ASSESSMENT OF GENETIC PARAMETERS FOR EARLY MATURING AND GRAIN YIELD IN SOME BREAD WHEAT CROSSES UNDER OPTIMUM AND LATE SOWING DATES

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ABSTRACT

Considerable attention is paid in the Egyptian National Wheat Research Program to develop early maturing and high yielding cultivars. Therefore, six early to moderate maturing bread wheat lines were crossed to produce three cross populations. The six populations model was used through three growing seasons from 2017/18 to 2019/20. The objective was to determine the intra- and inter-allelic gene interactions controlling earliness and some agronomic traits as well as identify the best germplasm which had accumulated early maturing gene pool. Results showed that late sowing date in end of December decreased all studied traits. Both additive and dominance gene effects and variances were important in inheritance of the studied traits. Additive effects and variance were larger than corresponding dominance ones in most cases. Heritability in broad and narrow sense and expected genetic advance as percent of F_2 mean were moderate to high for all the studied traits. Negative and significant phenotypic and genotypic correlation between grain yield and earliness traits were obtained. Generally, most biometrical parameters resulted from cross 2 (line 3 x line 4) and cross 3 (line 5 x line 6) were higher in magnitude compared to cross 1 (line 1 x line 2), thus, these two crosses would be used in breeding program for improving earliness and grain yield traits.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important and strategic cereal crops worldwide. In Egypt, wheat is the main winter cereal crop used as a staple food for urban and rural societies and the major source of straw for animal feed.

Considerable attention is paid in the Egyptian National Wheat Research Program to develop early maturing and high yielding cultivars. Early maturing allows to escape of environmental stresses like disease and heat in the end of growing season (**Acquaah, 2012**). Also, short-duration wheat varieties are often preferred by farmers for use in crop intensification. They also require fewer inputs, especially for irrigation,

due to the shorter crop cycle (**Mondal *et al*. 2016**). On the other hand, early maturity genotypes only partially exploit the growing season and economic yield may be significantly reduced. However, it is known that longer growth duration is associated with high grain yield (**Acquaah, 2012**).

Crop maturity in general is affected by many factors in the environment conditions, including photoperiod, temperature, altitude, relative humidity, soil fertility, and plant genotype (**Acquaah, 2012**). Accordingly, a better understanding of earliness inheritance and type of gene action would help wheat breeders to efficiently improve early maturing with high yielding cultivars.

Selection of early maturing genotypes under conflicting environments like sowing dates, receive more attention in wheat breeding programs. Late sowing dates in Egypt cause heat stress for wheat plants during grain filling period resulting in grain yield losses (**Abd El-Rady 2018, Abdallah *et al*. 2019, Farhat *et al*. 2019 and Koubisy 2019**).

Therefore, the present study aimed to enhance wheat breeding program efficiency through (1) determining intra- and inter-allelic gene interactions controlling earliness and agronomic traits in three cross populations of bread wheat, (2) assessing some genetic parameters which improve selection in segregating generations, and (3) identifying best genotypes had accumulated early maturing gene pool.

MATERIALS AND METHODS

The present study was carried out at the Experimental Farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt through three wheat growing seasons of 2017/18, 2018/19 and 2019/2020. Six moderate to early maturing bread wheat lines were used as parents. Name, pedigree and selection history in addition to days to heading and maturity in last 5 wheat growing seasons which were recorded by National Wheat Research Program for these parents are presented in Table (1).

In 2017/18, F_1 hybrids were obtained for Line 1 x Line 2 (cross 1), Line 3 x Line 4 (Cross 2) and Line 5 x Line 6 (cross 3). In 2018/19, BC_1 (F_1 x P_1), BC_2 (F_1 x P_2) and F_2 seeds were produced for each cross. In the third season (2019/20), the six populations of each cross (P_1, P_2, F_1, BC_1, BC_2 and F_2) were evaluated under optimum sowing date (24 November, 2019) and Late sowing date (24 December, 2019) in three replications. Each replication for each cross consisted of 6 rows for each population. The rows were 4 m long with 30 apart and 15 cm within rows. All the recommended cultural practices for wheat production in north Delta were applied at the proper time. Maximum and minimum temperatures were presented in Figure (1) according to Sakha meteorological station.

Table 1: Name, pedigree, days to heading and maturity in last 5 wheat growing seasons of the studied parents.

| Name	Pedigree	Selection history	Number of days to heading	Number of days to maturity
Line 1	**PRL/2*PASTOR//KACHU/3/TRCH/SRTU//KACHU**	CMSS10Y00993T-099TOPM-099Y-099M-14WGY-0B	**87-99**	**137-155**
Line 2	**CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /3/ 2*KAUZ /4/ HAAMA-11**	S. 16276 -018S-010S-3S-0S	**75-86**	**128-139**
Line 3	**DVERD 2 / AE - SQUARROSA (214) // 2* BCN /3/ GIZA 168 /8/MAI "S" / PJ // ENU "S" /3/ KITO / POTO. 19 // MO / JUP /4/ K 134 (60) / VEE/7/KAUZ /6/ ATL 66 / H567.71 // ATL 66 /5/ PMN5 // S948.A1 / 4*CNO67 /3/ PMNS /4/ CMH75A.66**	S. 16832 -020S -08S-1S -0S	**83-93**	**133-137**
Line 4	**NING MAI 50 /6/ SAKHA 12 /5/ KVZ // CNO 67 / PJ 62 /3/ YD "S" / BLO "S" /4/ K 134 (60) / VEE**	S. 16604 -073S -010S-6S -0S	**86-88**	**140-147**
Line 5	**WBLL1*2/BRAMBLING // HUBARA-21**	S. 17017 -056S -019S-1S -0S	**83-92**	**133-139**
Line 6	**TOBA97/ATTILA /8/ KAUZ / ATTILA /7/ KVZ /4/ CC / INIA /3/ CNO // ELGAU / SON 64 /5/ SPARROW "S" / BROCHIS "S" /6/ BAYA "S" / IMU**	S.2011-29-26S-08S-2S-0S	**75-85**	**126-132**
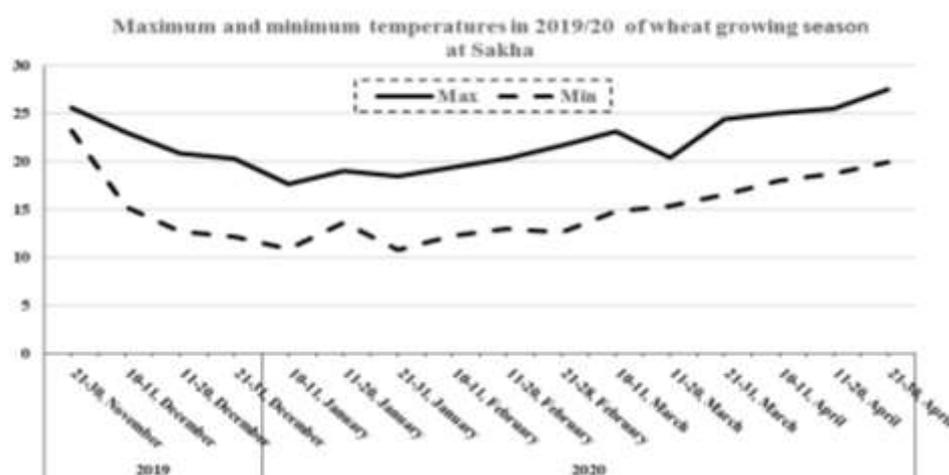
Figure 1: Maximum (Max) and minimum (Min) temperatures in 2019/20 season of wheat growing at Sakha.

Data were recorded on individual plants in the central four rows and represented by 20 plants for each parent and F_1, 50 plants for each backcross, and 70 plants for each F_2 in each replication. The studied traits were days to heading (DH), days to maturity (DM), grain filling period

(GFP), grain filling rate (GFR, g day^{-1} plant^{-1}), plant height (PH, cm), number of spikes plant^{-1} (SP) and grain yield plant^{-1} (GY, g).

The analysis of variance was performed using randomized complete block design and LSD were calculated to test the significance of differences among means according to **Steel *et al*. (1997).** Difference between F_2 and corresponding environmental variances was tested by F ratio. Significance of F ratio indicate enough variability in the studied material to estimate the components of genetic variance. **Mather's (1949)** scaling test was performed for confirmation of additive-dominance model reported by **Singh and Chaudhary (2010)**. Estimates of variances gene effects, allelic interaction and their test of significance were computed by six-parameter model of **Jinks and Jones (1958)**. Environmental variance was calculated as the average variances of the two parents and F_1 plants. Genotypic variance was estimated by subtracting the environmental variance from corresponding phenotypic variance in F_2 populations. Broad and narrow sense heritability and expected genetic advance from selection as percentage of F_2 mean were estimated according to **Mather and Jinks (1982).** The phenotypic and genotypic correlation between grain yield and other studied traits was estimated for every population under the two sowing dates according to **Steel *et al*. (1997)**.

RESULTS AND DISCUSSIONS

The variance for each population in each cross is presented in Table (2). Highest variance was obtained by the F_2 population for all studied traits in the three crosses, followed by that of backcross populations (BC$_1$'s and BC$_2$'s), reporting that the maximum heterogeneity exists in F_2 population. On the other hand, the lowest variance was obtained by parents (P$_1$'s and P$_2$'s) and F_1 populations, indicating to the homogeneity of these populations and their variance is due to environmental factors. These results may be logic and suggests the validity of estimating the appropriate genetic model and determine the different gene effects for the studied traits of the three cross populations.

Mean performance

Mean performance of the populations in the three studied crosses are given in Table (3). The wheat breeder prefers the lowest values of DH, DM, GFP and PH. Means values for all traits of studied crosses decreased under late sowing date compared to optimum one, except for GFR in cross 2 and 3.

Table 2: The variances for all studied traits of studied six populations in the three wheat crosses under optimum (SD1) and late (SD2) sowing dates.

Traits	Sowing date	P_1	P_2	F_1	F_2	BC_1	BC_2
Cross 1 (Line 1 x Line 2)							
DH	SD1	4.87	3.92	4.79	22.04	16.57	10.17
	SD2	7.64	7.79	5.28	26.06	11.66	24.23
DM	SD1	2.93	1.71	1.99	8.38	5.64	9.93
	SD2	4.43	2.14	3.05	10.43	6.55	7.86
GFP	SD1	5.58	4.73	4.99	15.23	12.55	12.91
	SD2	2.18	6.5	3.13	14.00	10.22	13.75
GFR	SD1	0.026	0.028	0.007	0.238	0.151	0.109
	SD2	0.028	0.021	0.006	0.077	0.075	0.035
PH	SD1	4.07	8.83	5.50	24.41	10.92	32.21
	SD2	6.35	6.18	7.80	67.59	38.85	36.58
SP	SD1	12.32	9.86	8.18	61.43	41.37	30.71
	SD2	17.26	3.58	8.71	47.06	25.24	32.02
GY	SD1	75.42	79.86	16.95	703.13	452.26	311.01
	SD2	55.45	39.73	10.15	162.43	138.95	73.56
Cross 2 (Line 3 x Line 4)							
DH	SD1	2.25	7.1	3.75	17.36	13.75	17.80
	SD2	5.95	7.70	8.88	23.17	15.97	17.83
DM	SD1	6.15	8.88	3.46	16.69	12.60	10.44
	SD2	4.3	2.06	4.30	10.70	11.09	7.70
GFP	SD1	8.15	14.29	4.38	18.91	20.06	16.09
	SD2	6.39	5.73	6.25	14.38	11.86	9.12
GFR	SD1	0.03	0.04	0.01	0.12	0.08	0.09
	SD2	0.001	0.001	0.001	0.06	0.05	0.08
PH	SD1	5.5	6.63	6.33	34.12	25.46	14.86
	SD2	4.77	4.77	9.07	42.45	29.67	24.64
SP	SD1	10.47	18.10	11.15	43.78	31.29	34.26
	SD2	15.34	15.68	12.08	41.79	28.68	32.57
GY	SD1	85.85	89.98	16.95	408.45	252.08	316.19
	SD2	3.13	1.36	3.84	164.54	92.62	153.17
Cross 3 (Line 5 x Line 6)							
DH	SD1	5.94	3.44	5.71	18.93	14.11	13.62
	SD2	8.44	1.34	7.12	35.05	20.43	21.47
DM	SD1	6.76	1.13	3.23	20.88	11.78	20.54
	SD2	7.17	1.30	3.23	13.49	10.85	10.29
GFP	SD1	8.12	4.00	8.52	15.27	14.96	15.41
	SD2	8.02	2.10	10.15	13.58	13.44	13.40
GFR	SD1	0.02	0.02	0.01	0.09	0.07	0.08
	SD2	0.04	0.03	0.01	0.07	0.07	0.06
PH	SD1	10.06	4.94	9.17	17.83	16.33	15.03
	SD2	13.07	12.28	9.17	49.61	31.80	31.35
SP	SD1	9.83	9.50	8.33	38.02	22.26	25.83
	SD2	10.89	8.19	11.83	26.12	20.44	17.31
GY	SD1	78.49	84.61	29.02	321.31	209.48	235.31
	SD2	73.75	54.24	7.58	152.82	153.12	115.72

DH = days to heading, DM = days to maturity, GFP = grain filling period, GFR = grain filling rate (g day^{-1} plant^{-1}), PH = plant height (cm), SP = number of spikes plant^{-1} and GY = grain yield plant^{-1}.

Table 3: Mean performance of the six populations in the three crosses for studied traits under optimum (SD1) and late (SD2) sowing dates.

Trait	Sowing date	P_1	P_2	MP	F_1	F_2	BC_1	BC_2	$LSD_{0.05}$
— Cross 1 (Line 1 x Line 2)								
DH	SD1	96.3	83.9	90.1	90.2	91.9	95.2	88.7	1.6
	SD2	91.0	81.7	86.4	88.9	87.2	88.2	82.4	2.1
DM	SD1	149.5	139.0	144.2	145.2	146.2	149.2	144.0	0.7
	SD2	135.9	126.9	131.4	133.4	131.8	132.9	129.0	1.5
GFP	SD1	53.3	55.1	54.2	54.9	54.2	54.0	55.3	1.3
	SD2	44.8	45.2	45.0	44.5	44.6	44.7	46.5	1.1
GFR	SD1	1.19	0.80	1.00	0.82	1.13	0.95	0.82	0.10
	SD2	0.88	0.64	0.76	0.98	0.78	0.78	0.57	0.07
PH	SD1	106.0	87.3	96.6	101.6	96.4	93.5	79.0	1.5
	SD2	82.4	72.1	77.3	88.0	80.0	89.7	77.9	1.5
SP	SD1	26.6	18.6	22.6	14.0	23.0	20.4	21.0	2.3
	SD2	25.6	17.8	21.7	11.9	22.0	19.5	18.2	2.6
GY	SD1	63.6	44.2	53.9	45.0	61.3	51.2	45.3	5.7
	SD2	39.3	29.0	34.2	43.4	34.9	34.5	26.3	2.7
Cross 2 (Line 3 x Line 4)								
DH	SD1	86.5	87.2	86.8	88.2	86.4	89.4	90.8	2.2
	SD2	83.5	86.9	85.2	85.9	79.3	86.8	89.2	3.1
DM	SD1	141.0	143.7	142.3	145.4	143.1	140.8	145.4	2.4
	SD2	126.9	134.8	130.8	130.9	132.8	131.0	133.5	2.9
GFP	SD1	54.6	56.5	55.5	57.2	56.7	51.4	54.6	3.7
	SD2	43.5	47.8	45.6	45.1	53.6	44.2	44.4	1.4
GFR	SD1	0.69	0.89	0.79	0.82	0.77	0.75	0.77	0.1
	SD2	0.83	0.79	0.81	0.88	0.66	0.69	0.87	0.07
PH	SD1	90.9	99.3	95.1	102.3	101.5	100.2	109.0	1.1
	SD2	91.3	96.3	93.8	99.5	96.4	90.2	88.8	1.6
SP	SD1	15.1	22.4	18.7	19.8	17.8	15.7	19.9	3.0
	SD2	13.6	20.3	16.9	16.6	16.8	15.0	17.4	1.9
GY	SD1	37.5	49.8	43.7	47.0	43.9	39	42.3	6.3
	SD2	36.2	37.8	37.0	39.5	35.4	30.5	38.4	2.8
Cross 3 (Line 5 x Line 6)								
DH	SD1	84.8	86.0	85.4	82.7	84.1	85.3	87.4	1.9
	SD2	82.0	84.3	83.2	79.6	83.3	82.1	83.6	2.2
DM	SD1	144.1	145.0	144.5	142.9	143.1	142.6	144.4	2.6
	SD2	129.0	130.5	129.8	130.9	129.8	129.7	129.6	1.7
GFP	SD1	59.3	59.0	59.1	60.2	59.1	57.3	57.0	2.2
	SD2	47.0	46.2	46.6	51.3	46.6	47.6	46.0	2.0
GFR	SD1	0.88	0.79	0.83	0.78	0.68	0.67	0.63	0.12
	SD2	0.80	0.77	0.79	0.78	0.71	0.72	0.60	0.11
PH	SD1	93.7	100.8	97.2	103.3	99.9	89.3	104.7	1.5
	SD2	90.3	94.9	92.6	98.3	86.9	87.5	93.8	1.6
SP	SD1	27.3	22.3	24.8	16.7	19.4	23.6	20.3	1.7
	SD2	25.8	20.3	23.0	18.6	18.7	14.2	16.7	1.1
GY	SD1	51.8	46.3	49.1	46.6	39.9	38.0	35.6	6.3
	SD2	37.7	35.6	36.6	39.9	32.8	34.1	27.6	4.7

P_1 = first parent, P_2 = second parent, MP = mid parent F_1 = first generation, F_2 = second generation, BC_1 = backcross first parent, BC_2 = backcross for second parent, DH = days to heading, DM = days to maturity, GFP = grain filling period, GFR = grain filling rate (g day^{-1} plant^{-1}), PH = plant height (cm), SP = number of spikes plant^{-1} and GY = grain yield plant^{-1}.

Reduction in agronomic and earliness traits under late sowing date may be a result of high temperature in end of growing season (**Abd El-Rady 2018, Abdallah *et al*. 2019, Farhat *et al*. 2019, Hagras 2019 and Koubisy 2019**). Previous studies have observed similar effects of high temperature on days to heading and maturity and plant height (**Mondal *et al*., 2013 and 2016 and Hagras 2019**). Genotype under late sowing date recorded a few numbers of growing days, then yield components decrease and hence the economic yield suffers negatively (**Menshawy *et al*. 2015 and Hagras 2019**).

The two parents differed significantly in each cross for all the studied traits, except for GFP under late sowing date in cross 1, GY under late sowing date in cross 2, and DM, GFP, and GFR under both sowing dates, DH under optimum sowing date and GY under late sowing date in cross 3. Differences were more pronounced between parents in cross 1, then cross 2 for most traits. Line 1 had the highest values of parents for DH, DM, GFP, PH, SP and GY, while Line 2 showed an opposite trend for the same traits under both sowing dates. Moreover, Line 3, 4 and 6 had close values for DH, DM and GFP. Similar results were obtained by **Abdelkhalik (2019), Morsy (2020) and Sharshar and Genedy (2020).**

Means of F_1 generation were in-between P_1 and P_2 means for DH and DM under both sowing dates, GFP, PH and GY under optimum sowing date in cross 1, SP under both sowing dates, GFR and GY under optimum sowing date and DH, DM and GFP under late sowing date in cross 2, and DM under late sowing date in cross 3. These results indicated presence of partial or absence of dominance as well as additive gene effects and similar to those of **Abd El-Rady (2018) and Koubisy (2019)**.

Moreover, means of F_1 population was higher than the respective parents for GFR, PH and GY under late sowing date in cross 1, PH under both sowing dates, DH and DM under optimum sowing date and GFR and GY under late sowing date in cross 2, and GFP and PH under both sowing dates and GY under late sowing date in cross 3. These results indicate the presence of overdominance with positive heterotic effect.

Also, F_1 means were lower than or close to the lower parent for SP under both sowing dates and GFP under late sowing date in cross 1, GFP under optimum sowing date in cross 2, and DH, GFR and SP under both sowing dates and DM and GY under optimum sowing date in cross 3.

Means of F_2 population were lower than respective F_1 population for PH under both sowing dates, GFP under optimum sowing date and DH, DM, GFR and GY under late sowing date in cross 1, DH, PH, GFR and GY under both sowing dates and DM, GFP and SP under optimum sowing date in cross 2, and GFP, GFR, PH and GY under both sowing dates and DM under late sowing date in cross 3. These results indicated to positive inbreeding depression for these cases.

On the contrary, F_2 population means were higher than F_1 means for SP under both sowing dates, DH, DM, GFR and GY under optimum sowing date and GFP under late sowing date in cross 1, DM, GFP and SP under late sowing

date in cross 2, and SP and DH under both sowing dates and DM under optimum sowing date in cross 3. These results indicated to negative inbreeding depression in these cases.

In general, means of the BC_1's were close to those of their respective female parents (P_1's) and means of the BC_2's were close to their respective male parents (P_2's) for all studied traits in the three crosses, that referred to highly homogeneity for BC with their parents. Similar results were obtained by **Abdallah *et al* (2019), Abdelkhalik (2019), Koubisy (2019) and Sharshar and Genedy (2020)**.

Gene effects

The simple scaling test (A, B and C) was used to detect the presence of non-allelic interaction (Table 4). Significance of any one of the epistatic scales would indicate the presence of non-allelic interactions amongst the genes controlled traits in view. The parameters A, B and C showed significance for the different traits, indicating the adequacy of the six parameters model to explain the type of gene action controlling the traits of the studied crosses.

Table 4. Scaling tests (A, B and C) for the studied traits under optimum (SD1) and late (SD2) sowing dates.

Trait	A		B		C	
	SD1	SD2	SD1	SD2	SD1	SD2
Cross 1 (Line 1 x Line 2)						
DH	3.9**	-3.55**	3.33**	-5.83**	7.12**	-1.94
DM	3.76**	-3.41**	3.98**	-2.33**	5.93**	-2.5*
GFP	-0.14	0.14	0.65	3.49**	-1.19	-0.56
GFR	-0.12	-0.3**	0.02	-0.49**	0.88**	-0.35**
PH	-20.52**	9.05**	-30.83**	-4.24**	-10.82**	-10.7**
SP	0.39	1.47	9.5**	6.79**	18.82**	20.73**
GY	-6.22	-13.79**	1.35	-19.77**	47.3**	-15.69**
Cross 2 (Line 3 x Line 4)						
DH	4.08**	4.33**	6.31**	5.53**	-4.42**	-25.05**
DM	-4.77**	4.21**	1.85**	1.26*	-2.85*	7.79**
GFP	-8.82**	-0.09	-4.43**	-4.14**	1.63	32.84**
GFR	0.00	-0.34**	-0.17**	0.06	-0.13	-0.73**
PH	7.15**	-10.42**	16.35**	-18.08**	11.07**	-1.00
SP	-3.51**	-0.08	-2.4*	-2.02	-5.64**	0.4
GY	-6.55*	-14.67**	-12.18**	-0.46	-5.89	-11.42**
Cross 3 (Line 5 x Line 6)						
DH	3.1**	2.57**	6.25**	3.33**	0.09	7.55**
DM	-1.85**	-0.63	0.96	-2.17**	-2.39	-2.01
GFP	-4.95**	-3.2**	-5.29**	-5.5**	-2.48	-9.57**
GFR	-0.32**	-0.14**	-0.3**	-0.35**	-0.51**	-0.32**
PH	-18.25**	-13.5**	5.47**	-5.5**	-1.32	-34.17**
SP	3.26**	-16.12**	1.57	-5.44**	-5.41**	-8.36**
GY	-22.42**	-9.34**	-21.76**	-20.19**	-31.72**	-21.94**

* **and** ** = **significance at 0.05 and 0.01 levels of probability levels, respectively, DH = days to heading, DM = days to maturity, GFP = grain filling period, GFR = grain filling rate (g day^{-1} plant^{-1}), PH = plant height (cm), SP = number of spikes plant^{-1} and GY = grain yield plant^{-1}.**

Estimates of gene effects calculated from the six-parameters model for the studied traits are presented in Table (5). Mean effect (m) refers to the role of the overall mean in addition to the locus effects and interactions of the fixed loci. All studied crosses exhibited significant (m)

static for all studied traits, indicating that these traits are under genetic control. Similar results were obtained by **Abdallah *et al* (2019), Abdelkhalik (2019), Koubisy (2019).**

Table 5. Mean estimates of the six gene effects for studied traits under optimum (SD1) and late (SD2) sowing dates.

Trait	Sowing date	m	d	h	i	j	l
		Cross 1 (Line 1 x Line 2)					
DH	SD1	91.94**	6.46**	0.27	0.11	0.28	-7.35**
	SD2	87.17**	5.78**	-4.88**	-7.44**	1.14*	16.82**
DM	SD1	146.17**	5.17**	2.74**	1.81	-0.11	-9.56**
	SD2	131.75**	3.95**	-1.22	-3.24**	-0.54	8.98**
GFP	SD1	54.24**	-1.29**	2.47	1.70	-0.39	-2.21
	SD2	44.58**	-1.83**	3.66**	4.2**	-1.68**	-7.84**
GFR	SD1	1.13**	0.12**	-1.16**	-0.98**	-0.07	1.07**
	SD2	0.78**	0.21**	-0.22*	-0.44**	0.09**	1.23**
PH	SD1	96.4**	14.53**	-35.58**	-40.53**	5.16**	91.88**
	SD2	79.95**	11.81**	26.26**	15.51**	6.65**	-20.31**
SP	SD1	22.98**	-0.59	-17.57**	-8.93**	-4.55**	-0.96
	SD2	21.95**	1.27*	-22.31**	-12.48**	-2.66**	4.23
GY	SD1	61.28**	5.89**	-61.08**	-52.18**	-3.79	57.05**
	SD2	34.88**	8.14**	-8.59*	-17.86**	2.99*	51.42**
		Cross 2 (Line 3 x Line 4)					
DH	SD1	86.4**	-1.47**	16.17**	14.81**	-1.12*	-25.21**
	SD2	79.28**	-2.32**	35.59**	34.91**	-0.60	-44.77**
DM	SD1	143.15**	-4.63**	2.98*	-0.07	-3.31**	3.00
	SD2	132.84**	-2.43**	-2.22	-2.31*	1.47**	-3.16
GFP	SD1	56.75**	-3.15**	-13.23**	-14.89**	-2.2**	28.14**
	SD2	53.56**	-0.17	-37.65**	-37.06**	2.03**	41.28**
GFR	SD1	0.77**	-0.02	-0.01	-0.04	0.08*	0.21
	SD2	0.66**	-0.18**	0.52**	0.45**	-0.2**	-0.18
PH	SD1	101.48**	-8.77**	19.68**	12.43**	-4.6**	-35.93**
	SD2	96.38**	1.33*	-21.75**	-27.5**	3.83**	56.00**
SP	SD1	17.85**	-4.19**	0.82	-0.27	-0.55	6.18
	SD2	16.83**	-2.38**	-2.85	-2.50	0.97	4.60
GY	SD1	43.87**	-3.35	-9.51	-12.84	2.81	31.56**
	SD2	35.37**	-7.94**	-1.26	-3.72	-7.1**	18.86**
		Cross 3 (Line 5 x Line 6)					
DH	SD1	84.06**	-2.13**	6.54**	9.25**	-1.57**	-18.6**
	SD2	83.28**	-1.55**	-5.2**	-1.65	-0.38	-4.25
DM	SD1	143.12**	-1.84**	-0.11	1.49	-1.41**	-0.60
	SD2	129.83**	0.04	0.38	-0.79	0.77	3.59
GFP	SD1	59.06**	0.29	-6.65**	-7.76**	0.17	18.00**
	SD2	46.55**	1.59**	5.58**	0.87	1.15*	7.83**
GFR	SD1	0.68**	0.04	-0.17	-0.11	-0.01	0.73**
	SD2	0.71**	0.12**	-0.18	-0.17	0.1**	0.66**
PH	SD1	99.9**	-15.4**	-5.43**	-11.47**	-11.86**	24.25**
	SD2	86.88**	-6.33**	20.83**	15.17**	-4.00**	3.83
SP	SD1	19.37**	3.33**	2.10	10.23**	0.84	-15.06**
	SD2	18.74**	-2.55**	-17.63**	-13.2**	-5.34**	34.76**
GY	SD1	39.9**	2.40	-14.92*	-12.47**	-0.33	56.65**
	SD2	32.77**	6.48**	-4.35	-7.59	5.43**	37.11**

* and ** = significance at 0.05 and 0.01 levels of probability levels, respectively, m = mean effect, d = additive effect, h = dominance effect, i = additive x additive, j = additive x dominance and l = dominance x dominance effects, DH = days to heading, DM = days to maturity, GFP = grain filling period, GFR = grain filling rate (g day^{-1} plant^{-1}), PH = plant height (cm), SP = number of spikes plant^{-1} and GY = grain yield plant^{-1}.

Additive gene effects (d) were either positive or negative and significant in 34 out of 42 cases (81.0 %) in all conditions. These cases include all traits, except for SP under optimum sowing date in cross 1, GFR and GY under optimum sowing date and GFP under late sowing date in cross 2, and GFP, GFR and GY under optimum sowing date and DM under late sowing date in cross 3. Most of the positive effect was found for the cross No. 1, referring to highly diversity for their parents compared to the other crosses and that improving of these traits by pedigree selection may be effective. These results are in accordance with the previous findings of **Abd El-Rady (2018), Elmassry and El-Nahas (2018) and Koubisy (2019)**.

The estimates of dominance (h) effects were positive and significant in 11 out of 42 cases (26.2 %) namely DM under optimum sowing date and GFP and PH under late sowing date in cross 1, DH under both sowing dates, DM and PH under optimum sowing date and GFR under late sowing date in cross 2, and DH under optimum sowing date and GFP and PH under late sowing date in cross 3. This indicates the importance of positive dominance of gene effects in inheritance of these traits and validity of heterosis breeding program for improving such traits.

On the contrary, negative and significant dominance gene effects occurred in 16 out of 42 cases (38.1 %). These cases included GFR, SP and GY under both sowing dates, PH under optimum sowing date and DH under late sowing date in cross 1, GFP under both sowing dates, PH under late sowing date in cross 2, and GFP, PH and GY under optimum sowing date and DH and SP under late sowing date in cross 3. In general, these results indicated that both additive and dominance gene effects were important in the inheritance of these traits. These results are in line with those obtained by **Abd El-Rady (2018)** and **Koubisy (2019)**.

Out of 42 cases, additive (d) was larger in magnitude than dominance (h) effect in 24 cases (57.1 %). These involved all traits, except for GFP under both sowing dates and PH under late sowing date in cross 1, DH and DM under both sowing dates, GFR and PH under optimum sowing date and GFP and GY under late sowing date in cross 2, and PH under both sowing dates, DH and DM under optimum sowing date and GFP under late sowing date in cross 3. On the contrary, dominance was larger than additive variance in the remaining 18 cases (42.9 %). These results were confound with the findings for relative importance of additive and dominance in the inheritance of studied traits

in bread wheat and this may be due to differences in genetic background of parental materials introduced in these studies (**EL-Nahas 2016, Elmassry and El-Nahas 2018, Abd El-Rady 2018, Abdallah *et al*. 2019 and Koubisy 2019**).

Significant epistatic gene effects were exhibited in 81 out of 126 studied cases (64.3 %) for all three types of epistasis (i, j and l). This indicates that epistatic gene effects were generally important in the inheritance of studied traits. Similar results were also obtained by **Koubisy (2019**), **Sharshar and Esmail (2019) and Sharshar and Genedy (2020).**

Dominance x dominance (l) gene effects were the highest in magnitude among the three digenetic epistatic effects in 27 out of 42 cases (64.3 %), followed by (i) effects in 12 cases (28.6 %) and then (j) effects in three cases (7.1 %). Similar trend was given by **Abd El-Rady (2018), Abdallah *et al*. (2019) and Koubisy (2019**).

Positive or negative and significant (i) gene effects were exhibited in 26 cases (61.9 %) for GFR, PH, SP and GY under both sowing dates and DH, DM and GFP under late sowing date in cross 1, DH, GFP and PH under both sowing dates, and DM and GFR under late sowing date in cross 2, and PH and SP under both sowing dates and DH, GFP and GY under optimum sowing date in cross 3. This indicates an enhancing effect of additive x additive type of epistasis for inheritance of these traits.

Additive x dominance (j) type of epistasis exhibited positive and significant effects in 12 cases (28.6 %), namely PH and SP under both sowing dates, DH, GFP, GFR and GY under late sowing date in cross 1, GFR under optimum sowing date and DM, GFP and PH under late sowing date in cross 2, and GFP, GFR and GY under late sowing date in cross 3. As additive × dominance epistasis tends to segregate in next generations, it would be better to delay selection to later generations with increased homozygosity, where additive and additive × additive variances are prevailing.

Negative and significant additive x dominance (j) epistatic gene effects were shown in 14 cases (33.3 %), namely SP under both sowing dates and GFP under late sowing date in cross 1, DH, DM, GFP and PH under optimum sowing date and GFR and GY under late sowing date in cross 2, and PH under both sowing dates, DH and DM under optimum sowing date and SP under late sowing date in cross 3.

Positive and significant dominance x dominance (l) epistatic gene effects were shown in 20 cases (47.6 %), namely GFR and GY under

both sowing dates, PH under optimum sowing date, DH, and DM under late sowing date in cross 1, GFP and GY under both sowing dates, and PH under late sowing date in cross 2, and GFP, GFR and GY under both sowing dates, PH under optimum sowing date and SP under late sowing date in cross 3.

Negative and significant dominance × dominance gene interactions were obtained in 10 cases (23.8 %), namely SP under both sowing dates and GFP under late sowing date in cross 1, DH and GFP under optimum sowing date and GFR and GY under late sowing date in cross 2, and PH under both sowing dates, DH and DM under optimum sowing date and SP under late sowing date in cross 3. These results indicated to reducing effect of dominance × dominance gene interactions in the expression of these traits.

In general, maximum number of inter- and intra-allelic interaction types of gene effects were exhibited by PH under both sowing dates and DH, GFR and GY under late sowing date in cross 1, PH under late sowing date in cross 2, and SP under optimum sowing date and GFP and GY under late sowing date in cross 3. This suggests that the selection in early segregating generations could be used for the improvement of these traits in the respective crosses.

Type of epistasis was considered as complementary when dominance and dominance × dominance gene effects have the same sign, and duplicate epistasis when the sign was different. Opposite signs of dominance and dominance x dominance type of gene effects were recorded for all the studied traits, except for SP under optimum sowing date in cross 1, DM under both sowing dates and SP under optimum sowing date in cross 2, and DM under both sowing dates and DH, GFP and PH under late sowing date in cross 3. These results reveal that duplicate epistatic gene action is important in the inheritance of most studied traits compared to complementary epistasis. Similar trends were also reported by **Abd El-Rady (2018), Koubisy (2019), Morsy (2020) and Sharshar and Genedy (2020).**

Components of variance and genetic parameters

Variance components and other genetic parameters are presented in Table (6). Phenotypic variance in F_2 populations differed significantly from the corresponding environmental variance for all studied traits. Consequently, the genotypic variance was the major part of the phenotypic variance.

Table 6. Variance components and some genetic parameters for studied traits under optimum (SD1) and late (SD2) sowing dates.

Trait	Sowing date	V_{ph}	V_G	V_E	h^2_b	h^2_n	GS %
				Cross 1 (Line 1 x Line 2)			
DH	SD1	22.04**	17.51	4.53	79.46	78.67	8.28
	SD2	26.06**	19.15	6.91	73.50	62.26	7.51
DM	SD1	8.38**	6.17	2.21	73.61	14.23	0.58
	SD2	10.43**	7.22	3.21	69.23	61.86	3.12
GFP	SD1	15.23**	10.13	5.10	66.51	32.77	4.86
	SD2	14.00**	10.07	3.94	71.89	28.81	4.98
GFR	SD1	0.24**	0.22	0.02	91.41	90.75	0.91
	SD2	0.08**	0.06	0.02	76.25	57.71	0.33
PH	SD1	24.41**	18.28	6.13	74.87	23.30	2.46
	SD2	67.59**	60.81	6.77	89.98	88.38	18.72
SP	SD1	61.43**	51.31	10.12	83.52	82.66	58.09
	SD2	47.06**	37.21	9.85	79.07	78.32	50.42
GY	SD1	703.13**	645.72	57.41	91.84	91.45	81.52
	SD2	162.43**	127.32	35.11	78.39	69.17	52.07
				Cross 2 (Line 3 x Line 4)			
DH	SD1	17.36**	12.99	4.37	74.84	18.23	1.81
	SD2	23.17**	15.65	7.51	67.57	54.10	6.77
DM	SD1	16.69**	10.52	6.16	63.07	61.98	3.64
	SD2	10.7**	7.15	3.55	66.81	24.45	1.24
GFP	SD1	18.91**	9.98	8.94	52.74	8.85	1.40
	SD2	14.38**	8.25	6.12	57.41	54.11	7.89
GFR	SD1	0.12**	0.10	0.02	80.61	58.41	0.42
	SD2	0.06**	0.06	0.001	94.57	0.49	0.00
PH	SD1	34.12**	27.97	6.15	81.97	81.81	9.70
	SD2	42.45**	36.25	6.20	85.39	72.06	10.03
SP	SD1	43.78**	30.54	13.24	69.76	50.27	38.40
	SD2	41.79**	27.43	14.37	65.62	53.45	42.31
GY	SD1	408.45**	344.19	64.26	84.27	60.87	57.77
	SD2	164.54**	161.76	2.78	98.31	50.62	37.83
				Cross 3 (Line 5 x Line 6)			
DH	SD1	18.93**	13.90	5.03	73.43	53.55	5.71
	SD2	35.05**	29.41	5.64	83.92	80.44	11.78
DM	SD1	20.88**	17.17	3.71	82.25	45.23	2.97
	SD2	13.49**	9.59	3.90	71.08	43.29	2.52
GFP	SD1	15.27**	8.39	6.88	54.94	1.15	0.16
	SD2	13.58**	6.82	6.75	50.26	2.30	0.38
GFR	SD1	0.09**	0.07	0.02	78.85	39.15	0.25
	SD2	0.07**	0.05	0.02	69.32	24.24	0.14
PH	SD1	17.83**	9.77	8.06	54.82	24.11	2.10
	SD2	49.61**	38.10	11.51	76.80	72.71	12.14
SP	SD1	38.02**	28.80	9.22	75.75	73.52	48.23
	SD2	26.12**	15.82	10.30	60.56	55.52	31.20
GY	SD1	321.31**	257.27	64.04	80.07	61.57	56.98
	SD2	152.82**	107.63	45.19	70.43	24.08	18.71

* and ** = significance at 0.05 and 0.01 levels of probability levels, respectively, V_{ph} = phenotypic variation, V_G = genotypic variance, V_E = environmental variance, h^2_b = broad sense heritability, h^2_n = narrow sense heritability , GS % = expected genetic advance as percentage of F_2 mean, DH = days to heading, DM = days to maturity, GFP = grain filling period, GFR = grain filling rate (g day^{-1} plant^{-1}), PH = plant height (cm), SP = number of spikes plant^{-1} and GY = grain yield plant^{-1}.

Heritability is very important for wheat breeder to predict behavior of succeeding the breeding program and effective selection. Heritability in broad-sense was found to be moderate to high for all studied traits. Narrow sense heritability ranged from moderate to high in most cases, except for DM and PH under optimum sowing date and GFP under late sowing date in cross1, DH and GFP under optimum sowing date and DM and GFR under late sowing date in cross 2, and GFP under both sowing date, PH under optimum sowing date and GFR and GY under late sowing date in cross 3. These results indicated that additive gene action was important in the inheritance of most traits and selection may be more effective for improving such traits of all genotypes in early segregating generations. In addition, the remaining traits are inherited by non-additive gene action and selection for these traits will be effective in late generations. These results were corroborated with those obtained by **Ataei *et al* (2017), Abd El-Rady (2018) and Koubisy (2019).**

Heritability along with genetic advance are more helpful in predicting the gain under selection than heritability alone (**Johnson *et al*., 1955**). According to **Johnson *et al*. (1955)** genetic advance as percent of mean classified as low (<10%), moderate (10-20%) and high (>20%). Accordingly, the expected genetic advance as percent of F_2 mean was moderate to high for GFR, SP and GY under both sowing dates and PH under late sowing date in cross 1, SP and GY under both sowing dates, GFR under optimum sowing date and PH under late sowing date in cross 2, and GFR, SP and GY under both sowing dates and DH and PH under late sowing date in cross 3. These results indicated the possibility of practicing selection in early generations to select high yielding genotypes. Meanwhile, the remaining traits, which showed the lowest values of expected genetic advance, suggesting the role of environmental factors and dominance gene action in inheritance of these traits.

Generally, most biometrical parameters resulted from cross 2 and 3 were higher in magnitude compared to cross 1. Consequently, it could be concluded that these two crosses would be of interest in breeding program for improving earliness and grain yield traits.

Correlation coefficients.

High genotypic correlation, which is the correlation of breeding values helps in selection for genetically controlled traits. Phenotypic and genotypic correlation coefficients between GY and other studied traits are presented in Table (7). At both sowing dates, genotypic correlation coefficient was higher than corresponding phenotypic correlation

coefficient for most studied traits in the three studied cross populations, indicating to the inherent association among these traits and the phenotypic expression of these traits were less influenced by the environment. Similar results were reported by **Dabi *et al*. (2016) and Baye *et al*. (2020**).

Table 7. Coefficient of phenotypic and genetic correlation between grain yield and studied traits under optimum (SD1) and late (SD2) sowing dates.

Correlation	Sowing date	DH	DM	GFP	GFR	PH	SP
Cross 1 (Line 1 x Line 2)							
Phenotypic correlation	SD1	-0.04	0.07	0.11	0.81*	0.21*	0.68*
	SD2	-0.19*	-0.02	0.25*	0.41*	0.20*	0.91*
Genotypic correlation	SD1	-0.04	0.07	0.11	0.81*	0.21*	0.68*
	SD2	-0.19*	-0.02	0.25*	0.41*	0.20*	0.91*
Cross 2 (Line 3 x Line 4)							
Phenotypic correlation	SD1	-0.20*	0.001	0.19*	0.98*	0.02	0.32*
	SD2	-0.26*	-0.31*	-0.05	0.71*	0.07	0.34*
Genotypic correlation	SD1	-0.26*	0.11	0.41*	0.58*	0.03	0.45*
	SD2	-0.32*	-0.54*	-0.06	0.96*	0.05	0.46*
Cross 3 (Line 5 x Line 6)							
Phenotypic correlation	SD1	-0.10	-0.03	0.07	0.99*	0.19*	0.42*
	SD2	-0.48*	-0.35*	0.13	0.87*	0.001	0.39*
Genotypic correlation	SD1	-0.20*	-0.10	0.12	0.50*	0.25*	0.45*
	SD2	-0.40*	-0.50*	0.23*	0.16*	0.05	0.56*

* and ** = significance at 0.05 and 0.01 levels of probability levels, respectively, DH = days to heading, DM = days to maturity, GFP = grain filling period, GFR = grain filling rate (g day⁻¹ plant⁻¹), PH = plant height (cm), SP = number of spikes plant⁻¹ and GY = grain yield plant⁻¹.

Positive and significant phenotypic and genotypic correlations were observed between GY and each of GFR, PH and SP under both sowing dates and GFP under optimum sowing date in cross 1, GFR, and SP under both sowing dates and GFP under optimum sowing date in cross 2, and SP under both sowing dates, GFR and PH under optimum sowing date and GFP under late sowing date in cross 3. Accordingly, selection for such traits could be helpful for grain yield improvement in segregating populations. These results were in line with those obtained by **Hassani *et al*. (2017)**.

Phenotypic and genotypic correlation were negative and significant between GY and DH under late sowing date in cross 1, DH under both sowing dates and DM under late sowing date in cross 2, and DH under late sowing date and DM under late sowing date in cross 3. Only phenotypic correlation was negative and significant between GY and DH under optimum sowing date in cross 3. These results referred to the change in the weather conditions (**Mondal *et al*. 2013 and 2016 and**

Pask *et al*. 2014). This negative correlation could be used as indicator to select the promising genotypes that combine early maturing and high yield potential especially in cross 2 and 3.

CONCLUSION

Generally, the biometrical parameters resulted from cross 2 and 3 were higher in magnitude compared to cross 1. Consequently, it could be concluded that these crosses would be used in breeding program for improving earliness and grain yield traits. Negative correlation between grain yield and earliness traits indicated that earliness could be used as a criterion in breeding for tolerance to high temperature stress in end of growing season. This negative correlation also enables to select the promising genotypes which had early maturing and high yield potentiality especially in cross 2 and 3.

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تقدير المعالم الوراثية للتبكير في النضج والمحصول في بعض هجن قمح الخبز

تحت ميعاد الزراعة الأمثل والمتأخر

وليد ذكي اليماني فرحات

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يُولي البرنامج القومي لبحوث القمح في جمهورية مصر العربية اهتماما متزايدا لتطوير أصناف مبكرة النضج وذات إنتاجية عالية. لذلك، تم استخدام ست سلالات مبكرة إلى متوسطة التبكير من قمح الخبز لإنتاج ثلاثة هجن. وتم استخدام نموذج الست عشائر خلال مواسم النمو 2017/18 إلى 2019/20. وكان الهدف هو تحديد التفاعلات الأليلية وغير الأليلية التي تتحكم في صفات التبكير ومحصول الحبوب، وكذلك تحديد أفضل التراكيب الوراثية التي تراكمت فيها جينات التبكير في النضج. وتم الحصول على اختلافات كبيرة بين ميعاد الزراعة الأمثل

والمتأخر وفيما بين العشائر الستة لكل الصفات. وقد تسببت الزراعة المتأخرة في نهاية شهر ديسمبر في انخفاض جميع الصفات المدروسة. وكانت تأثيرات الفعل الجيني المضيف والسيادي ذات أهمية في وراثة الصفات المدروسة. وكان تأثير الفعل الجيني المضيف أكبر من السيادي في معظم الحالات. وكذلك كانت قيم المكافئ الوراثي بالمعنى الواسع والضيق والتقدم الجيني المتوقع كنسبة مئوية من متوسط الجيل الثاني متوسطة إلى مرتفعة لمعظم الصفات المدروسة. وكان معامل الارتباط الظاهري والوراثي سالبا ومعنويا بين محصول الحبوب وصفات التبكير في معظم الظروف. وبصفة عامة، كانت معظم المعالم الوراثية الناتجة عن الهجين 2 (سلالة 3 x سلالة 4) والهجين 3 (سلالة 5 x سلالة 6) أعلى في قيمتها مقارنة بالهجين 1 (سلالة 1 x سلالة 2)، وبالتالي، فإن هذين الهجينين سيكونان مهمين في برنامج التربية لتحسين صفات التبكير في النضج ومحصول الحبوب.