis measured the variance components of three crosses of five diverse parents. This work carried during three years 2010-13 at the experimental farm of Sakha Agricultural Research Station, Kafr El-Sheikh governorate, Egypt. The Data were recorded on days to heading, days to maturity, grain filling period and rate, plant height, number of spikes per plant, number of kernels per spike, 100-kernel weight and grain yield. The F_3 families had highly significant differences in most cases. The ranges of the performance of the F_3 families exceeded the limits of the minus and plus directions of their parents for most characters, showing the ability of selection for the desirable directions for these characters. The magnitude of genetic variance among the F_3 families exceeded corresponding environmental variance, while the environmental variance was higher than or almost equal to the corresponding genetic variance among plants within families for most characters. The additive and dominance variances were important in all cases. The broad and narrow sense heritability and genetic advance estimates were relatively medium to high for most characters. 5% of plants for each cross were selected for early mature and high yielding to evaluate in sperate experment in the next season.

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1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops in Egypt and world. In Egypt, early maturing cultivars aid to fit in crop intensive rotation. Development of early-maturing wheat cultivars without losses in grain yielding ability is a major objective of many wheat breeding programs. Some wheat cultivars, differing in maturity date, can produce similar grain yields, suggesting the effectiveness of yield enhancement by manipulating earliness potentiality.

Various biometrical analyses were used in the early and advanced generations to study the inheritance of earliness and agronomic characters. Farhat [1], El-Hawary [2], El-fadly [3] and Yasin [4] indicated the importance of additive and dominance role in the inheritance of most studied characters.

Generally, the values of heritability in broad and narrow sense were moderate to high for most studied characters in wheat [1,2,3]. On the other hand, [5,6] found low to moderate heritability estimates for grain yield and its components.

The expected genetic advance from selection was found to be low to moderate for days to heading and maturity and grain filling period [5,6,3]. Meanwhile, it was medium to high for grain filling rate and grain yield and its components [3].

The purpose of this research is (a) to investigate the genetic basis of characters of earliness and yield and its components, (b) to estimate heritability in both broad and narrow senses, (c) to predict the genetic advances from selection for these characters and (d) to obtain early and high yielding genotypes for advanced generation analysis.

2. MATERIAL AND METHODS

This study was carried out during three years 2010-13 at the Experimental Farm of Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, Egypt.

Five genetically diverse bread wheat (*Triticum aestivum* L.) parents representing a wide range of maturing earliness response were studied. The name, pedigree and earliness of maturing of these genotypes are given in Table 1.

Three crosses derived from the above parents have been chosen as follows: Misr 2 x Gemmeiza 9 (Cross 1, Late x Late), Line 1 x Line 2 (Cross 2, Early x Early) and Gemmeiza 9 x Line 3 (Cross 1, Late x Early).

The hybrid seed from each cross were obtained from a proceeding study and grown in 2010/2011 wheat growing season to obtain the F₂ seed. In 2011/2012, out of each F₂ population, 60 plants were randomly selected and their F₃ seed were taken to grow F₃ families. On 25th, November 2012, the parents and the three crosses were evaluated and the recommended cultural practices for wheat production were applied at the proper time.

Table 1. Name, pedigree and earliness of maturing of the studied bread wheat parents

Name	Cross Name & Pedigree	Earliness of maturing
Misr 2	SKAUZ / BAV92 CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S	Late
Gemmeiza 9	Ald "S" / Huac // C74A. 630 / Sx CGM 4583-5GM-1GM-0GM	Late
Line 1	GIZA168/5/MAI"S"/FJ//ENU"S"/3/KITO/POTO19//MO/JUP/4/K 134(60)VEE S.15410-19S-7S-2S-0SS.15410-19S-7S-2S-0S	Early
Line 2	KAUZ/ATTILA/7/KVZ/4/CC/INIA/3/CNO//ELGAU/SON64/5/SP ARROW"S"/BROCHIS"S"/6/BAYA"S"/IMU S.15563-9S-3S-1S-0S	Early
Line 3	ATTILA*2/GIZA168 S.15612-1S-1S-4S-0S	Early

The evaluation experiment was conducted using the replicated complete block design with three replicates. For a replicate, each cross consisted of 62 rows, one row for P₁ and P₂ and sixty rows for F₃ families (one row for each family). Each row was 3 meters long and 25 cm apart. Plants within rows were 20 cm spaced, so, each row comprised fifteen plants. In each row, data were taken on five random competitive plants for P₁, P₂ and F₃ families.

The Data recorded were days to heading (DH, days), days to maturity (DM, days), grain filling period (GFP, days) and rate (GFR, gm days⁻¹), plant height (PH, cm), number of spikes per plant (SP⁻¹), number of kernels per spike (KS⁻¹), 100-kernel weight (100KW, gm) and Grain yield (GY, gm).

Statistical analyses were performed using the statistical routines available in Microsoft EXCEL [7]. The "t" test was used to test the significance of difference between means of the two parents in each cross according to [8]. Basic generations' variances for each cross including three populations (P₁, P₂ and F₃) were statistically analyzed on plot mean and individual plant bases according to [9]. These values were used in estimation of additive and dominance genetic variances. A direct F test was made to determine if the differences among F₃ families are significant. In addition, the heritability in the broad (h_{2b}) and narrow (h_{2n}) senses for F₃ family means were estimated as described by [10]. The expected genetic advance from selection (Δg) was computed according to [11] and [12] Table 12.

3. RESULTS AND DISCUSSION

3.1 The t-test and Analysis of Variance

The t-test in Table 2 showed that the two parents in each cross are significantly different in heading (DH, days), days to maturity (DM, days), grain filling period (GFP, days), plant height (PH, cm), number of spikes per plant (SP⁻¹), except for number of kernels per spike (KS⁻¹) in all crosses, 100-kernel weight (100KW, gm) in cross 1 and grain filling rate (GFR, gm days⁻¹) and Grain yield (GY, gm) in cross 2.

Table 2. The "t" test estimates of the two parents in each cross for the studied characters

DH	DM	GFP	GFR	GY	PH	SP ⁻¹	KS ⁻¹	100-KW
(Cross1) Misr 2 x Gemmeiza 9								
**	**	**	**	**	**	**	ns	ns
(Cross 2) Line 1 x Line 2								
**	**	**	ns	ns	**	*	ns	**
(Cross 3) Gemmeiza 9 x Line 3								
**	**	**	**	**	**	**	ns	**

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

Table 3. Analysis of variance for the studied characters for the F₃ families in the three wheat crosses

Source of variation	DF	DH	DM	GFP	GFR	GY	PH	SP ⁻¹	KS ⁻¹	100-KW
MS										
(Cross1) Misr 2 x Gemmeiza 9										
Replication (R)	2	111.0**	161.7**	8.0	0.146	278.4	834.4*	101.6	2370.4**	0.6
Among F3 families (F)	59	116.9**	121.0**	27.0**	0.803	1732.8**	742.0**	274.1**	830.3**	1.9**
R x F (Error)	118	21.8	21.8	9.4	0.169	356.3	210.0	56.1	273.6	0.6
Plants within F3 families	720	13.7	13.1	6.9	0.129	273.6	73.3	36.3	204.4	0.3
(Cross 2) Line 1 x Line 2										
Replication (R)	2	32.7	72.8	10.1	0.421	858.2	2783.5**	606.0**	165.8	0.2
Among F3 families (F)	59	123.1**	120.2**	41.6**	0.375	908.3**	1068.3**	123.0**	589.6**	3.2**
R x F (Error)	118	33.4	27.2	17.9	0.179	398.0	290.0	46.6	315.5	1.2
Plants within F3 families	720	17.1	12.9	14.5	0.097	224.1	96.2	28.8	194.0	0.5
(Cross 3) Gemmeiza 9 x Line 3										
Replication (R)	2	25.3	54.8*	74.6**	0.023	114.4	864.7*	148.9	387.5	7.6**
Among F3 families (F)	59	123.7**	133.0**	43.0**	0.398	856.3**	641.2**	266.8**	924.7**	2.2**
R x F (Error)	118	18.4	17.7	11.4	0.167	382.1	215.9	111.6	267.4	0.5
Plants within F3 families	720	13.0	14.0	8.4	0.118	252.3	67.3	61.4	212.6	0.3

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

Analysis of variance of all characters for the F_3 families is presented in above Table 3. Highly significant differences among the F_3 families were found in all crosses for all characters, except for GFR in all crosses. These significant differences indicate the size of the difference among the parents, which were expressed in the amount of the variability produced from segregation in the F_3 families. It could be permit to select for extreme types such as earlier, shorter, yielder and heavier kernel weight. Transgressive segregation occurred even in crosses involving parents that were similar in phenotypic performance, indicating that these parents were different genotypically. In general, these results were in harmony with those obtained by [1].

3.2 Means Performance

The mean values of all characters in the three crosses are presented in Table 4. The superior parents were Gemmeiza 9 for DH, DM and PH; Misr 2 for GFR, GY and KS^{-1} ; Line 2 for GFP; Line 3 for 100KW and Line 1 for SP^{-1} . On the other hand, the inferior parents were Gemmeiza 9 for GFP, GFR, GY and SP^{-1} ; Line 3 for DH and DM and Line 1 for PH, KS^{-1} and 100KW.

F_3 means of cross 1 surpassed the other F_3 populations for DH, DM, PH, SP^{-1} and KS^{-1} , while cross 3 surpassed the others in GFR and GY, in addition cross 2 had the highest GFP and 100KW. The lowest F_3 means belonged to cross 1 for GFP, GFR, GY and 100KW and cross 2 for DH, DM, PH, SP^{-1} and KS^{-1} .

The F_3 family means went in line with the corresponding highest parent for GFP and 100KW in cross 2; DH, DM and GFP in cross 3. Meanwhile, the F_3 family means were in line with the corresponding lowest parent for GFR, GY and KS^{-1} in cross 1. Moreover, the F_3 family means went in midway between the two corresponding parents in cross 1 for GFP and SP^{-1} ; cross 3 for DH, GFR, GY and 100KW. In addition, the F_3 family means were higher the highest corresponding parents for DH, DM and PH in cross 1 and 2; KS^{-1} in cross 2 and PH in cross 3. Moreover, the F_3 family means were lower than lowest corresponding parent for 100KW in cross 1; GFR, GY and SP^{-1} in cross 2 KS^{-1} in cross 3.

The ranges of the performance of the F_3 families exceeded the limits of the minus and plus directions of their parents for all characters, except for DH in all crosses, DM in cross 2 and 3, PH in cross 3 and SP^{-1} in cross 2. These results showed the ability to selection for the desirable directions for these characters.

3.3 Genetic and Environmental Variances

The estimation of the genetic variance and its components was made according to [9]. This model for computing the variance components carries the assumptions of: (1) no linkage, (2) no epistasis, (3) normal diploid meiosis, (4) random choice of the material and (5) gene frequency of 0.5 for segregating loci. Assumptions (3), (4) and (5) were most probably fulfilled.

The genetic and environmental variance components among F_3 families and among plants within families for all caharacters are illustrated in Table 5.

Table 4. Means of the parents and their F₃ generations, in addition to the ranges of F₃ family means (between brackets) for the studied characters in the three wheat crosses

Population		DH	DM	GFP	GFR	GY	PH	SP ⁻¹	KS ⁻¹	100-KW
Parents										
	Misr 2	96.6	144.9	48.3	1.500	67.7	89.7	26.1	82.9	3.72
	Gemmeiza 9	102.0	146.7	44.7	0.794	36.26	98.7	15.1	79.6	3.84
	Line 1	89.3	134.7	45.5	1.141	51.99	72.7	27.4	62.9	3.70
	Line 2	83.5	133.2	49.7	1.151	56.78	82.3	24.4	67.1	4.48
	Line 3	83.3	131.9	48.5	1.127	54.96	82.3	26.6	76.9	4.63
	Mean	90.9	138.3	47.3	1.133	53.53	85.1	23.9	73.9	4.07
F₃ s										
	Misr 2 x Gemmeiza 9	104.6	151.3	46.7	0.880	40.97	106.0	21.5	76.3	3.65
	(Cross1)	(99.6-114.1)	(141.7-158.3)	(42.1-49.1)	(0.352-1.654)	(16.05-79.77)	(87.0-127.0)	(14.0-34.7)	(58.1-95.4)	(2.81-4.51)
	Line 1 x Line 2	90.9	139.6	48.6	0.933	45.25	97.8	20.8	69.3	4.39
	(Cross2)	(84.0-96.9)	(133.4-145.3)	(43.3-52.2)	(0.557-1.358)	(26.92-65.79)	(80.7-114.0)	(14.3-26.3)	(50.8-81.9)	(3.54-5.33)
	Gemmeiza 9 x Line 3	96.9	144.4	47.5	0.967	45.77	102.7	21.2	71.9	4.16
	(Cross3)	(91.3-102.4)	(135.8-150.1)	(43.5-51.1)	(0.602-1.352)	(29.32-61.74)	(86.0-114.7)	(8.9-32.7)	(54.1-91.8)	(3.28-4.97)
	Mean	97.5	145.1	47.6	0.927	44.00	102.2	21.2	72.5	4.07
	Total Mean	93.1	140.6	47.4	1.065	50.58	90.8	23.0	73.4	4.07

Table 5. Genetic (σ^2G) and environmental (σ^2E) variance components among F_3 families and among plants within F_3 families for the studied characters in the three wheat crosses

Source		DH	DM	GFP	GFR	GY	PH	SP-1	KS ⁻¹	100-KW
(Cross1) Misr 2 x Gemmeiza 9										
Among families	σ^2G	6.3	6.6	1.2	0.042	103.5	35.5	15.9	37.1	0.09
	σ^2E	1.5	1.5	0.6	0.011	23.8	14.0	3.7	18.2	0.04
Among plants within families	σ^2G	10.4	8.5	3.1	0.016	28.3	44.9	5.3	57.7	0.08
	σ^2E	3.3	4.6	3.8	0.110	245.4	28.45	31.0	146.7	0.22
(Cross 2) Line 1 x Line 2										
Among families	σ^2G	6.0	6.2	1.6	0.013	36.0	51.9	5.1	18.3	0.13
	σ^2E	2.2	1.8	1.2	0.012	26.5	19.3	3.1	21.0	0.08
Among plants within families	σ^2G	7.7	11.3	6.7	0.007	14.0	89.5	3.5	20.9	0.12
	E	9.4	1.6	7.8	0.090	210.1	6.67	25.3	173.1	0.40
(Cross 3) Gemmeiza 9 x Line 3										
Among families	σ^2G	7.0	7.7	2.1	0.015	40.7	28.4	10.3	43.8	0.11
	σ^2E	1.2	1.2	0.8	0.011	25.5	14.4	7.4	17.8	0.04
Among plants within families	σ^2G	3.6	11.2	1.0	0.018	2.2	48.9	18.5	49.2	0.15
	σ^2E	9.4	2.8	7.4	0.100	250.1	18.45	42.8	163.	0.18

5

The magnitude of genetic variance among the F_3 families exceeded corresponding environmental variance for all characters, except for KS^{-1} in cross 2. In addition, the genetic variance among plants within families was higher than the corresponding environmental variance for DM and PH in all crosses and DH only in cross 1. For the remaining characters, the environmental variance was higher than or almost equal to the corresponding genetic variance. It is evident that the variance of DH, DM and PH were mostly due to the genetic effects.

The genetic variance among F_3 families were higher than those among plants within families for GY in all crosses; GFR, SP^{-1} and 100KW in cross 1 and 2 and DH and GFP in cross 3. These results are similar to those obtained by [1] for the grain yield and its components and plant height. Moreover, [13] reported that the selection is much more effective because the environmental variation is reduced by working with means and the non-additive variation is reduced by inbreeding.

3.4 Genetic Varince Components, Heritability and Expected Genetic Advance

Estimates of variance components, heritability in broad ($h^2_{(b)}$) and narrow senses ($h^2_{(n)}$) and expected genetic advance for all characters within F_3 families in each cross are presented in Table 6.

Because of the negative estimates of the dominance variance, heritability estimates in broad and narrow sense were the same for GY in crosse 2 and 3; GFR and SP^{-1} in cross 1 and GFP in cross 3. For the remaining characters, the narrow sense heritabilities were much lower than the broad heritabilities, except for GFR and SP^{-1} in cross 2 and DH in cross 3. These results indicate that the additive portions were including of the genetic variations in the F_3 generation.

Table 6. Estimates of additive (σ^2_A) and dominance (σ^2_D) variances, heritability in broad ($h^2_{(b)}$) and narrow senses ($h^2_{(n)}$) and expected genetic advance (Δg) within F_3 family means for the studied characters

Parameters	DH	DM	GFP	GFR	GY	PH	SPI ⁻¹	KS ⁻¹	100-KW
(Cross1) Misr 2 x Gemmeiza 9									
V A	1.5	3.1	0.3	0.046	55.9	17.4	15.9	11.0	0.06
¼ V D	4.8	3.5	1.0	-0.003	35.8	18.1	-1.3	26.1	0.02
Hertability (b)	81.4	82.0	71.5	80.19	79.4	71.7	80.9	67.0	67.51
Hertability (n)	19.7	38.7	18.3	80.19	48.4	35.1	80.9	19.9	49.70
$\Delta g F_3$	5.0	6.0	1.8	0.39	12.9	11.6	7.4	9.0	0.55
(Cross 2) Line 1 x Line 2									
V A	2.8	0.8	0.3	0.01	36.0	9.5	4.4	10.5	0.10
¼ V D	3.2	5.4	1.5	0.000001	-2.0	42.4	0.7	7.8	0.03
Hertability (b)	72.9	77.4	67.2	52.344	57.6	72.9	62.1	46.5	62.4
Hertability (n)	34.3	9.4	12.1	52.348	57.6	13.3	54.0	26.6	46.7
$\Delta g F_3$	4.8	3.0	1.5	0.17	9.4	9.5	3.9	5.4	0.60
(Cross 3) Gemmeiza 9 x Line 3									
V A	7.0	2.8	2.1	0.01	69.3	5.2	1.4	25.7	0.05
¼ V D	0.03	4.9	-0.036	0.007	-37.7	23.1	8.9	18.2	0.10
Hertability (b)	85.1	86.7	73.9	58.2	73.1	66.3	58.2	71.1	75.4
Hertability (n)	84.7	31.0	73.9	32.7	73.1	12.2	8.1	41.6	31.3
$\Delta g F_3$	5.1	7.0	2.6	0.2	14.7	5.8	2.2	13.1	0.70

The additive variance components exceeded the dominance portions for GFR and GY in all crosses; SP⁻¹ and 100KW in cross 1 and 2; KS⁻¹ in cross 2 and 3 and DH and GFP in cross 3. The remaining characters showed dominance variance higher than or almost equal to the additive variance component.

Since variances cannot be negative, any negative estimates of variance may be an estimates of zero. Thus dominance component was an estimates of zero in many cases. These negative values could have resulted from larger genotyp x environment interaction for among plants within families than that for among families and therefore might underestimate the variance.

In this respect, [1] obtained similar results and found relatively moderate to high broad and narrow sense heritability and expected genetic advance values estimates were found for most agronomic characters.

Relatively medium to high broad and narrow sense heritability estimates for all characters were recorded, except for the narrow sense heritability in all cross for DM and PH; cross 1 and 2 for DH and KS⁻¹ and cross 3 for GFR, SP⁻¹ and 100KW. The comparatively high environmental and low genetic variance for the excepted characters accounted for their low heritability values. Meanwhile, the high estimates of heritability indicate the importance of the additive component in the inheritance of these characters.

High heritability alone is not enough to make sufficient improvement through selection generally in advance generations unless accompanied by substantial amount of genetic advance [14]. The expected genetic advance values were low for GFR and 100KW in all crosses; SP⁻¹ in cross 2 and 3; DM in cross 2 and GFP in cross 3. The remaining characters had medium to high estimates of genetic advance.

4. CONCLUSION

Dominance and additive types of gene action were involved in the inheritance of all studied characters, with predominant for dominance gene action. According to the high estimates of heritability and genetic advance for GFP, GY, SP⁻¹, KS⁻¹ and 100KW it could be concluded that selection for these characters would be effective in early generation, whereas, selection for DH, DM, GFR and ph⁻¹ would be effective in late generation. 5% of plants for each cross were selected for early mature and high yielding to evaluate in separate experiment in the next season.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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