

GENE ACTION AND GENETIC DIVERSITY IN A SIX PARENTAL DIALLEL CROSSES OF WHEAT

H. A. Dawwam⁽¹⁾; Marwa M.El-Nahas⁽¹⁾; SH. D. Ibrahim⁽²⁾; W.M.EL-Orabey⁽³⁾;
M.S. Abd El- Aal⁽¹⁾ and Amira A. Ali⁽¹⁾

⁽¹⁾Crop Science Dept., Faculty of Agriculture, Menoufia Univ., Egypt.

⁽²⁾Agriculture Genetic Engineering Res. Institution (AGERI)- ARC- Giza, Egypt.

⁽³⁾Wheat Dis. Res. Dept., Plant Pathol. Res. Inst. A. R. C., Giza, Egypt.

Received: May 9, 2022

Accepted: Jul. 31, 2022

ABSTRACT: Six varieties of bread wheat were crossed in half diallel analysis. The fifteen F₁'s and their parents were evaluated. The experiment in a randomized complete block design with three replications at the Experimental farm, Faculty of Agriculture, Menoufia University Shebin El – Kom, Egypt during 2020/2021. The results cleared that genotypes, parents and the resultant fifteen crosses mean squares were found to be highly significant for all traits studied. Parent vs. crosses mean squares as an indication to average heterosis over all crosses were found to be highly significant for all traits studied. Variance of general combining ability was found to be highly significant for all traits studied. The parental variety Shandaweeel-1 proved to be good general combiner for grain yield per spike and grain yield per plant. Also, Giza-171 was good general combiner in heading date, grain yield per spike. The most desirable SCA effects for grain yield per plant were detected by the seven hybrids i.e. Shandaweeel-1 × Giza-171, Shandaweeel-1 × Misr-3, Giza-171× Misr-3, Misr-3 × Sakha-95, Sakha-95 × Sids-1, Sakha-95 × Morocco and Sids-1 × Morocco. Desirable and significant useful heterosis for grain yield per plant was detected in all 15 F₁'s. The results show the dendrogram on the basis of the molecular parameters on two groups and on the basis of the crop characteristics on three main groups and they were not identical, which indicates the existence of morphological and molecular differences between the varieties. The study indicates that the molecular parameters and yield characteristics can be used successfully in estimating the genetic diversity in wheat.

Keywords: Bread wheat, Diallel, Combining ability, Heterosis, Molecular markers.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important crops, with an annual production of about 8 to 9 million tons while our needs vary between 15 to 16 million tons, accordingly the self-sufficiency is 54% only (FAO., 2020). The Egyptian government's main goal is to close the gap between wheat output and consumption. The use of a plant breeding programme is critical for producing a productive wheat harvest. Cultivation of crops with various genetic backgrounds is an efficient technique for crop enhancement maintenance and weakness reduction. Combining ability analysis is one of the most effective approaches for finding the best combiners to utilize in crosses. It also helps breeders comprehend the genetic architecture of different qualities, allowing them to create an effective breeding plan for future material enhancement. Estimates of general and specific combining ability can aid with parent selection,

and a true grasp of genetic traits for various qualities is helpful in deciding on an acceptable breeding system. The ability of parents (GCA) and hybrids (SCA) to combine traits is used to determine the type of gene activity involved in feature inheritance. Heterosis depends on the balance of different combinations of gene effects as well as on distribution of plus and minus alleles in the parents of the mating system. In self-pollinated crops, like wheat, the scope for utilization of heterosis depends mainly upon the direction and magnitude of heterosis. The economic feasibility of hybrid wheat would be considerably improved if sufficient heterosis were retained in the F₁ generation to render its production value. The segregation that occurs in an F₂ generation could, however, cause problems. Better information could be obtained when both F₁ and F₂ generations are compared at the same year (Ali *et al.*, 2020). Tolerance to biotic and abiotic stress in crops necessitates a

high level of genetic variation. The genetic diversity is critical in crop breeding projects, because they are abundant and independent of environmental effects, molecular markers are useful companions to morphological and molecular characterization. They allow cultivar identification in the early stages of development (Caboet *et al.*, 2014). Collard and Mackill (2009) have described Start Codon Targeted (SCoT) Polymorphism, a simple and innovative DNA marker approach. The 18-mer marker is used in this procedure. PCR products are resolved using normal agarose gel electrophoresis and a single primer in PCR with an annealing temperature of 50°C. The primers are simple to construct since they are based on the conserved region surrounding the translation initiation codon and therefore do not require genomic sequence information. Furthermore, this technique is suitable for analysing genetic diversity in different crops due to high repeatability and polymorphism, as well as being very informative (Abdel-Lateifet *et al.*, 2018). The primary purpose of the study was to determine the genetic variability of the six cultivars employed (Giza-171, Sids-1, etc.).

MATERIALS AND METHODS

Experimental procedures

This investigation was carried out at the Experimental Farm, Faculty of Agriculture, Menoufia University, Shebin El-Kom, Egypt (latitude 30°31'39''N, longitude 31°04'03''E)

during the two growing successive seasons of 2018/2019 and 2020/2021. Six varieties of spring wheat representing a wide range of diversity for several agronomic traits were selected for this study. The names, pedigree and origin of these varieties are presented in Table (1).

The aforementioned genotypes were used in a diallel fashion without reciprocals giving a total of 15 F₁ crosses during 2018/2019 growing season. In 2020/2021 season, all parents, their F₁'s were evaluated.

All genotypes were grown under normal condition and normal agriculture practices were applied as usual for ordinary wheat fields in the area. The experiment was laid a randomized complete blocks design (RCBD) with three replications in rows with 3 m long and 20 cm between rows and 10 cm between plants within rows. Observation were recorded on 10 garded plants from each plot of parents and F₁.

Measurements:

Heading date (day), maturity date (day), plant height (cm), Grain yield per spike (g), 1000-grain weight (g) and grain yield per plant (g).

Statistical procedures:

The analysis of variance for combining ability and estimation of genetic effects was done following the technique of (Grifing, 1956) model1 method2

Table 1. The code number, name, pedigree and origin of the studied parental varieties

No.	Variety	Pedigree	Origin
1	Shandawee-1	SITE//MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC.CMSS93 B00567S-72Y-010M-010Y-010M-0HTY-0SH	Egypt
2	Giza-171	Sakha 93 / Gemmeiza 9 S.6-1GZ-4GZ-1GZ-2GZ-0S	Egypt
3	Misr-3	ATTILA*2/ABW65*2/KACHU CMSS06Y002582T-099TOPM-099Y-099ZTM-099Y-099M-10WGY-0B-0EGY	Egypt
4	Sakha-95	PASTOR//SITE/MO/3/CHEN/AEGILOPSSQUARROSA(TA US)//BCN /4/WBLL1CMSA01Y00158S-040P0Y-040M-030ZTM-040SY-26M-0Y-0SY-0S	Egypt
5	Sids-1	HD2172/PAVON"S"//1158.574"S". SD46-4SD-2SD-1SD-0SD.	Egypt
6	Morocco	Tob's /1/NP/2/CC/Inia/3/ Cha	Morocco

DNA markers:

Six Egyptian cultivars of wheat grains were obtained from Agricultural Genetic Engineering Research Institute (AGERI) and cultivated in the department of Agricultural Genetic Engineering Research Institute. The seedling leaves were used for DNA extraction.

Genomic DNA extraction:

The genomic DNA was extracted from the seedling leaves by (Thermo Scientific Gene JET Plant Mini Kit). Agarosegel electrophoresis definite that the DNA was of high molecular weight with nodegradation.

SCoTanalysis:

a- Twelve SCoT primers were used in this study (Table 2). The amplification reaction was carried out in 25 μ l reaction volume containing 1X PCR buffer, 2mM MgCl₂, 0.2mM dNTPs, 25pmol primer, 1 U Taq DNA polymerase and 30ng template DNA.

b- Thermocycling Profile PCR:

PCR amplification was performed in a Perkin-Elmer/GeneAmp® PCR System 9700 (PE Applied Biosystems) programmed to fulfill 40 cycles after an initial denaturation cycle for 5 min at 94°C. Each cycle consisted of a denaturation step at 94°C for 45s, an annealing step at 50°C for 50s, and an elongation step at 72°C for 1min. The primer extension segment was extended to 7 min at 72°C in the final cycle.

c- The amplification products were resolved by electrophoresis in a 1.5% agarose gel containing ethidium bromide (0.5ug/ml) in 1X TBE buffer at 95 volts.

RESULTS AND DISCUSSION

Analysis of variance:

The analysis of variance revealed highly significant mean squares for all sources of variations (genotypes, parents, F₁ crosses and parents vs F₁ crosses (heterosis). Meanwhile, F₂ generation all genotypes, parents, F₂ hybrids and parents vs F₂ hybrids were highly significant for all traits .The results indicate that, the differential in the material and sufficient amount of genetic variability adequate for further biometrical assessment. Large magnitude of parents vs crosses mean squares were found in F₁ analysis compared with F₂ ones for all traits studied. These results are logic consequence inbreeding depression present in F₂ which would decrease the heterosis effect.

Significant differences among wheat genotypes for yield and its components in different sets of material were reported by Farhat and Darwish (2016).

Both types of combining ability mean squares for all traits in both F₁ and F₂ generations are presented in Table (3).

Table (2): Data of SCoTprimers:-

Primer Name	Sequence
SCoT-1	5'-ACGAC <u>ATG</u> GCGACCACGC-3'
SCoT-2	5'-ACC <u>ATGG</u> CTACCACCGGC-3'
SCoT-3	5'-ACGAC <u>ATG</u> GCGACCCACA-3'
SCoT-4	5'-ACC <u>ATGG</u> CTACCACCGCA-3'
SCoT-5	5'-CA <u>ATG</u> GCTACCACTAGCG-3'
SCoT-6	5'-CA <u>ATGG</u> GCTACCACTACAG-3'
SCoT-7	5'-ACA <u>ATGG</u> GCTACCACTGAC-3'
SCoT-8	5'-CAACA <u>ATG</u> GCTACCACCA-3'
SCoT-9	5'-ACA <u>ATGG</u> GCTACCACTGCC-3'
SCoT-10	5'-ACA <u>ATGG</u> GCTACCAACCAGC-3'
SCoT-11	5'-ACA <u>ATGG</u> GCTACCACTACC-3'
SCoT-12	5'-CAACA <u>ATG</u> GCTACCAACCG-3'

Both types of combining ability (GCA and SCA) mean squares were found to be highly significant for all traits. These results indicated that both types of combining ability are important in the inheritance of these traits.

For development of an efficient hybridization program and select the suitable way of selection, must determine the relative importance of additive and non-additive gene action. To determine the genetic effects of greatest importance, GCA/SCA ratio were computed. Values exceeding largely the unity were detected for plant height and grain yield per plant in F₁ generation, but in F₂ generation, detected for all traits except, heading date and grain yield per spike. This indicates that the largest part of the

total genetic variability was due to additive and additive × additive types of gene effects. For the exceptional cases, however, non-additive types of gene action seemed to be more prevalent.

The GCA/SCA ratio were higher in magnitude in F₂ than F₁ generation for all traits revealing that the additive and additive × additive gene effects were increased and non-additive gene effects were also reduced in F₂ generation.

Both general and specific combining ability mean squares were previously obtained by Ahmad *et al.* (2003), Ahmad *et al.* (2006), Adel and Ali (2013), Kalhoro *et al.* (2015), Ahmad *et al.* (2016), Afridi *et al.* (2017).

Table 3: Ordinary analysis of variance and combining ability analysis in F₁ and F₂ generations for all traits studied.

S.O.V.	d. f	Heading date (days)	Maturity date (days)	Plant height (cm)	Grain yield per spike (g)	1000-grain weight (g)	Grain yield per plant (g)
		NI	NI	NI	NI	NI	NI
F ₁ hybrids							
Rep.	2	0.21	2.23	0.53	0.001	0.02	0.04
Genotypes	20	64.62**	88.40**	110.54**	2.94**	82.01**	21.63**
Parents	5	5.13**	63.78**	54.55**	0.96**	79.57**	15.77**
F ₁ Crosses	14	73.74**	101.52**	122.38**	1.63**	88.73**	13.57**
P. VS. F ₁ .	1	234.42**	27.97**	224.64**	31.09**	0.27**	163.67**
Error	40	1.55	1.92	1.19	0.001	0.02	0.05
GCA	5	3.13**	30.90**	47.41**	0.33**	20.45**	11.99**
SCA	15	27.67**	28.99**	33.32**	1.19**	29.63**	5.61**
Error	40	0.52	0.63	0.39	0.003	0.01	0.02
GCA/ SCA		0.11	1.06	1.42	0.27	0.69	2.13
Rep.	2	0.03	0.16	0.39	0.00	0.00	0.29
Genotypes	20	11.56**	110.28**	118.07**	1.78**	70.99**	22.12**
Parents	5	4.63**	61.03**	56.10**	0.96**	90.60**	20.22**
F ₂	14	2.63**	131.36**	143.64**	1.16**	68.93**	18.53**
P. VS. F ₂ .	1	171.28**	61.47**	69.89**	14.49**	1.87**	81.84**
Error	40	0.57	0.96	1.11	0.01	0.01	0.05
GCA	5	1.14**	37.23**	61.67**	0.31**	25.15**	16.62**
SCA	15	4.75**	36.60**	31.92**	0.68**	23.17**	4.29**
Error	40	0.19	0.32	0.37	0.003	0.004	0.02
GCA/ SCA		0.24	1.02	1.93	0.46	1.09	3.87

Mean performance:

Mean values of all studied wheat genotypes for F₁ and F₂ generations for all studied traits are presented in Table (4).

The mean of heading date for parents was 82.12 days, the earliest parents were Morocco (P₆) and was headed after 80.15 from sowing. While, the last parents Sakha-95 (P₄) was headed after 83.85. The earliest F₁ hybrids were

Shandawee-1 (P₁) × Misr-3 (P₃) was headed after 73.25. While, the last F₁-hybrid was Shandawee-1 (P₁) × Morocco (P₆) that headed after 90.65 from sowing, the late planting date reduced days to heading over all F₁-hybrids from 77-85 days. The mean of heading date for F₂ generations ranged from 76.15 for Shandawee-1(P₁) × Sakha-95 (P₄) to 79.65 for Giza-171(P₂) × Sids-1(P₅) with an average of 78.26.

Table (4): The genotypes mean performance for all traits studied.

Parents	Heading date (days)	Maturity date (days)	Plant height (cm)	Grain yield per main spike (g)	1000-grain weight (g)	Grain yield per plant (g)
	NI	NI	NI	NI	NI	NI
Shandawee-1(P ₁)	82.65	119.65	104.90	5.22	50.30	16.18
Giza-171 (P ₂)	82.70	117.20	98.75	4.21	46.34	12.62
Misr-3 (P ₃)	81.10	113.90	92.15	4.18	48.18	9.10
Sakha-95 (P ₄)	83.85	125.85	95.20	5.68	44.22	13.10
Sids-1(P ₅)	82.25	114.30	97.55	4.30	52.08	10.63
Morocco (P ₆)	80.15	114.55	98.75	3.93	55.28	11.52
Mean P	82.12	117.57	97.88	4.58	49.40	12.19
P ₁ × P ₂	73.65	114.65	87.95	2.71	48.05	18.20
P ₁ × P ₃	73.25	113.80	90.60	3.36	49.41	17.17
P ₁ × P ₄	74.30	106.90	91.20	3.02	50.68	17.47
P ₁ × P ₅	80.90	112.70	100.95	3.06	60.14	18.55
P ₁ × P ₆	90.65	108.35	95.65	2.03	39.98	15.44
P ₂ × P ₃	83.10	112.25	102.80	5.42	50.14	13.55
P ₂ × P ₄	74.40	112.60	90.95	3.41	49.15	13.48
P ₂ × P ₅	75.05	111.90	101.10	2.95	50.64	12.80
P ₂ × P ₆	73.70	117.30	95.45	2.92	47.36	13.18
P ₃ × P ₄	77.40	122.90	78.65	2.73	57.75	14.42
P ₃ × P ₅	84.00	125.35	90.35	2.74	50.23	15.05
P ₃ × P ₆	77.65	120.65	98.20	2.61	49.45	12.47
P ₄ × P ₅	77.65	121.50	87.85	2.71	40.51	14.30
P ₄ × P ₆	78.25	125.15	95.40	3.54	48.64	16.00
P ₅ × P ₆	73.75	115.50	98.45	2.95	56.35	14.35
Mean C	77.85	116.10	93.70	3.07	49.89	15.09
Mean T	79.06	116.52	94.89	3.50	49.64	13.65
L.S.D 0.05	2.05	2.28	1.79	0.05	0.23	0.33
L.S.D 0.01	2.74	3.05	2.40	0.06	0.29	0.43

For maturity date, the mean performance for parents was 117.52 days. The best parent for maturity was Misr-3 (P_3) (113.90 days). The hybrid Shandaweeel-1 (P_1) \times Sakha-95 (P_4) was the earliest in maturity 106.90. While, Misr-3 (P_3) \times Sids-1(P_5) and Sakha-95(P_4) \times Morocco (P_6) hybrids were late maturity. The average of F_1 hybrids were 116. 10 days. The average of maturity date for F_2 -generation were 104.10 for Shandweel-1(P_1) \times Sakha-95(P_4). In general, F_2 populations were average was 99.52 days. These results are also in a line with those obtained by El-Said (2018) and Ali *et al.*, (2020).

Concerning plant height, the mean of parents ranged from 92.15 cm for Misr-3 (P_3) to 104.90 cm for Shandaweeel-1 (P_1).

Mean of plant height for F_1 hybrids showed that the tallest hybrids were Giza-171(P_2) \times Misr-3(P_3) by 102.80, but the shortest hybrids were Misr-3 (P_3) \times Sakha-95 (P_4) by 78.65. The mean of plant height for F_2 -generation was 114.30 for Giza-171(P_2) \times Sids-1(P_5) Generally, plant height of F_2 -populations were tallest than F_1 hybrids.

For grain yield per spike, the average of parents was over 5g for weight per spike. The hybrids Giza -171(P_2) \times Misr- 3 (P_3) out of 15 F_1 'swas the higher in its value. Also, the hybrids Shandaweeel-1 (P_1) \times Sids - 1 (P_5) and Sids-1(P_5) \times Morocco (P_6) were highly the weight was high from 4g in F_2 – generation.

For 1000-grain weight, mean of parents ranged from 59.34 g to for 55.43 g for Morocco (P_6) and sids-1(P_5). The mean of 1000-grain weight for F_1 hybrids, it noticed that the heaviest F_1 hybrids was Shandaweeel-1(P_1) \times Sids-1(P_5). The F_2 population performance ranged from 57.75 g to 42.20 g for Giza-171(P_2) \times Misr-3(P_3).

For grain yield per plant, the mean over all parents was 13.70 g. The parental variety Shandaweeel-1(P_1) had the highest yield (17.39). the parental Misr-3 (P_3) gave the lowest values 10.28 g. The mean of grain yield per plant for F_1 hybrids noted that the high value was 22.42 g for Shandaweeel-1 (P_1) \times Giza- 171 (P_2). The mean of grain yield per plant for the F_1 hybrids was

17.26 g. With regard to grain yield per plant, the performance of F_2 - populations showed that the high mean was 20.80 g for Shandaweeel-1 (P_1) \times Giza -171 (P_2), while the low value was 11.80 g for Misr-3 (P_3) \times Sids-1 (P_5). While, the performance of F_2 - populations were 15.74. These results are in line with those obtained by Farooqi *et al* (2006), Verma *et al.* (2016), El-Said (2018), Joshi *et al.* (2020) and Abro *et al.* (2021).

General Combining ability (GCA) effects

General combining ability effects GCA of each parent for all traits studied are presented in Table (5). General combining ability effects computed here in were found to be differ significantly from zero in most traits.

High positive values of general combining ability effects would be of interest in most traits. On the contrary, for heading data, maturity data and plant height, high negative values would be useful from the wheat breeder point of view.

The parental varieties Giza-171 (P_2) and Sakha-95(P_4) showed highly significant negative (GCA) effects in F_1 generation, as well as the two parents Misr-3 (P_3) and Morocco (P_6) expressed significant desirable GCA effects.

For maturity data, the two parents Shandaweeel-1 (P_1) and Giza-171 (P_2) were found to be highly significant negative (GCA) effects in F_1 generation. revealing that these parental varieties could be considered as excellent combiners for developing early genotypes.

For plant height, the two parental varieties Misr-3(P_3) and Sakha-95 (P_4) exhibited highly significant negative (GCA) effects in F_1 generation. While, the three parents Misr-3 (P_3), Sakha-95 (P_4) and Morocco (P_6) in F_2 generation in prove to be good combiner for shortness and releasing varieties resistance to lodging.

For grain yield per spike, the three parental varieties Giza-171 (P_2), Misr-3 (P_3) and Sakha-95 (P_4) was significant in F_1 generation. Shandaweeel-1(P_1), Sids-1 (P_5) and Morocco (P_6) showed significant GCA in F_2 generation.

For 1000-grain weight, the three parental varieties Shandaweeel-1 (P_1), Sids-1 (P_5) and Morocco (P_6) were highly significant under both experiments and the parental variety Misr-3 (P_3) under artificial inoculation infection with leaf rust in F_1 generation. The two parents Giza-171 (P_2) and Morocco (P_6) showed significant GCA effects under both experiments in F_2 generation proving to be good combiners in this concern.

For grain yield per plant, the parental variety Shandaweeel-1 (P_1) was highly significant. The

three parental varieties Shandaweeel-1 (P_1), Giza-171 (P_2), Sakha-95 (P_4) were found to be significant GCA effects proving to be good combiners for this trait.

General combining ability effect was also detected by Iqbal and Khan (2006), Hassan *et al.* (2007), Adel and Ali (2013), Kalhoro *et al.* (2015), Mahpara *et al.* (2017), Joshi *et al.* (2020) and Abro *et al.* (2021).

Table (5): Estimates of parental (GCA) effects for all traits studied in F_1 and F_2 generations.

Parents	Heading date (days)		Maturity date (days)	Plant height (cm)	Grain yield per main spike (g)	1000-grain weight (g)	Grain yield per plant (g)
	NI	NI	NI	NI	NI	NI	NI
F_1 generation							
Shandaweeel-1 (P_1)	0.57*	-2.49**	1.48**	-0.03**	0.29**	2.15**	
Giza-171 (P_2)	-1.02**	-1.56**	1.43**	0.11**	-1.41**	0.17**	
Misr-3 (P_3)	0.52*	0.88**	-2.42**	0.21**	-0.25**	-1.54**	
Sakha-95 (P_4)	-0.47*	3.13**	-3.73**	0.15**	-2.04**	-0.15**	
Sids-1(P_5)	0.29	-0.01	1.18**	-0.08**	2.29**	0.05	
Morocco (P_6)	0.10	0.05	2.04**	-0.35**	1.12**	-0.67**	
L.S.D \hat{g}_i	0.05	0.46	0.51	0.40	0.01	0.04	0.08
	0.01	0.62	0.68	0.54	0.02	0.05	0.11
L.S.D $\hat{g}_i - \hat{g}_j$	0.05	0.71	0.78	0.63	0.02	0.06	0.12
	0.01	0.95	1.05	0.84	0.02	0.08	0.16
Shandaweeel-1 (P_1)	0.04	-2.86**	1.85**	0.25**	-0.40**	2.38**	
Giza-171 (P_2)	0.55**	-0.22	3.94**	-0.05**	1.87**	0.65**	
Misr-3 (P_3)	-0.28*	-0.24	-3.26**	-0.24**	-1.09**	-0.82**	
Sakha-95 (P_4)	0.01	3.85**	-0.47*	-0.06**	-1.76**	0.12**	
Sids-1(P_5)	0.22	-0.24	0.79**	0.22**	-1.14**	-1.82**	
Morocco (P_6)	-0.53**	-0.29	-2.84**	-0.13**	2.54**	-0.51**	
L.S.D \hat{g}_i	0.05	0.28	0.36	0.38	0.04	0.04	0.08
	0.01	0.38	0.48	0.51	0.05	0.05	0.11
L.S.D $\hat{g}_i - \hat{g}_j$	0.05	0.44	0.56	0.63	0.06	0.06	0.12
	0.01	0.59	0.75	0.84	0.08	0.08	0.16

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

Specific Combining ability (SCA) effect:

Estimates of the specific combining ability SCA effects for the fifteen hybrid combinations studied in F₁ and F₂ generations are presented in Table (6).

Nine hybrids out of 15 F₁'s showed highly significant negative specific combining ability SCA effects for heading date, while, seven hybrids exhibited highly significant negative SCA in F₂ generation.

Six and seven hybrid combinations studied were detected to show highly significant negative SCA effects in F₁ and F₂ generations, respectively, for maturity date in the two experiments. These hybrids in both generations showed desirable heterosis for earliness.

Nine and five hybrid combinations were detected to show highly significant negative SCA effects for plant height in F₁ and F₂ generations, respectively. The two parental cultivars Misr-3 and Sakha-95 were found to be the best general combiners for plant height.

Table 6: Estimates of specific combining ability (SCA) effects for the fifteen wheat crosses for F₁ and F₂ generations for all traits studied.

Crosses	Heading date(days)		Maturity date (days)		Plant height (cm)	
	F1	F2	F1	F2	F1	F2
	NI	NI	NI	NI	NI	NI
P1xP2	-4.96**	-1.29**	2.19**	1.72**	-9.86**	-0.96
P1x P3	-6.91**	-1.01*	-1.12**	0.25	-3.35**	-0.34
P1x P4	-4.86**	-3.21**	-10.26**	-12.75**	-1.45*	-3.99**
P1x P5	0.96	-0.42	-1.32**	-2.20**	3.37**	6.43**
P1x P6	10.91**	-0.32	-5.73**	-5.75**	-2.77**	-4.40**
P2x P3	4.54**	-1.42**	-3.59**	-6.19**	8.89**	0.36
P2x P4	-3.18**	-0.92*	-5.49**	6.51**	-1.65**	4.42**
P2x P5	-3.29**	-0.43	-3.04**	-5.79**	3.57**	10.39**
P2x P6	-4.45**	-0.13	2.29**	0.60	-2.92**	2.84**
P3x P4	-1.71**	-0.58	2.35**	-4.52**	-10.09**	4.02**
P3x P5	4.11**	-0.29	7.95**	8.57**	-3.31**	-4.19**
P3x P6	-2.03**	-1.24**	3.19**	3.62**	3.67**	2.39**
P4x P5	-1.24**	-2.59**	1.85*	2.48**	-4.51**	3.86**
P4x P6	-0.45	-1.04**	5.44**	4.38**	2.18**	-1.89**
P5x P6	-5.72**	-0.75	-1.05	-0.32	0.32	-8.97**
LSD (sij)	0.05	1.28	0.77	1.41	1.01	1.13
	0.01	1.72	1.03	1.89	1.35	1.45
LSD (sij-skl)	0.05	1.76	1.07	1.96	1.39	1.55
	0.01	2.34	1.43	2.62	1.86	2.07
LSD (sij-sik)	0.05	1.89	1.15	2.12	1.49	1.67
	0.01	2.54	1.54	2.84	1.99	2.24

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

Table 6: Cont.

Crosses	Grain yield per spike (g)		1000- grain weight (g)		Grain yield per plant (g)	
	F1	F2	F1	F2	F1	F2
	NI	NI	NI	NI	NI	NI
P1xP2	-0.86**	0.13**	-0.33**	3.29**	3.85**	2.73**
P1x P3	-0.33**	-1.07**	-2.03**	-2.43**	1.63**	2.75**
P1x P4	-0.57**	-0.60**	1.24**	3.53**	-0.18	-2.07**
P1x P5	-0.37**	0.41**	7.04**	-8.04**	1.18**	-0.79**
P1x P6	-1.07**	-0.23**	-11.17**	-5.12**	-0.19	2.19**
P2x P3	1.57**	-0.02	1.95**	6.24**	0.64**	2.83**
P2x P4	-0.38**	-0.01	2.06**	2.11**	-0.78**	0.50**
P2x P5	-0.55**	-0.28**	-0.37**	1.43**	2.27**	0.58**
P2x P6	-0.36**	-0.33**	-0.93**	1.55**	-0.27*	-1.15**
P3x P4	-1.06**	-0.75**	9.48**	3.92**	1.51**	1.12**
P3x P5	-0.90**	-0.94**	-0.91**	-5.45**	2.43**	-0.58**
P3x P6	-0.71**	0.26**	-2.76**	-0.42**	-0.46**	0.10
P4x P5	-1.06**	-0.87**	-8.85**	2.06**	0.15	1.15**
P4x P6	0.12**	-0.86**	-0.73**	-3.71**	2.67**	0.77**
P5x P6	-0.08**	0.64**	5.68**	2.62**	0.82**	0.65**
LSD (sij)	0.05	0.03	0.08	0.13	0.10	0.24
	0.01	0.05	0.11	0.18	0.14	0.32
LSD (sij-skl)	0.05	0.04	0.12	0.19	0.14	0.32
	0.01	0.05	0.16	0.24	0.19	0.43
LSD (sij-sik)	0.05	0.05	0.14	0.20	0.16	0.36
	0.01	0.07	0.18	0.27	0.22	0.46

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

For grain yield per spike, the hybrid combinations neamly (Giza-171(P₂) × Misr-3(P₃) and Sakha-95 (P₄) × Morocco (P₆) estimates of SCA effects in F₁ generation. While, the hybrids shandweel (P₁)× Giza171(P₂) and Sids1 (P₅) × Morocco(P₆) were significant eatimates of SCA effects in F₂ generation.

For 1000 – grain weight, six and nine hybrid combinations showed highly significant SCA effects in F₁ and F₂ generations, respectively. These hybrids also showed useful heterosis, Shandaweeel-1 (P₁), Giza-171(P₂) and Sakha-95 (P₄) wheat varieties involved in these hybrids

were found to be good combiners for grain weight.

For grain yield per plant, nine and nine hybrid combinations showed highly significant SCA effects in F₁ and F₂ generations, respectively. All of these hybrids showed also useful heterotic effects. The two parental Shandaweeel-1 and Sakha-95 were found to be good general combiner for this trait and could be used in wheat breeding program. The best crosses in most traits could be attributes to high × high, high × low and low × low general combiners.

In general, such combinations of high SCA specially in F₂ generation in the same time, involved good combiner for both parents, they could be exploited for breeding varieties. Nevertheless, if the parental combination showed desirable high SCA involve only one good combiner, such combinations would throughout desirable transgressive segregates provided that the additive genetic system in the good combiner (as well as complementary and epistatic effects in the hybrids) act in the same direction to reduce undesirable characteristics and maximize the character under consideration.

The same conclusion was also drawn by Masood and Kornstad (2000), Nazir *et al.*

(2005), Al-Hamdany (2010), Ammar *et al.* (2014), Farhat and Darwish (2016), Khilwat *et al.* (2017), El-Gammaal and Yahya (2018), Ali *et al.* (2020) and Abro *et al.* (2021)

Heterosis:

Useful heterosis expressed as the percentage deviation of F₁ and F₂ mean performance from the mid parent for all traits studied in Table 7.

For heading date, eleven out of the fifteen hybrids studied in F₁'s were found to be exhibit highly significant negative useful heterotic effect which ranged from -1.87% to -10.92% relative to the respective mid parent values. Generally, all hybrids were earlier than their parents.

Table (7): Percentage of heterosis for F₁ and F₂ hybrids relative to mid parent for all traits.

Hybrids	Heading date (days)		Maturity date (days)		Plant height (cm)	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
	NI	NI	NI	NI	NI	NI
P1xP2	-10.92**	-4.73**	-3.18**	-3.17**	-13.62**	2.45**
P1x P3	-10.53**	-4.53**	-2.54**	-3.42**	-8.04**	-0.61
P1x P4	-10.75**	-8.25**	-12.91**	-15.02**	-8.85**	-3.21**
P1x P5	-1.87	-3.76**	-3.65**	-5.31**	-0.27	7.45**
P1x P6	11.36**	-3.38**	-7.47**	-8.39**	-6.06**	-7.61**
P2x P3	1.46	-4.40**	-2.85**	-5.65**	7.70**	5.47**
P2x P4	-10.65**	-4.87**	-7.34**	3.92**	-6.21**	10.65**
P2x P5	-9.00**	-3.16**	-3.33**	-5.11**	3.01**	16.93**
P2x P6	-9.48**	-2.52**	1.23	0.38	-3.34**	4.67**
P3x P4	-6.15**	-4.62**	2.52**	-4.21**	-16.03**	6.65**
P3x P5	2.85*	-3.13**	9.85**	8.49**	-4.74**	-1.86*
P3x P6	-3.68**	-4.04**	5.62**	4.11**	2.88**	0.47
P4x P5	-6.50**	-7.01**	1.18	1.84**	-8.85**	7.66**
P4x P6	-4.57**	-4.89**	4.12**	3.38**	-1.62*	-2.89**
P5x P6	-9.17**	-3.39**	0.94	0.87	0.31	-9.82**
L.S.D 0.05	1.77	1.07	1.97	1.39	1.56	1.50
L.S.D 0.01	2.38	1.43	2.65	1.86	2.08	1.99

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

Table 7: Cont.

Hybrids	Grain yield per spike (g)		1000-grain weight		Grain yield per plant (g)	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
	NI	NI	NI	NI	NI	NI
P1xP2	-32.52**	-6.11**	-2.03**	9.22**	44.00**	34.29**
P1x P3	-25.49**	-34.71**	-3.67**	-7.98**	33.58**	39.88**
P1x P4	-34.21**	-27.67**	1.43**	6.69**	14.12**	-3.18**
P1x P5	-32.07**	-3.23**	11.51**	-22.24**	29.57**	4.72**
P1x P6	-43.66**	-12.86**	-26.10**	-14.94**	13.05**	26.89**
P2x P3	19.84**	-14.58**	8.23**	21.42**	29.23**	48.38**
P2x P4	-22.36**	-15.94**	7.33**	16.77**	10.56**	15.98**
P2x P5	-26.53**	-12.44**	1.67**	6.42**	40.70**	18.16**
P2x P6	-20.95**	-11.94**	-5.24**	7.35**	13.08**	6.59**
P3x P4	-36.10**	-35.99**	24.63**	13.74**	30.95**	24.61**
P3x P5	-34.66**	-31.74**	2.24**	-13.39**	48.30**	11.60**
P3x P6	-30.21**	-9.46**	-7.05**	-2.26**	13.55**	20.08**
P4x P5	-41.73**	-31.28**	-14.53**	4.54**	19.98**	13.98**
P4x P6	-20.38**	-31.57**	-4.54**	-5.76**	29.82**	13.09**
P5x P6	-25.21**	4.66**	6.71**	-0.87**	24.03**	13.22**
L.S.D 0.05	0.05	0.14	0.20	0.14	0.32	0.32
L.S.D 0.01	0.59	0.18	0.27	0.19	0.43	0.41

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

Eight hybrids were highly significant negative useful heterotic effects for maturity date in F₁ generation. It's ranged from -2.54% to -12.91% relative to mid parent values. The best cross was Shandawee-1 (P₁) × Sakha-95 (P₄) which come to maturity after 105.22 days from sowing and thirteen days earlier than its early parent. Meanwhile, eight hybrids were highly significant negative remain heterotic effect in F₂ generation which ranged from -3.17% to -15.02% relative to mid parent values. Also, the hybrid Shandawee-1 (P₁) × Sakha-95 (P₄) was the earlier in F₂ generation. Therefore, it could be concluded that these previous hybrids would be of interest in wheat breeding program for earliness. These results are in conformity with those previously obtained by Fellahi *et al.* (2017) and Noorka *et al.* (2013).

Concerning plant height, ten and five hybrid combinations showed useful heterosis which ranged from (-1.62% to -16.03%) and (-1.86% to -9.82%) in F₁ and F₂ generations. Useful heterotic effects were previously obtained for plant height by Noorka *et al.* (2013), Ahmed *et al.* (2016), Farhat and Darwish (2016) and Ali *et al.* (2020).

The hybrid Giza-171 (P₂) × Misr-3 (P₃) and Sids-1 (P₅) × Morocco (P₆) were highly significant useful heterotic effect for grain yield per main spike under both experiments in F₁ and F₂ generations, respectively.

For 1000-grain weight, eight and eight hybrid combinations in F₁ and F₂ generations had significantly heavier grains than that of their respective mid parents. This useful heterosis ranged from (1.67% to 24.63%) and (4.54% to

21.42) in F₁ and F₂ generations, respectively. Significant heterosis was also found by Khilwat *et al.* (2017), Fellahi *et al.* (2017) and Ayoob (2020)

For grain yield per plant, all hybrid combinations in F₁ generation had significant useful heterotic effect which varied from 10.56% to 48.30% and 4.81% to 52.53% over the respective mid parent. thirteen hybrids has significant useful remain hetrotic effect which ranged from 11.92% to 51.45% over mid parents in F₂ generation. The superiority of these crosses could be attributed to the increases in one or more of yield components i.e. number of spikes per plant, number of grains per spike, spike yield and 1000-grain weight. Significant heterosis was also found by El-Noorka *et al.* (2013), Gammaal and Yahya (2018) and Ayoob (2020).

Regarding to heterosis, the mean performance of the parents and their hybrids, it could be concluded that these hybrids had highly promising characters for breeding wheat genotypes. Thus, it should possess the genetic factors for high yield potential. These results could be confirmed the possibility of selection for these characters through the hybrids.

Moreover, it allowed the greed light in the front of plant breeders to build future breeding program for high potential yield in wheat crop.

Genetic Polymorphism Detected using SCoT Markers:

In total, twelve SCoT primers were tested for their ability to generate banding patterns from DNA corresponding and evaluate the genetic diversity of 6wheat cultivars. The amplification results of the SCoT primers used in this investigation are presented in Table (8). These primers produced good reproducible and scorable patterns and the amplification profiles were screened for the presence of polymorphisms *among* the 6 wheat cultivars as shown in (Fig. 1 and 2).

A total of (158) fragments were amplified with average of 11.4 fragments / primer. The lowest number of fragments (5) was produced by the SCoT-05, while the highest number of fragments (20) was revealed by the SoT-02.

The number of monomorphic fragments reached (91) with an average of 7.6 fragments /primer.

Table 8: The list of primer, Total number of Bands (TB), Monomorphic Bands (MB), Polymorphic Bands (PB), Percentage of Polymorphism (%P), Frequency (F) and Polymorphism Information Content (PIC) as revealed by SCoT analysis 6 wheat cultivars.

Primer	TB	MB	PB	% P	F	PIC
SCoT-01	17	8	9	53	0.7	0.33
SCoT-02	20	10	10	50	0.7	0.31
SCoT-03	16	12	4	25	0.9	0.21
SCoT-04	13	12	1	8	1.0	0.14
SCoT-05	5	5	0	0	1.0	0.00
SCoT-06	14	4	10	71	0.6	0.36
SCoT-07	11	8	3	27	0.8	0.22
SCoT-08	13	4	9	69	0.5	0.37
SCoT-09	14	9	5	36	0.8	0.25
SCoT-10	9	5	4	44	0.7	0.33
SCoT-11	12	9	3	25	0.8	0.23
SCoT-12	14	5	9	64	0.6	0.36
Total	158	91	67	-	-	-
Average	13.2	7.6	5.6	39	0.76	0.26

Gene action and genetic diversity in a six parental diallel crosses of wheat

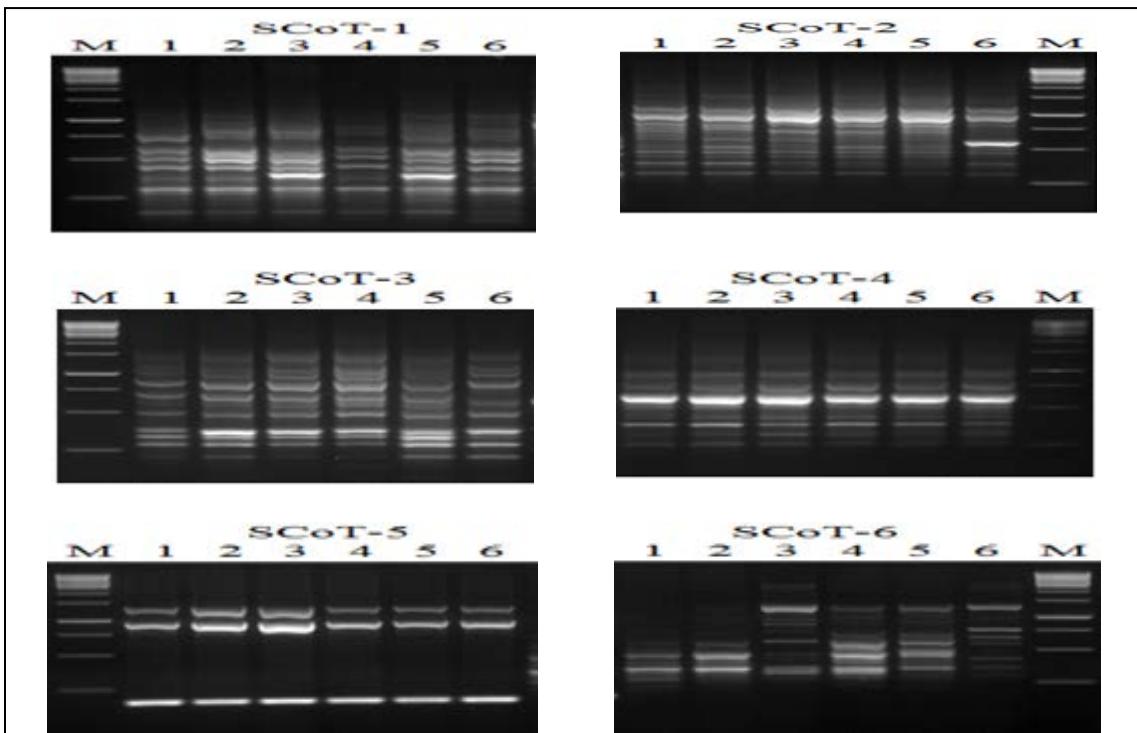


Fig (1): SCoT profiles for the 6 wheat cultivars as detected with primers SCoT-01, SCoT-02, SCoT-03, SCoT04, SCoT-05 and SCoT-06. Lanes 1 to 6 represent: Misr-3, shandawee-1, Sakha-95, Giza-171, sidsandMorocco. M: 1 Kb ladder DNA marker

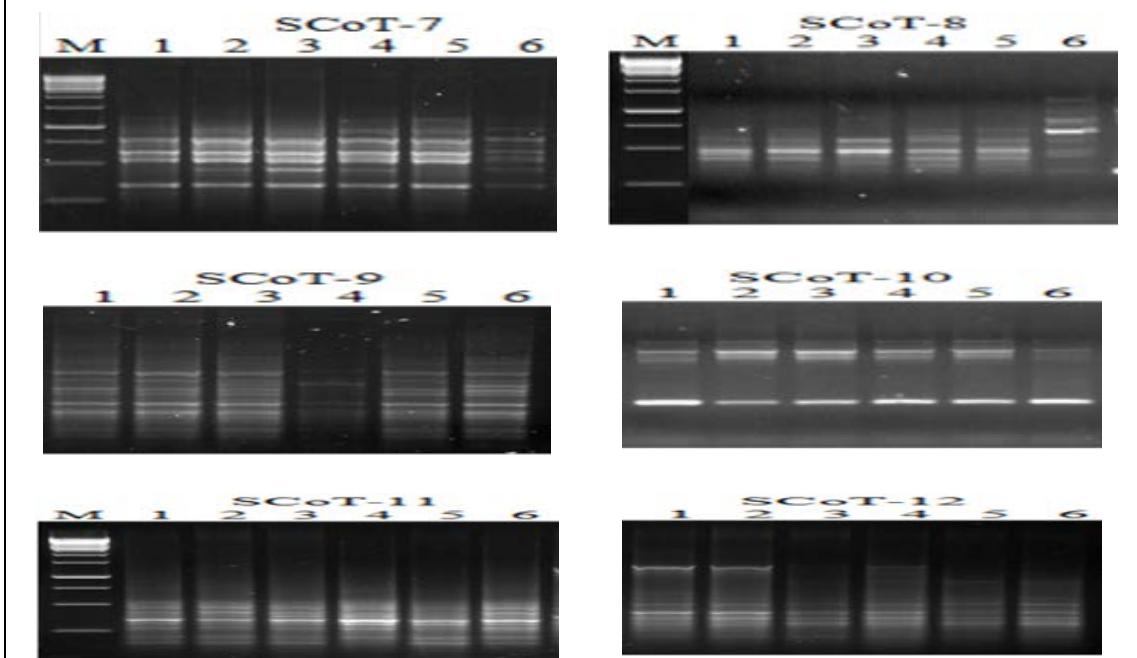


Fig (2): SCoT profiles for the 6 wheat cultivars as detected with primers SCoT-07, SCoT-09, SCoT-08, SCoT10, SCoT-11 and SCoT-12. Lanes 1 to 6 represent: misr-3, Shandawee-1, Sakha-95, Giza-171, sids and Morocco. M: 1 Kb ladder DNA marker

The maximum number of monomorphic bands (12) was generated by the SCoT-03 and SCoT-4, while the lowest (4) was produced by the SCoT-06.

The total number of polymorphic bands (67) was averaged as 5.6 fragments /primer. The lowest number of polymorphic fragments (1) was generated by the SCoT-04, while the highest number of polymorphic fragments (10) was revealed by the SCoT-02 and SCoT-06.

The percentage of polymorphism was ranged from 0% (SCoT-05) to 64% (SCoT-12). The average level of polymorphism was estimated as 39%. The frequency ranged from 0.5 (SCoT-08) to 1.0 (SCoT-4and SCoT-5).

The PIC value of the marker is defined as the expected fraction of informative offspring from this type of pedigree, the PIC values ranged from 0.00 (SCoT-05) to 0.37 (SCoT-08) with an average of 0.26. These results agree with those obtained by Abd El-lateif and Hewedy (2018), Hendawy (2019) and Nosair (2020).

- **Genetic relationship and diversity among 6 wheat cultivars;**

To examine the genetic relationships among the 6 wheat cultivars based on SCoT results, the scored data obtained from the 12 primers were analyzed using the Dice coefficient to compute the similarity matrices. These similarity matrices were used to generate a dendrogram using the UPGMA method. As shown in Table (9), the

estimated genetic similarities ranged from 83% to 93% revealing high levels of genetic similarity among the studied cultivars. The highest genetic similarity (93%) was observed among the cultivars Misr-3 and Shandwal-1 (resistant cultivars) followed by (91%) between cultivars Misr-3 and Sids-1., while the lowest genetic similarity (83%) was detected between Misr-3 (resistant cultivar) and Morocco (hypersensitive cultivar). These results agree with Abd El-lateif and Hewedy (2018) and Nosair (2020).

- **Cluster Analysis as Revealed by SCoT:**

Matrices of similarities between pairs of individuals may be used as a starting point for statistical procedures such as cluster analysis. In a cluster analysis, relatively homogeneous groups of individuals cluster together in a hierarchical way and this clustering is visually displayed in a dendrogram.

The similarity matrix developed by analyzing only the common fragments between the different cultivars, a dendrogram (Fig 3) was constructed using UPGMA cluster analysis. The obtained dendrogram was divided into two main clusters; one cluster included cultivar Morocco (Hypersensitive)". While, the second cluster included two subclusters, the first subcluster included cultivars "Giza-171, Sids-1, Shandawee-1 and Misr-3", and the second subcluster included cultivar "Sakha-95".

Table (9): Genetic similarity estimates for the 6 wheat cultivars based on twelve SCoT markers.

Variety	Misr-3	Shandawee-1	Sakha-95	Giza-171	Sids-1	Morocco
Misr-3	100					
Shandawee-1	<u>93</u>	100				
Sakha-95	87	90	100			
Giza-171	88	89	86	100		
Sids-1	91	90	88	88	100	
Morocco	<u>83</u>	85	88	<u>83</u>	85	100

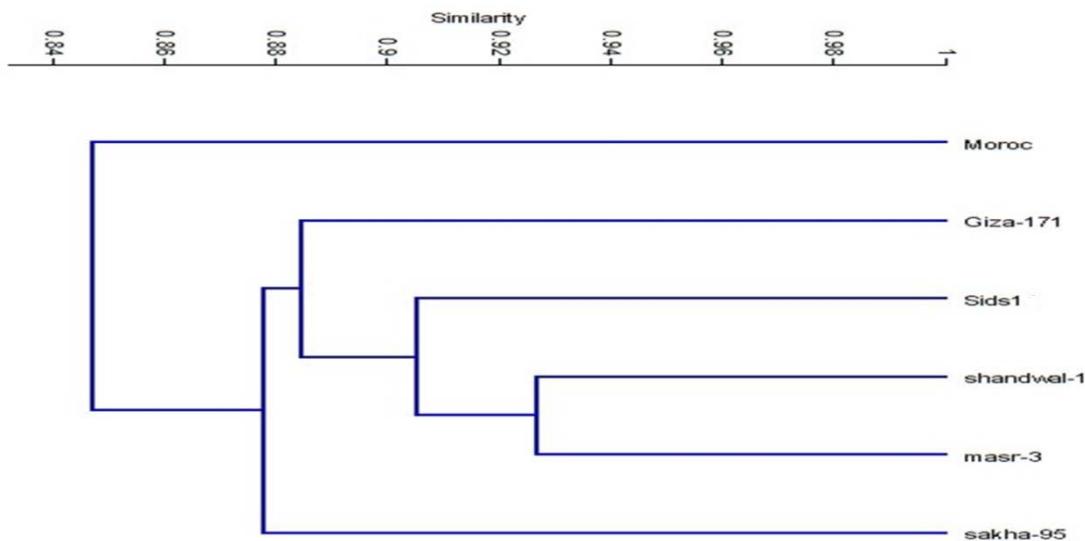


Fig. (3): Dendrogram for the 6 wheat cultivars constructed from the SCoT data using Un weighted Pair-group Arithmetic (UPGMA) and similarity matrices computed according to Dice coefficients.

DISCUSSION

Because of their great resolving capacity, SCoT is useful in genetic diversity research (Hamidet al., 2014 and Cao et al., 2006). These markers are effective and low-cost analytical tools for evaluating genetic variants in a wide range of plants. The effectiveness of SCoT markers is evaluated in this study using factors such as PIC and polymorphism percentage. PIC has traditionally been used to assess the informative capability of markers in different farmed cultivars. SCoT markers were used in wheat germplasm. We compared the genetic diversity of two groups of people in this study. The current study revealed considerable genetic diversity among the six wheat cultivars, which could be valuable for breeding purposes. Genetic corrosion in cultivated wheat provides a good motivation for evaluating genetic diversity among different cultivars, as well as determining the possibility of improving plant material efficiency, which could lead to increased food production.

REFERENCES

- Abdel-Lateif, K. and Hewedy, O. (2018). Genetic diversity Egyptian wheat cultivars using SCoTand SSR markers. SAB.J. Gene., 50(1): 36-45.

- Abro, T. F; Rajput, A. A.; Sootaher, J. K.; Shar, P. A.; Chang, M. S.; Naeem, M.; Siyal, A.L.; Siya, F. H.; Menghwar, K. K.; Baloch, A.; Keerio, A. and Vistro, M. A. (2021). Estimation of combining ability in F₂ hybrids of bread wheat (*Triticum aestivum* L.) .Enviro.Scien., 58(2): 69-81.
- Adel, M. M. and Ali, E. A. (2013). Gene action and combining ability in a six parent diallel cross of wheat. Asian. J. Sci., 5 (1): 14-23.
- Afridi, K.; Khan, U.N.; Mohammad, F.; Shah, A. J. S.; Gul, S.; Khalil, A. L.; Sajjad, M.; Ali, S.; Ali, L. and Khan, M. S. (2017). Inheritance pattern of earliness and yield traits in half-diallel crosses of spring wheat. J. Plant Sci. 97: 865–880.
- Ahmad, J.; Zali, A.; Samadi, B. Y.; Talai, A.; Ghannadha, M. R. and Saiedi, A. (2003). A study of combining ability and gene effect in bread wheat under drought stress conditions by diallel method Iranian J. Agri. Sci. 34: 1-8.
- Ahmad, I.; Mahmood, N.; Khaliq, I. and Khan, N. (2016). Genetic analysis for five important morphological attributes in wheat (*Triticum aestivum*L.). J. Ani. Sci., 26 (3): 725-730.
- Ahmed, I. H.; Mohammad, F.; Din, S. O.; Hassan, G. and Gul, R. (2006). Diallel

- analysis of the inheritance pattern of agronomic traits of bread wheat. J. Botany, 38(4): 169-175.
- Al – Hamdany A.T. (2010). Genetic analysis of F₂diallel crosses in durum wheat. J. of Agric, 38: (4)2-8.
- Ali, A. M; Hassan, S.M. and Ali, A. L. (2020). Combining ability in some genotypes of bread wheat (*Triticum aestivum* L.) under different sowing dates. J. Agric. Sci., 2 (2): 291-305.
- Ammar, A. A; I.S. liaqat; Ahmed, R.I.; Qayym, A.; Mahmood, S.; Noor, E.; Aziz, M. K.; Asim, A.; manzoor, S.A. and Malik, W. (2014). Line × Tester mating d design analysis for grain yield and yield related traits in bread wheat. Journal of Food, Agriculture and Environment, 12 (2): 383-386.
- Ayoob, H. M. (2020). Combining ability analysis estimation of heterosis and some genetic paramrters using half diallel cross in bread wheat (*Triticum aestivum*L.). J. edu. sci., 29(1): 93-106.
- Cabo, S.; Ferreira, L.; Carvalho, A.; Martins-Lopes, P. and Lima-Brito, J. (2014). Potential of startcodon targeted (SCoT) markers for DNA finger printing of newly synthesized tritordeums and their respective parents. J. Appl Genet., 55: 307–312.
- Cao, P.; Yao, Q.; Ding, B.; Zing, H.; Zeng, H.; Zhong, Y. and Jin, X. (2006). Genetic diversity of *inojackiadolichocarpa* (Styracaceae), species endangered and endemic to China, detected by inter-simple sequence repeat (ISSR). Biochem. Syst Ecol. 34: 231–239.
- Collard, B. and Mackill, D. (2009). Start codon targeted (SCoT) polymorphism: a simple, novel DNA marker technique for generating gene-targeted markers in plants. Plant. Mol. Biol. Rep., 27: 86–93.
- El-Gammaal and Yahya (2018). Genetic variability and heterosis in F₁ and F₂ generations of diallel crosses among seven wheat genotypes. J. Plant Production, Mansoura Univ., 9 (12): 1075 – 1086.
- El-Said, A. Rania (2018). Assessment of genetical parameters of yield and its attributes in bread wheat (*triticumaestivum*, l.). J. Agric. Chem. 9 (10): 243–251.
- FAO (2020). Food and Agriculture organization <http://www.fao.org/faostat/en/data>.
- Farhat, W. Z. E and Darwish, M. A. H. (2016) combining ability for earliness, agronomic and leaf and stem rusts resistance traits in f₁ and f₂ bread wheat diallel crosses. J. Plant Production, Mansoura Univ., 7(12): 1535 - 1541.
- Farooq, J.; Habib, I.; saeed, A.; Nawab, N. N.; Khalia, I. and Abbas, G. (2006). Combining ability for yield and its components in bread wheat (*Triticum aestivum*L.) J. Agri. Sci., 2(4): 208-211.
- Fellahi, Z. E. A.; Hannachi, A.; Bouzerzour, H.; Dreisigacker, S.; Yahyaoui, A. and Sehgal, D. (2017). Genetic analysis of morphophysiological traits and yield components in F₂ partial diallel crosses of bread wheat (*Triticum aestivum* L.). Revista Facultad Nacional de Agronomia Medellin, 70(3): 8237–8250.
- Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. Aust. J. Biol.sci., 9: 463-493.
- Hamidi, H; Talebi, R. and Keshavarzi, F. (2014). Comparative efficiency of function algene-based markers, start codon targeted polymorphism (SCoT) and conserved DNA-derived polymorphism (CDDP) with ISSR markers for diagnostic finger printing in wheat (*Triticum aestivum* L.). Cereal Res Commun.42(4):558–567.
- Hassan, G.; Mohammad, F.; Afridi, S.S. and Khalil, I. (2007) Combining ability in the F₁ generations of diallel crosses for yield and yield components in wheat. Sarhad . J. Agri. 23: 937–942.
- Hendaway, F. Marwa (2019). Breeding for some quantitative traits in common wheat (*Triticum aestivum* L.) using molecular marker technique. Ph.D. Thesis, Faculty of Agric. Minufiya Univ., Egypt.

- Iqbal, M. and Khan, A. A. (2006). Analysis of Combining Ability for Spike Characteristics in Wheat (*Triticum aestivum* L.). *J. Agri.Biol.* 8(5): 684 – 687.
- Joshi, A; Kumar, A. and Kashyap, S. (2020). Genetic analysis of yield and yield contributing traits in bread wheat. *Inte. J. Agri. Biot.*, 13(2): 119-128.
- Kalhoro, F. A.; Rajpar, A. A.; Kalhoro, S. A.; Mahar, A.; Ali, A.; Otho, S. A.; Soomro, R. N.; Ali, F. and Baloch, Z. A. (2015). Heterosis and combinig ability in F₁ population of hexaploid wheat (*Triticum aestivum* L.). *American. J. Plant Sci.*, 6: 1011 – 1026.
- Khilwat, A.; Khan, U. N.; Mohammad, F.; Shah, A. J. S.; Gul, S.; Khalil, A. L.; Sajjad, M.; Ali, S.; Ali, L. and Khan, M. S. (2017). Inheritance pattern of earliness and yield traits in half-diallel crosses of spring wheat. *J. Sci.*, 97: 865–880.
- Mahpara, S.; Ali, Z.; Rehmani, M. I. A.; Iqbal, J. and Shafiq, M. R. (2017). Studies of genetic and combining ability analysis for some physio – morphological traits in spring wheat using 7 x 7 diallel crosses. *Int. J. Agric. Appl. Sci.*, 9(1): 33–40.
- Masood, M.S. and Kornstad, W.E. (2000). Combining ability analysis over various generation in a diallel cross of bread wheat. *Pakistan J. Agric. Res.*, 16: 1-4.
- Nazir, S.; Khan, A. S. and Ali, Z. (2005). Combining ability analysis for yield and yield contributing traits in bread wheat. *J. Agri. Sci.*, 1: 129–132.
- Noorka, I. R.; Batool, A.; Rauf, S.; Teixeira da Silva, J. A. and Ashraf, E. (2013). Estimation of heterosis in wheat (*Triticum aestivum*L.) under contrasting water regimes. *Inte. J. Plant Breeding*, 7(1): 55-60.
- Nosair, H. R. (2020). Genetic diversity studies on seven Egyptian wheat (*Triticum aestivum* L) cultivars using SCoT and ISSR polymorphism markers. *Taeckholmia.*, 40: 143-151.
- Verma, S; Maurya, R. and Maurya, S. (2016). Prediction of gene action and combining ability for yield and quality traits in F₁ and F₂ generations of wheat (*Triticum aestivum* L.) *Tro. Plant. Res.*, 3(2): 449–459.

ال فعل الجيني والتتنوع الوراثي في ستة أباء من القمح باستخدام الهجن التبادلية

حسان عبد الجيد دوام^(١)، مروة محمد النحاس^(١)، شفيق درويش ابراهيم^(٢)،
وليد محمد العرابي^(٣)، محمد سيد عبد العال^(١)، أميرة عبد العزيز علي قنديل^(١)

^(١) قسم المحاصيل كلية الزراعة جامعة المنوفية

^(٢) معهد بحوث الهندسة الوراثية الزراعية - مركز البحوث الزراعية - الجيزة

^(٣) معهد بحوث امراض النبات - مركز البحوث الزراعية

الملخص العربي

جرى هذا البحث في مزرعة كلية الزراعة بشبين الكوم جامعة المنوفية بهدف دراسة :-

(١) دراسة أهمية كل من القدرتين العامة والخاصة على الاختلاف للمحصول ومكوناته في الجيل الأول والثاني.

(٢) تقدير قوة الهجين الموجودة في الجيل الأول والمتبقية في الجيل الثاني.

(٣) توصيف وتقييم أليات التنوع الوراثي لبعض التراكيب الوراثية من قمح الخبز باستخدام المعلمات الوراثية SCoT.

- وقد تم استخدام ستة أصناف من قمح الخبز لهذه الدراسة وهم (شندوبل ١ ، جيزة ١٧١ ، مصر ٣ ، سخا ٩٥٤ ، سدس ١ ، موركوا)

- وقد اجري هذا البحث في ثلاثة مواسم زراعية متتالية هي: ٢٠١٨/٢٠١٩ ، ٢٠٢٠/٢٠١٩ ، ٢٠٢١/٢٠٢٠ .

١- موسم الزراعة ٢٠١٨/٢٠١٩

تم زراعة الستة أصناف وعمل جميع الهجن الممكنة بينها من خلال التهجين النصف تبادلي وتم الحصول على ١٥ هجين فردي .

٢- موسم الزرعة ٢٠١٩/٢٠٢٠

تم زراعة هجن الجيل الأول (١٥ هجين) الناتج من الهجن السابقة للحصول على حبوب الجيل الثاني ، وفي نفس الوقت تم تهجين الآباء مرة أخرى للحصول على حبوب الجيل الأول .

٣- موسم الزراعة ٢٠٢٠/٢٠٢١

تم تقييم الأباء (الستة) وهجن كلا من الجيل الأول(١٥) والجيل الثاني (١٥ هجين) في تصميم القطاعات الكاملة العشوائية في ٣ مكررات.

وقد تم تحليل بيانات كل من التجربتين باستخدام طريقة جريفنج (١٩٥٦) الطريقة الثانية ، الموديل الأول لتقدير المكونات الوراثية للهجن التبادلية ، وقد تم دراسة كلا من الصفات التالية :-

ميعاد طرد السنابل (يوم) - ميعاد النضج (يوم) - طول النبات (سم) - محصول السنبلة الرئيسية — وزن ١٠٠٠ حبة (جم)
— محصول النبات الفردي (جم).

ويمكن تلخيص النتائج المتحصل عليها كما يلى :-

- كانت قيم التباين الراجعة إلى التراكيب الوراثية والأباء والهجن عالية المعنوية لكل من الجيل الأول والثاني .
- كانت القيم الراجعة إلى متوسط قوة الهجين عالية المعنوية لمعظم الصفات المدروسة في كلا الجيلين.
- كانت قيم المتوسطات لصفات محصول السنبلة الرئيسية، عدد حبوب السنبلة ، محصول السنبلة ، وزن ١٠٠٠ حبة ،
ومحصول النبات الفردي في حالة الإصابة المرضية أقل منها عن الزراعة في الظروف العادية مما يدل على تأثير
الإصابة بمرض صدأ الأوراق على هذه الصفات.
- كانت قيم التباين الوراثي الراجعة للقدرة العامة على التألف عالية المعنوية لكل من الصفات المدروسة ، مما يوضح أهمية
كل من الفعل الجيني فقط في وراثة هذه الصفات .

- كانت النسبة بين تباينى كل من القدرتين العامة والخاصة على التالفة أعلى في الجيل الثاني عن الجيل الأول لكن الصفات المدروسة مما يؤكد أن التباين الوراثي المضييف والفعل الوراثي المضييف \times المضييف يزداد والتباين الوراثي الغير مضييف ينخفض في الجيل الثاني.
- أظهر صنف القمح شندويل ١ قدرة عامة عالية على التالفة لصفات محصول السنبلة الرئيسية ومحصول النبات الفردي وذلك في كل من نباتات الجيل الأول والثاني ، كما أظهر صنف القمح جيزة ١٧١ قدرة عامة عالية على الخلط لصفات ميعاد النضج ومحصول سنبلة الساق الرئيسية لنباتات الجيل الأول ، بالإضافة إلى صفات وزن ١٠٠٠ جبة ومحصول النبات الفردي لنباتات الجيل الثاني .
- تم الحصول على أفضل التأثيرات المرغوبة للقدرة الخاصة على الانلاف لصفة محصول النبات الفردي في سبعة هجن هي (شندويل \times ج ١٧١)، (شندويل \times مصر ٣)، (ج ١٧١ \times مصر ٣)، (سخا ٩٥ \times سدس ١)، (سخا ٩٥ \times مرووكو)، (سدس ١ \times مرووكو) تم الحصول على ١٥٨ فرجمنت وراثياً بإستخدام اثنى عشر معلم جزيئي .
- تتراوح عدد الفرجمنت ٥ إلى ٢٠ بمتوسط ١٣,٢ فرجمنت DNA
- تراوحت قيم المحتوى المعلوماتي (PIC) بين ٠,٣٧ ، متوسط المعلم الجزيئي SCoT ١١ (٠,٢٣) ، ومتوسط المعلم الجزيئي ١٢ SCoT (٠,٣٦).
- أظهر متوسط قيم المحتوى المعلوماتي (PIC) للمعلمات الجزيئية SCoT متوسط قيمة ٠,٢٦ مما يؤكد أن علامات SCoT في القمح كانت ذات كفاءة في تقدير التنوع الوراثي .
- أظهر dendrogram الناتج من التحليل العنقودي UPGMA على أساس معامل المصفوفة GS للأصناف الستة وجود مجموعتين رئيسيتين .
- أوضحت هذه الدراسة انه يمكن الحصول على أعلى اختلافات وراثية بين أصناف القمح المستخدمة بإستخدام أقل عدد من المعلم الجزيئي SCoT وكذلك عمل البصمة الوراثية لهذه الأصناف .
- توضح هذه الدراسة أهمية استخدام المعلم الجزيئي SCoT في تحديد الاختلافات الوراثية بين الأصناف وأهمية هذه التراكيب الوراثية في برامج التربية وكذلك في استخدام المعلمات الجزيئية في الانتخاب للصفات تحت الدراسة في برامج تربية القمح .

MENOUFIA JOURNAL OF PLANT PRODUCTION

<https://mjppf.journals.ekb.eg/>