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CHARACTERZATION AND EVALUATION OF SOME GENOTYPES IN BREAD WHEAT USING SSR MARKERS UNDER DIFFERENT HEAT CONDITIONS

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ABSTRACT: *Heterosis and specific combining ability analysis were studied in a half diallel set of bread wheat for number of spikes per plant, 1000- grain weight, number of kernels per spike, grain yield per plant, protein and carbohydrate percentages under Gemmeiza location (normal temperature) and Mataana location (high temperature). Eight genotypes and the resultant twenty eight crosses mean squares were found to be highly significant for all studied traits at the two different locations and their combined data. Parents vs. crosses mean squares as an indication to average heterosis overall crosses, were found to be highly significant for protein and carbohydrate percentages at the two different locations and their combined data. For1000-grain weight and number of kernels per spike the estimated values of parents vs. crosses were highly significant at Gemmeiza location and their combined data. Specific combining ability was found to be highly significant for all studied characters under study at each location and the combined data. For grain yield per plant, three hybrid combinations Line 1 x Sids 1, Line 2 x Line 5 and Line 4 x Line 5 showed significant specific combining ability effects at the two different locations and their combined data. Simple Sequence Repeats (SSR) analysis was performed using ten SSR primers on the eight wheat genotypes. A total of 39 alleles ranging from 95.475 bp to 301.471 bp were obtained by the tested primers with an average 3.9 alleles per locus. SSR data analysis using the similarity matrix and the genetic distance estimates showed that similarity index ranged from 62% to 93%. The most distantly related cultivar and landraces were Sahel 1 and Line 1 with lowest similarity index (0.62) between them. The most related genotypes were Line 4 and Sids 1 with highest similarity index (0.93). Most examined traits showed low correlation coefficient between genetic distances coefficient, heterosis over better parent and specific combing ability at Gemmeiza and Mataana locations. Information generated from this study is useful to predict hybrids for selecting parents out to maximize the grain yield and its components.*

Key words: *SSR Markers, Wheat, Heterosis, SCA and Genetic distances coefficient.*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the first important and strategic cereal crop for the majority of world's populations. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. Old bread wheat (landrace) an important genetic resource that can be used to improve modern varieties Feldman and Sears (1981) by introducing new alleles or combinations of genes. This heterogeneity has not been analyzed systematically Nevo and Payne (1987) and such landraces may include genetic sources of biotic and abiotic stress tolerance, especially in environments not tested in major breeding programmes, and also quality, yield and resistance genes. Heat stress is an important constraint to wheat productivity affecting different growth stages specially anthesis and grain filling Kamaluddin, *et al* (2011). It has already been established that heat stress can be a significant factor in reducing the yield and quality of wheat Stone and Nicolas (1995). Molecular markers provide the best estimate of genetic diversity since they are independent of the confounding effects of environmental factors. Simple sequence repeats (SSR) have now provided the opportunity to monitor genetic integrity at the genotype level and laboratory tests are available to determine any unintentional genetic erosion or change in genetic identity. The objectives of the present study are (I) establish The potentiality of heterosis expressed as better parent and specific combining ability in order to formulate the most efficient breeding procedures. (II) Using Simple Sequence Repeats (SSR) to detect DNA polymorphism, identify genotypes and estimate genetic diversity among wheat genotypes. (III) Examine the relationship between genetic distance based on SSR with heterosis and SCA effects for yield, yield components and studied chemical traits.

MATERIALS AND METHODS

Plant materials

Five promising landraces for heat tolerance were collected from diverse areas of Egypt as well as three commercial cultivars used to establish the experimental materials for this investigation. The names, pedigree and source of these varieties and lines are presented in Table (1).

Filed experiments

A half diallel crosses set were carried out among the eight parents in 2008/2009 growing season. The parental genotypes and their possible 28 crosses were sown in 2009/2010 under two different heat conditions , which would be mentioned in the text as Gemmeiza location (L1) and Mataana location (L2),. The two experiments were arranged in a randomized complete block design with three replicates per each location. Each plot comprised single rows 3 meters long with 30 cm. between rows, plants within rows were 10 cm. apart allowing a total of 30 plants per plot. Normal agricultural practices were applied as usual for the ordinary wheat fields in the area. Ten guarded plants were randomly selected from each plot to detect number of spikes per plant, 1000 grain weight, number of kernels per spike, grain yield per plant, protein and carbohydrate percentages.. The combined analysis of two experiments was carried out whenever homogeneity of error variance was detected.

Molecular analysis

DNA extraction:

DNA was extracted using CTAB method suggested by Lansser *et al.* (1989) with some modifications. Leaves were ground to fine powder in the presence of liquid nitrogen then 100 µl of extraction buffer 140 mM Sorbitol, 220 mM Tris-HCl, pH 8.0, 22 mM EDTA, 800 mM NaCl, 1.0% CTAB, 1% Sarkosyl, 0.2 β-mercaptoethanol (adding just before use) was added and mixed gently. The content were transferred to sterile tubes and placed in 65 ºC for 20 min. The Tubes were centrifuged for 15 min at 12.000 rpm at 4 ºC. 400 µl Chloroform: Isoamayl (24:1) was added to the tubes and centrifuged for 15 min at 14.000 rpm at 4 ºC. The aqueous phase was transferred to a clean tube, then steps were repeated for second time. The supernatant was poured off and DNA pellet was washed using 70% ethanol and dried at room temperature. A volume of 50 µl TE was added (warmed at 65 ºC). DNA was assessed by Spectrophotometer at wave length 260/280 and the DNA was diluted to 100 ng/µl and stored at -20°C to be used in subsequent analysis.

SSR analysis

Ten SSR primer pairs (Table 2) developed and provided by Dr. P. Cregan, USDA-ARS, Aryland, USA were used in this study.

Table (1). Name, pedigree and source of the studied bread wheat genotypes.

Code No.	Name	Pedigree	source
1	Line 1	Landraces	New valley
2	Line 2	Landraces	Sohag
3	Line 3	Landraces	Sohag
4	Line 4	Landraces	Sohag
5	Line 5	Landraces	Qena
6	Sahel 1	NS732/PIMA//Veery"S"#5	Local variety
7	Sids 1	HD2172/Pavon "S" // 158-57 Maya 74 "S" Sd 46-45d-2Sd-1Sd-0Sd	Local variety
8	Gemmeiza 9	ALD"s"/HUAC//CMH74A-630/SX	Local variety

Table (2): Description of 10 wheat microsatellite, their chromosomal location, motif and annealing temperature

No	Primer pair ID[a]	Chromosomal Location	Motif	Annealing Tm(ºC)
1	BARC004	5AL	(TTA)15	52
2	BARC012	3AS	(TAA)28	52
3	BARC048	*4DS,4BS* 1AS,1AL	(TATC)11	55
4	BARC066	1DL	(TC)8(TAGA)5	55
5	BARC072	7BS	(CT)4(TCTA)8(TC)8	60
6	BARC078	4A	(TC)27(TATC)43	55
7	BARC079	6BL	(TAGA)10 + (TC)9	52
8	BARC003	*4AL*	(CCT)17	52
9	BARC010	2B,5A	(GAA)13	52
10	BARC011	2BL	(TAA)9+(TTA)12	52

PCR reaction:

PCR reactions were performed in a thermal cycler (MJ RESEACH 2000 TC thermal cycler). A standard 20 µl reaction mixture contained 1 x buffer, 2 mM MgCl2, 1 unit tag polymerase, 0.5 µM of each primer, 0.2 mM of each deoxyribonucleotide and 40 ng of template DNA. The amplification was carried out using the following profile 94 °C for 4 min, then 35 cycles at 94°C for 45 sec, 30 sec. depending on the individual primer set, 2 min at 72°C with a final extension step of 5 min. The PCR products were run on 8% PAGE sequencing gel at 120 volt. The gel was stained using Ethidium Bromide and photographed by Alpha Innotech gel . All data were analyzed by non linear dynamics phoretics program.

Cluster analysis:

DNA fragments amplified by microsatellite markers were scored in binary format with presence of a band scored as 1 and the absence of a band scored as 0. Genetic distances were estimated according to Nie and Li (1979) and the data were used to compare pair wise similarity coefficients according to Jaccard (1908). The similarity matrix UPGMA (unweighted pair – group method with arithmetic average) algorithm to generate the dendrogram showing the genetic relationship among studied genotypes .

RESULTS AND DISCUSSION.

Mean performance

Mean performance of the eight parents and their twenty eight crosses under Gemmeiza location (L1), Mataana location (L2) and the combined data for all studied traits are presented in Table (3). The parental Sahel 1 at L1 and Line 1 at L2 and combined analysis recorded the highest number of spikes per plant Also, the cross Line 1 x Sahel 1 at L1 and the combined analysis as well as Line 4 x Line 5 recorded the highest values. For 1000-grain weight, the Line 2 at L1, Sahel 1 at L2 and Gemmeiza 9 at the combined analysis recorded the greatest mean value. The crosses Sahel 1 x Gemmeiza 9, Line 5 x Sids 1 and Line 4 x Gemmeiza 9 at L1, L2 as well as the combined analysis had the highest mean values. The parental Sahel 1 at L1 and combined analysis and Gemmeiza 9 at L2 recorded the highest number of kernels per spike. While, the crosses Line 5 x Sahel at L1 and the combined analysis as well as Sids 1 x Gemmeiza 9 at L2 showed the highest mean values. For grain yield per plant, the parental variety Gemmeiza 9 at L1 and Line 1 at L2 as well as the combined analysis had the greatest mean values. The crosses Line 3 x Sahel 1 at L1 and Line 1 x Sahel 1 at L2 as well as the combined analysis had the greatest mean value. The high yielding of these genotypes could be attributed to number of spikes per plant, 1000-grain weight and number of kernels per spike. The parental Line 4 at L1 as well as the combined analysis and Line 2 at L2 expressed the highest values of protein percentage. Also, Line 2 x Sids 1 at L1 as well as the combined analysis and Line 2 x Sids 1 at L2 recorded the high mean values of protein percentage. For carbohydrate percentage the parental variety Sids 1 at L1, L2 as well as the combined analysis recorded the highest mean values. The crosses Sids 1 x Gemmeiza 9 at L1 as well as the combined analysis and Sahel 1 x Gemmeiza 9 at L2 had the greatest mean value.

Heterosis

Useful heterosis expressed as the percentage deviation of F_1 mean performance from the better parent for all traits studied are presented in Table (4).

For number of spikes per plant, the cross Line 4 x Line 5 exhibited significant useful heterosis at L2. Concerning 1000-grain weight four hybrid combinations Line 1 x Line 4 , Line 1 x Line 5, Line 1 x Sahel 1 and Line 4x Line 5 showed significant heterosis at L1. Kumar *et al.* (2011) found significant heterosis effects for this trait. As for number of kernels per spike, the cross Line 1 x Line 4 showed significant useful heterosis at L1, L2 and their combined data. Significant heterosis was also found by Dawwam *et al.* (2007) and Kumar *et al.* (2011) for this trait. For grain yield per plant, two hybrid combinations Line 2 x Line 5 and Line 4 x Line 5 showed significant heterosis at L2 and their combined data. The heterosis found in yield / plant could be attributed the heterosis in one or more yield component such as number of spikes per plant and 1000-grain weight. Sharief *et al.* (2006) and Kumar *et al.* (2011) found significant heterosis effects for this trait. As for protein percentage, four, three and two hybrid combinations which showed highly significant useful heterosis at L1, L2 and their combined respectively. Deshpande and Nayeem (1999) found significant heterosis effects for this trait. For carbohydrate percentage, the cross Line 1 x Line 5 showed significant useful heterosis at L2 and their combined .

Table (3): The genotypes mean performance under the two different locations and their combined data for all studied traits.

Genotypes	No. of spikes per plant			1000-grain weight			No. of kernels per spike		
	L1	L2	Comb	L1	L2	Comb	L1	L2	Comb
Line 1	14.80	13.93	14.37	30.11	26.93	28.52	53.07	45.33	49.20
Line 1x Line 2	14.40	9.67	12.03	41.39	32.86	37.12	58.87	52.33	55.60
Line 1x Line 3	16.40	8.93	12.67	39.20	37.23	38.22	52.47	51.80	52.13
Line 1x Line 4	16.20	11.53	13.87	37.33	34.25	35.79	61.60	56.80	59.20
Line 1x Line 5	15.00	9.89	12.45	38.29	35.92	37.11	52.00	49.67	50.83
Line 1x Sahel 1	16.61	13.93	15.27	38.70	39.24	38.97	58.67	55.67	57.17
Line 1x Sids 1	15.93	13.13	14.53	37.01	33.41	35.21	57.67	51.93	54.80
Line 1x Gemmeiza 9	15.73	12.61	14.17	39.48	45.10	42.29	58.53	56.11	57.32
Line 2	14.67	9.60	12.13	45.98	36.46	41.22	53.93	49.93	51.93
Line 2x Line 3	14.73	10.87	12.80	40.78	34.06	37.42	52.20	46.80	49.50
Line 2x Line 4	15.13	11.13	13.13	44.14	39.75	41.94	51.07	48.27	49.67
Line 2x Line 5	15.87	13.40	14.63	45.63	36.83	41.23	60.67	58.33	59.50
Line 2x Sahel 1	15.37	13.42	14.39	46.95	35.85	41.40	59.67	59.50	59.58
Line 2x Sids 1	13.93	9.83	11.88	41.64	38.51	40.07	55.33	48.33	51.83
Line 2x Gemmeiza 9	13.33	10.20	11.77	37.87	34.96	36.42	50.25	46.20	48.23
Line 3	15.07	12.53	13.80	43.84	39.15	41.50	56.87	55.80	56.33
Line 3x Line 4	14.20	14.53	14.37	37.13	33.54	35.33	58.00	51.67	54.83
Line 3x Line 5	15.47	14.53	15.00	42.17	40.47	41.32	55.60	56.80	56.20
Line 3x Sahel 1	16.27	12.07	14.17	43.27	37.79	40.53	58.00	53.77	55.88
Line 3x Sids 1	13.70	13.00	13.35	41.87	39.60	40.73	60.47	50.47	55.47
Line 3x Gemmeiza 9	14.33	12.13	13.23	47.99	41.65	44.82	53.27	58.47	55.87
Line 4	15.07	10.40	12.73	31.57	31.34	31.46	46.40	47.00	46.70
Line 4x Line5	15.07	14.60	14.83	39.22	39.82	39.52	57.07	59.93	58.50
Line 4x Sahel 1	12.07	12.00	12.03	36.58	48.19	42.38	62.87	56.07	59.47
Line 4x Sids` 1	10.80	9.80	10.30	31.50	50.32	40.91	62.13	58.20	60.17
Line 4x Gemmeiza 9	14.47	11.13	12.80	47.18	47.33	47.25	57.07	58.87	57.97
Line 5	14.87	11.73	13.30	33.26	39.36	36.31	56.13	53.27	54.70
Line 5x Sahel 1	15.47	12.13	13.80	37.59	43.90	40.75	69.47	59.67	64.57
Line 5x Sids 1	15.47	11.20	13.33	35.22	50.93	43.08	64.07	56.47	60.27
Line 5x Gemmeiza 9	15.80	8.60	12.20	48.63	39.18	43.90	68.33	60.60	64.47
Sahel 1	15.67	12.87	14.27	32.76	48.92	40.84	67.73	60.07	63.90
Sahel 1x Sids 1	15.30	8.20	11.75	42.26	41.30	41.78	67.60	59.67	63.63
Sahel 1 xGemmeiza 9	14.93	5.40	10.17	49.92	38.74	44.33	63.53	47.87	55.70
Sids 1	12.73	11.00	11.87	38.38	47.91	43.14	51.47	54.47	52.97
Sids 1x Gemmeiza 9	13.87	8.67	11.27	39.62	41.71	40.67	64.33	64.00	64.17
Gemmeiza 9	15.27	10.20	12.73	45.75	42.83	44.29	66.73	60.20	63.47
mean of parents	14.77	11.53	13.15	37.71	39.11	38.41	56.54	53.26	54.90
mean of crosses	14.85	11.31	13.08	41.02	39.73	40.37	58.96	54.79	56.88
mean of Genotypes	14.83	11.36	13.09	40.28	39.59	39.94	58.42	54.45	56.44
L.S.D 5%	1.67	2.20	1.91	4.63	5.71	5.09	5.97	5.67	5.70
L.S.D 1%	2.22	2.92	2.51	6.16	7.59	6.68	7.94	7.53	7.48

L1= Gemmeiza , L2 = Mataana and Comb. = combined data.

Table (3). Cont.

Genotypes	Grain yield/plant (g)			Protein percentage			Carbohydrate percentage		
	L1	L2	Comb	L1	L2	Comb	L1	L2	Comb
Line 1	29.30	26.46	27.88	11.74	14.49	13.12	62.13	60.80	61.47
Line 1x Line 2	27.99	19.37	23.68	12.46	13.65	13.06	62.23	62.13	62.18
Line 1x Line 3	31.16	18.97	25.07	11.86	12.66	12.26	63.10	66.53	64.82
Line 1x Line 4	30.78	23.20	26.99	11.43	12.48	11.96	63.27	62.27	62.77
Line 1x Line 5	28.50	18.79	23.64	12.48	12.65	12.57	62.03	62.93	62.48
Line 1x Sahel 1	31.56	27.93	29.74	11.66	13.42	12.54	62.83	62.03	62.43
Line 1x Sids 1	31.27	26.95	29.11	11.12	13.95	12.53	63.57	61.87	62.72
Line 1x Gemmeiza 9	29.89	26.48	28.19	11.90	13.61	12.75	62.87	62.20	62.53
Line 2	26.87	19.57	23.22	12.53	16.62	14.58	63.93	61.73	62.83
Line 2x Line 3	26.99	22.05	24.52	13.76	13.45	13.60	61.67	62.77	62.22
Line 2x Line 4	28.75	22.04	25.40	14.14	14.00	14.07	61.17	61.93	61.55
Line 2x Line 5	30.15	25.46	27.80	13.59	17.18	15.39	61.33	59.40	60.37
Line 2x Sahel 1	29.37	24.82	27.10	12.90	12.96	12.93	62.47	65.33	63.90
Line 2x Sids 1	25.08	18.68	21.88	16.13	14.90	15.52	60.37	62.47	61.42
Line 2x Gemmeiza 9	25.00	20.25	22.62	15.03	13.22	14.13	61.27	62.80	62.03
Line 3	28.99	24.81	26.90	11.81	15.05	13.43	64.00	64.57	64.28
Line 3x Line 4	26.65	26.28	26.46	12.23	14.04	13.13	63.57	62.03	62.80
Line 3x Line 5	27.61	27.84	27.73	11.75	14.77	13.26	63.17	60.93	62.05
Line 3x Sahel 1	32.81	22.32	27.56	13.09	14.56	13.82	63.60	62.10	62.85
Line 3x Sids 1	24.70	25.59	25.14	10.83	12.56	11.69	65.13	64.53	64.83
Line 3x Gemmeiza 9	27.23	21.84	24.54	13.42	15.58	14.50	61.60	60.30	60.95
Line 4	26.96	20.81	23.89	15.61	15.96	15.78	63.13	62.90	63.02
Line 4x Line5	29.63	27.74	28.68	11.46	14.31	12.88	63.53	62.33	62.93
Line 4x Sahel 1	24.55	19.83	22.19	12.72	14.87	13.80	62.57	63.20	62.88
Line 4x Sids` 1	20.04	17.95	19.00	11.75	14.41	13.08	65.53	65.03	65.28
Line 4x Gemmeiza 9	27.49	21.15	24.32	13.63	15.70	14.67	61.60	60.20	60.90
Line 5	28.25	19.32	23.78	12.39	14.92	13.65	62.43	60.60	61.52
Line 5x Sahel 1	28.12	21.24	24.68	12.32	13.12	12.72	64.17	61.83	63.00
Line 5x Sids 1	29.21	20.16	24.69	11.97	12.47	12.22	63.17	63.83	63.50
Line 5x Gemmeiza 9	30.02	16.34	23.18	12.27	8.65	10.46	62.50	62.13	62.32
Sahel 1	29.43	24.11	26.77	13.14	14.74	13.94	64.77	65.10	64.93
Sahel 1x Sids 1	28.50	15.58	22.04	11.48	12.24	11.86	63.73	66.13	64.93
Sahel 1 x Gemmeiza 9	26.75	14.93	20.84	11.82	12.49	12.16	64.03	66.87	65.45
Sids 1	28.25	20.83	24.54	11.79	11.66	11.73	65.53	67.57	66.55
Sids 1x Gemmeiza 9	24.32	16.47	20.39	11.45	14.30	12.88	66.20	66.27	65.83
Gemmeiza 9	30.71	21.05	25.88	13.20	13.00	13.10	61.30	65.47	63.78
mean of parents	28.59	22.12	25.36	12.78	14.55	13.67	63.40	63.69	63.55
mean of crosses	28.00	21.79	24.90	12.52	13.65	13.09	62.94	62.91	62.93
mean of Genotypes	28.14	21.87	25	12.58	13.85	13.22	63.04	63.09	63.06
L.S.D 5%	2.79	2.70	2.69	0.26	0.32	0.28	0.69	0.56	0.62
L.S.D 1%	3.71	3.59	3.53	0.34	0.42	0.37	0.92	0.74	0.81

L1= Gemmeiza , L2 = Mataana and Comb. = combined data

Table (4). Percentage of heterosis over better parent for all studied traits under the two different locations and their combined data .

Parents	No. of spikes per plant			1000-grain weight (gm)			No. of kernels per spike		
	L1	L2	Comb.	L1	L2	Comb.	L1	L2	Comb.
Line 1x Line 2	-2.703	-30.622**	-16.241*	-9.986	-9.875	-9.937	9.147	4.806	7.060
Line 1x Line 3	8.850	-35.885**	-11.833	-10.58*1	-4.904	-7.903	-7.737	-7.168	-7.456
Line 1x Line 4	7.522	-17.225*	-3.480	18.237*	9.274	13.772	16.080**	20.851**	20.325**
Line 1x Line 5	0.897	-29.019**	-13.376*	15.123*	-8.739	2.189	-7.363	-6.758	-7.069
Line 1x Sahel 1	6.021	0.000	6.299	18.106*	-19.789**	-4.588	-13.386**	-7.325	-10.537*
Line 1x Sids 1	7.658	-5.742	1.160	-3.550	-30.272**	-18.387**	8.668	-4.651	3.461
Line 1x Gemmeiza 9	3.057	-9.498	-1.357	-13.704**	5.292	-4.519	-12.288**	-6.794	-9.682*
Line 2x Line 3	-2.212	-13.298	-7.246	-11.293*	-13.017	-9.823	-8.206	-16.129**	-12.130*
Line 2x Line 4	0.442	7.051	3.141	-3.992	9.024	1.764	-5.315	-3.338	-4.365
Line 2x Line 5	6.726	14.205	10.025	-0.747	-6.427	0.040	8.076	9.512	8.775
Line 2x Sahel 1	-1.915	4.275	0.876	2.107	-26.719**	0.435	-11.909**	-0.943	-6.755
Line 2x Sids 1	-5.000	-10.606	-2.060	-9.430	-19.627**	-7.115	2.596	-11.261	-2.140
Line 2x Gemmeiza 9	-12.664	0.000	-7.592	-17.622**	-18.383**	-17.781**	-24.700**	-23.256**	-24.015**
Line 3x Line 4	-5.752	15.957	4.106	-15.316**	-14.345	-14.858*	1.993	-7.407	-2.663
Line 3x Line 5	2.655	15.957	8.696	-3.804	2.811	-0.423	-2.227	1.792	-0.237
Line 3x Sahel 1	3.830	-6.218	-0.701	-1.308	-22.753**	-2.338	-14.370**	-10.488*	-12.546**
Line 3x Sids 1	-9.071	3.723	-3.261	-4.499	-17.352**	-5.589	6.331	-9.558	-1.538
Line 3x Gemmeiza 9	-6.114	-3.191	-4.106	4.896	-2.747	1.200	-20.180**	-2.879	-11.975**
Line 4x Line 5	0.000	24.432*	11.529	17.919*	1.152	8.831	1.663	12.516*	6.947
Line 4x Sahel 1	-22.979**	-6.736	-15.654*	11.636	-1.492	3.774	-7.185	-6.659	-6.938
Line 4x Sids 1	-28.319**	-10.909	-19.110*	-17.916**	5.030	-5.175	20.725**	6.854	13.593*
Line 4x Gemmeiza 9	-5.240	7.051	0.524	3.116	10.507	6.689	-14.486**	-2.215	-8.666
Line 5x Sahel 1	-1.277	-5.699	-3.271	13.022	-10.249	-0.227	2.559	-0.666	1.043
Line 5x Sids 1	4.036	-4.545	0.251	-8.225	6.310	-0.155	14.133*	3.672	10.177
Line 5x Gemmeiza 9	3.493	-26.705**	-8.271	6.283	-8.530	-0.879	2.398	0.664	1.576
Sahel 1x Sids 1	-2.34	-36.269**	-17.640**	10.11	-15.571**	-3.163	-0.20	-0.666	-0.417
Sahel 1 x Gemmeiza 9	-4.68	-58.031**	-28.738**	9.12	-20.797**	0.095	-6.20	-20.487**	-12.833**
Sids 1x Gemmeiza 9	-9.170**	-21.21*	-11.518	-13.393*	-12.93*	-8.178	-3.596	6.31	1.103

L1= Gemmeiza , L2 = Mataana and Comb. = combined data.

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

Table (4) cont.

Parents	Grain yield/plant (g)			Protein percentage			Carbohydrate percentage		
	L1	L2	Comb.	L1	L2	Comb.	L1	L2	Comb.
Line 1x Line 2	-4.449	-26.799**	-15.054**	-0.585	-17.887**	-10.449**	-2.659**	0.648	-1.034*
Line 1x Line 3	6.360	-28.285**	-10.080*	0.423	-15.840**	-8.688**	-1.406*	3.046**	0.830
Line 1x Line 4	5.063	-12.297*	-3.175	-26.762**	-21.767**	-24.237**	0.211	-1.007*	-0.397
Line 1x Line 5	-2.719	-28.982**	-15.182**	0.780	-15.237**	-7.971**	-0.641	3.509**	1.571**
Line 1x Sahel 1	7.229	5.556	6.698	-11.289**	-8.912**	-10.032**	-2.985**	-4.711**	-3.850**
Line 1x Sids 1	6.747	1.877	4.436	-5.709**	-3.750**	-4.447**	-3.001**	-8.436**	-5.760
Line 1x Gemmeiza 9	-2.649	0.101	1.118	-9.874**	-6.073**	-2.770*	1.180	-6.137**	-1.960**
Line 2x Line 3	-6.898	-11.136*	-8.853	9.761**	-19.110**	-6.699**	-3.646**	-2.788**	-3.215**
Line 2x Line 4	6.652	5.894	6.322	-9.419**	-15.781**	-10.856**	-4.327**	-1.537**	-2.327**
Line 2x Line 5	6.726	30.075**	16.903**	8.457**	3.369**	5.556**	-4.067**	-3.780**	-3.926**
Line 2x Sahel 1	-0.204	2.917	1.201	-1.826	-22.017**	-11.295**	-3.551**	0.358	-1.591**
Line 2x Sids 1	-11.211**	-10.291	-10.821	28.670**	-10.347**	6.425**	-7.884**	-7.548**	-7.713**
Line 2x Gemmeiza 9	-18.584**	-3.801	-12.572*	13.889**	-20.453**	-3.087**	-4.171**	-5.231**	-2.744**
Line 3x Line 4	-8.094	5.911	-1.635	-21.657**	-12.012**	-16.781**	-0.677	-3.924**	-2.307**
Line 3x Line 5	-4.760	12.198*	3.060	-5.167**	-1.839	-2.893**	-1.302*	-5.627**	-3.474**
Line 3x Sahel 1	11.461**	-10.048	2.453	-0.406	-3.257**	-0.837	-1.801**	-4.608**	-3.208**
Line 3x Sids 1	-14.808**	3.117	-6.542	-8.298**	-16.549**	-12.920**	-0.610	-4.489**	-2.580**
Line 3x Gemmeiza 9	-11.311**	-11.983*	-8.797	1.667	3.567**	7.993**	-3.750**	-9.004**	-5.185**
Line 4x Line 5	4.886	33.280**	20.081**	-26.570**	-10.341**	-18.365**	0.634	-0.901*	-0.132
Line 4x Sahel 1	-16.580**	-17.750**	-17.107**	-18.475**	-6.789**	-12.567**	-3.397**	-2.919**	-3.157**
Line 4x Sids 1	-29.054**	-13.796*	-22.578**	-24.733**	-9.693**	-17.130**	0.000	-3.749**	-1.903**
Line 4x Gemmeiza 9	-10.486*	0.507	-6.016	-12.666**	-1.588	-7.065**	-2.429**	-9.155**	-4.521**
Line 5x Sahel 1	-4.462	-11.902*	-7.812	-6.215**	-12.042**	-8.717**	-0.926	-5.018**	-2.977**
Line 5x Sids 1	3.410	-3.201	0.605	-3.337**	-16.421**	-10.486**	-3.611**	-5.525**	-4.583**
Line 5x Gemmeiza 9	-2.236	-22.363**	-10.421	-7.071**	-42.024**	-23.401**	0.107	-6.237**	-2.299**
Sahel 1x Sids 1	-3.17	-35.388**	-17.679**	-12.66**	-16.919**	-14.911**	-2.75**	-2.121**	-2.429**
Sahel 1 x Gemmeiza 9	-12.87**	-38.098**	-22.161**	-10.43**	-15.268**	-12.794**	-1.13*	0.905	0.79
Sids 1x Gemmeiza 9	-20.799**	-21.76**	-21.190**	-13.232**	9.97**	-1.717	1.017	-3.11**	-1.077**

L1= Gemmeiza , L2 = Mataana and Comb. = combined data.
* and ** significant and highly significant at 0.05 and 0.01 levels of probability, respectively

Specific combining ability

Estimates of specific combining ability effects (Ŝi) for the twenty eight hybrid combinations at the two different locations and their combined data are presented in Table (5). For number of spikes per plant, the cross Line 1 x Sids 1 showed significant specific combining ability effects at the two different locations and their combined data. For 1000-grain weight, the hybrid combinations Line 4 x Gemmeiza 9 showed highly significant desirable specific combining ability effects at the two different locations and their combined data. For number of kernels per spike, the two crosses Line 1 x Line 4 and Line 2 x Line 5 showed significant desirable specific combining ability effects at the two different locations and their combined data. Concerning grain yield per plant, three hybrid combinations Line 1 x Sids 1, Line 2 x Line 5 and Line 4 x Line 5 exhibited significant specific combining ability effects at the two different locations and their combined data. For protein percentage, five crosses Line 2 x Line 5, Line 2 x Sids 1, Line 3 x Sahel 1, Line 3 x Gemmeiza 9 and Line 4 x Gemmeiza 9 exhibited highly significant specific combining ability effects at the two different locations and their combined data. With regard to carbohydrate percentage, three crosses Line 4 x Sids 1, Sahel 1 x Gemmeiza 9 and Sids 1 x Gemmeiza 9 showed highly significant desirable specific combining ability effects at the two different locations and their combined data.

Simple Sequence Repeats (SSR) finger printing:

The SSR analysis was performed using ten SSR primer pairs on the eight DNA samples representing the eight wheat genotypes. A total of 39 fragments ranging from 95.475 bp to 301.471 bp were obtained by the tested primers with an average 3.9 fragment per locus. SSR primers BARC004 and BARC079 exhibited the highest alleles number (7), followed by primers BARC066 and BARC011 (5 alleles each), while primers BARC012, BARC048 and BARC010 exhibited (3 alleles each). However, primers BARC072, BARC078 and primer BARC003 revealed the lowest number of alleles (2) as shown in Table (6).

The total number of polymorphic bands was 26; which represents a level of polymorphism around 66.67% Table (7). The number of amplified polymorphic markers varied among the different primers. Primers BARC004 and BARC079 showed 7 polymorphic alleles with 100 % polymorphism. Similarly, BARC011 showed 5 polymorphic alleles with 100% polymorphism, while BARC066 generated 5 alleles , four of which were polymorphic giving 80% polymorphism. Primers BARC012, BARC048 and BARC010 generated 3 alleles each with a percentage of polymorphism 33.33 % for both BARC012 and BARC010, while primer BARC048 showed no polymorphic alleles (0%). However, primers BARC072, BARC078 and BARC003 amplified 2 bands each , with 50 % polymorphism for primer BARC078 and no polymorphisms (0%) was revealed by the two primers BARC072 and BARC003. These results are in agreement with Salem (2009) Tahir (2010) and Gorji and Zolnoori (2011).

Although three of the SSR primer pairs BARC048, BARC072 and BARC003 were non polymorphic and could not discriminate between the eight genotypes, the other seven SSR primers BARC004, BARC012, BARC066, BARC078, BARC079, BARC010 and BARC011 together generated unique profiles for the eight genotypes. The SSR primer pairs BARC004 and BARC079 which gave the highest number of polymorphic (7 bands each) generated unique profiles for most of the wheat studied genotypes. Whereby, BARC004 gave 7 different allelic for the eight genotype (Table 7) with Line 3 and Line 4 sharing the same profile, i.e. BARC004 did not differentiate between two Lines. BARC079 gave 7 different allelic profiles with the variety Gemmeiza 9 and Line 4 having the same profile and also Line 3 and Line 5 had are identical profile. Similarly, out of the eight genotypes studied, SSR primers BARC066 and BARC011 generated three different profiles, while BARC012, BARC078 and BARC010 identified two different profiles. All the eight genotypes tested gave identical allelic profiles according two non polymorphic SSR primers used (BARC048, BARC072 and BARC003). These results agree with previous studies by Zeb *et al.* (2009).

Table (5). Estimates of specific combining ability effects for the twenty eight studied crosses under two different locations and their combined data.

Parents		No. of spikes per plant			1000-grain weight (g)			No. of kernels per spike		
		L1	L2	Comb.	L1	L2	Comb.	L1	L2	Comb.
Line 1x Line 2		-0.93	-1.78*	-1.35**	1.42	0.77	1.09	5.418**	3.43	4.43**
Line 1x Line 3		0.76	-3.85**	-1.55**	0.26	3.46	1.86	-1.764	0.73	-0.52
Line 1x Line 4		1.27*	-0.69	0.29	2.77	-0.85	0.96	7.483**	5.48**	6.48**
Line 1x Line 5		-0.91	-2.56**	-1.74**	2.03	-0.17	0.93	-5.804**	-4.07*	-4.94**
Line 1x Sahel 1		0.75	1.97**	1.36**	1.68	1.44	1.56	-2.717	1.50	-0.61
Line 1x Sids 1		1.37*	1.88**	1.62**	1.49	-5.27**	-1.89	0.356	-0.80	-0.22
Line 1x Gemmeiza 9		0.31	2.02**	1.17**	-1.67	8.15**	3.24**	-0.202	1.92	0.86
Line 2x Line 3		-0.13	-0.93	-0.53	-4.03**	-1.11	-2.57*	-1.029	-3.74*	-2.38
Line 2x Line 4		0.98	-0.11	0.44	3.71*	3.26	3.49**	-2.049	-2.51	-2.28
Line 2x Line 5		0.74	1.93**	1.33**	3.50*	-0.64	1.43	3.864*	5.13**	4.50**
Line 2x Sahel 1		0.29	2.44**	1.36**	4.06**	-3.33	0.36	-0.716	5.87**	2.58
Line 2x Sids 1		0.14	-0.44	-0.15	0.24	-1.55	-0.65	-0.976	-3.87*	-2.42
Line 2x Gemmeiza 9		-1.31*	0.60	-0.36	-9.16**	-3.37	-6.26**	-7.484**	-7.45**	-7.47**
Line 3x Line 4		-0.26	1.95**	0.84	-2.28	-4.64*	-3.46**	4.103*	-1.29	1.41
Line 3x Line 5		0.02	1.72*	0.87	1.06	1.30	1.18	-1.984	1.43	-0.28
Line 3x Sahel 1		0.88	-0.25	0.31	1.41	-3.09	-0.84	-3.164	-2.04	-2.60*
Line 3x Sids 1		-0.404	1.39	0.49	1.50	-2.15	-0.33	3.376	-3.91*	-0.27
Line 3x Gemmeiza 9		-0.62	1.19	0.28	1.99	1.63	1.81	-5.249**	2.64	-1.30
Line 4x Line 5		0.34	2.35**	1.34**	2.50	-0.68	0.91	-0.404	4.32*	1.96
Line 4x Sahel 1		-2.61**	0.24	-1.18**	-0.90	5.99**	2.55**	1.816	0.02	0.92
Line 4x Sids 1		-2.59**	-1.25	-1.92**	-4.48**	7.25**	1.38	5.156**	3.58	4.37**
Line 4x Gemmeiza 9		0.23	0.75	0.49	5.56**	5.98**	5.77**	-1.336	2.80	0.73
Line 5x Sahel 1		-0.19	0.15	-0.02	-1.59	0.72	-0.44	4.729*	1.20	2.96
Line 5x Sids 1		1.10*	-0.08	0.51	-2.47	6.87**	2.20	3.403	-0.57	1.42
Line 5x Gemmeiza 9		0.58	-2.01**	-0.72	5.31**	-3.16	1.07	6.244**	2.11	4.18**
Sahel 1x Sids 1		0.99	-2.59**	-0.80	3.82*	-4.47**	-0.33	3.356	2.20	2.78*
Sahel 1 x Gemmeiza 9		-0.24	-4.72**	-2.48**	5.85**	-5.299**	0.28	-2.136	-11.06**	-6.60**
Sids 1x Gemmeiza 9		-0.014	-0.75	-0.38	-2.96	-3.205	-3.08	2.738	6.51**	4.62**
LSD (sij)	5%	1.07	1.41	0.87	2.97	3.66	2.31	3.829	3.63	2.59
	1%	1.43	1.87	1.14	3.95	4.87	3.03	5.093	4.83	3.39
LSD (sij-sik)	5%	1.59	2.09	1.28	4.39	5.41	3.42	5.666	5.37	3.83
	1%	2.11	2.77	1.68	5.84	7.20	4.48	7.535	7.15	5.02
LSD (sij-ski)	5%	1.50	1.97	0.43	4.14	5.10	1.14	5.34	5.07	1.28
	1%	1.99	2.61	0.56	5.51	6.79	1.49	7.10	6.74	1.67

L1= Gemmeiza , L2 = Mataana and Comb. = combined data.

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

Table (5) cont.

Parents		Grain yield/plant (g)			Protein percentage			Carbohydrate percentage		
		L1	L2	Comb.	L1	L2	Comb.	L1	L2	Comb.
Line 1x Line 2		-1.18	-3.78**	-2.48**	-0.42**	-0.67**	-0.55**	0.41	0.42*	0.41**
Line 1x Line 3		1.18	-6.45**	-2.63**	0.23**	-1.17**	-0.47**	0.13	4.01**	2.07**
Line 1x Line 4		2.13*	-0.75	0.69	-1.00**	-1.75**	-1.38**	0.53*	0.30	0.42**
Line 1x Line 5		-1.94*	-4.80**	-3.37**	0.85**	-0.71**	0.07	-0.43	1.79**	0.68**
Line 1x Sahel 1		1.04	4.47**	2.76**	-0.15	0.05	-0.05	-0.44	-1.42**	-0.93**
Line 1x Sids 1		2.84**	4.68**	3.76**	-0.29**	1.07**	0.39**	-0.29	-2.27**	-1.28**
Line 1x Gemmeiza 9		0.21	4.56**	2.39**	-0.27**	0.59**	0.16*	0.62**	-0.74**	-0.06
Line 2x Line 3		-0.72	-1.09	-0.90	0.46**	-1.50**	-0.52**	-0.72**	0.37*	-0.17
Line 2x Line 4		2.37*	0.37	1.37*	0.04	-1.35**	-0.66**	-0.99**	0.09	-0.45**
Line 2x Line 5		1.97*	4.15**	3.06**	0.29**	2.70**	1.50**	-0.55*	-1.62**	-1.08**
Line 2x Sahel 1		1.12	3.64**	2.38**	-0.57**	-1.53**	-1.05**	-0.23	2.00**	0.89**
Line 2x Sids 1		-1.08	-1.31	-1.19	3.05**	0.91**	1.98**	-2.91**	-1.54**	-2.23**
Line 2x Gemmeiza 9		-2.41**	0.60	-0.90	1.20**	-0.91**	0.14*	-0.40	-0.01	-0.21
Line 3x Line 4		-0.54	2.34**	0.90	-0.62**	-0.82**	-0.72**	0.27	-0.61**	-0.17
Line 3x Line 5		-1.37	4.26**	1.45*	-0.31**	0.78**	0.24*	0.14	-0.89**	-0.38**
Line 3x Sahel 1		3.75**	-1.13	1.31*	0.87**	0.55**	0.71**	-0.24	-2.03**	-1.14**
Line 3x Sids 1		-2.27*	3.33**	0.53	-0.99**	-0.95**	-0.97**	0.71**	-0.28	0.21
Line 3x Gemmeiza 9		-0.98	-0.07	-0.53	0.84**	1.94**	1.39**	-1.22**	-3.31**	-2.27**
Line 4x Line 5		1.98*	5.63**	3.81**	-1.40**	-0.08	-0.74**	0.74**	1.06**	0.90**
Line 4x Sahel 1		-3.17**	-2.14*	-2.66**	-0.30**	0.47**	0.09	-1.04**	-0.38*	-0.71**
Line 4x Sids 1		-5.59**	-2.84**	-4.22**	-0.88**	0.50**	-0.19**	1.34**	0.78**	1.06**
Line 4x Gemmeiza 9		0.60	0.71	0.66	0.24**	1.66**	0.95**	-0.98**	-2.86**	-1.92**
Line 5x Sahel 1		-1.40	-0.37	-0.88	0.10	-0.41**	-0.16*	0.83**	-0.93**	-0.05
Line 5x Sids 1		1.78	-0.27	0.76	0.14	-0.56**	-0.21**	-0.75**	0.40*	-0.18
Line 5x Gemmeiza 9		1.34	-3.74**	-1.20	-0.32**	-4.52**	-2.42**	0.19	-0.11	0.04
Sahel 1x Sids 1		0.99	-4.72**	-1.86**	-0.52**	-0.80**	-0.66**	-1.00**	0.39*	-0.31*
Sahel 1 x Gemmeiza 9		-2.00*	-5.02**	-3.51**	-0.93**	-0.70**	-0.82**	0.91**	2.32**	1.61**
Sids 1x Gemmeiza 9		-2.35*	-2.30**	-2.32**	-0.91**	1.61**	0.35**	2.49**	0.24	1.36**
LSD (sij)	5%	1.79	1.73	1.22	0.17	0.20	0.13	0.44	0.36	0.28
	1%	2.38	2.30	1.60	0.22	0.27	0.17	0.59	0.47	0.37
LSD (sij-sik)	5%	2.65	2.56	1.80	0.24	0.30	0.19	0.66	0.53	0.41
	1%	3.52	3.41	2.37	0.33	0.40	0.25	0.87	0.70	0.54
LSD (sij-ski)	5%	2.50	2.41	0.60	0.23	0.28	0.06	0.62	0.50	0.14
	1%	3.32	3.21	0.79	0.31	0.38	0.08	0.82	0.66	0.18

L1= Gemmeiza , L2 = Mataana and Comb. = combined data.
* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table (6): Description of 10 wheat microsatellite, their losation, size range of alleles and number of alleles

No	Primer pair ID[a]	Chromosomal location	Fragment size		Number of alleles
			Min Allele	Max Allele	
1	BARC004	5AL	153.507	192.166	7
2	BARC012	3AS	118.531	145.343	3
3	BARC048	*4DS,4BS* 1AS,1AL	175.066	195.189	3
4	BARC066	1DL	95.475	124.195	5
5	BARC072	7BS	171.609	222.307	2
6	BARC078	4A	199.732	204.63	2
7	BARC079	6BL	155.364	189.491	7
8	BARC003	*4AL*	195.424	263.551	2
9	BARC010	2B,5A	268.085	296.381	3
10	BARC011	2BL	263.956	301.471	5
Total					39
Mean					3.9

Table (7): Total number of SSR amplified fragments, polymorphic fragments and polymorphic % in the eight wheat genotypes using the SSR primers.

AF SSR primers	Amplified fragments		
	Total amplified fragments	Polymorphic fragments	Percentage of polymorphism (%)
BARC004	7	7	100
BARC012	3	1	33.33
BARC048	3	0	0
BARC066	5	4	80
BARC072	2	0	0
BARC078	2	1	50
BARC079	7	7	100
BARC003	2	0	0
BARC010	3	1	33.33
BARC011	5	5	100
Total	39	26	66.67

Estimate of genetic relationships among eight genotypes based on SSR analysis:

SSR data analysis using the similarity matrix and the genetic distance estimates are presented in Table (8). It appeared that similarity index ranged from 62% to 93% . The most distant cultivar and landraces were Sahel 1 and Line 1 with lowest similarity index (0.62) between them. The most related genotypes were Line 4 and Sids 1 with highest similarity index (0.93) followed by Gemmeza9 and line4 (0.91).

To assess the genetic diversity of wheat genotypes, marker data were converted into binary matrix, which in turn allowed to calculate the genetic similarity index. A dendrogram was created with the use of these data and presented in Fig. (1). All genotypes were divided into two clusters , the first group contained Sahel 1 only, while, the second group contained the rest of studied genotypes (Line 1 , Line 2, Line 3, Line 4, Line 5, Gemmeiza 9 and Sids 1) . The similarity coefficient between Sahel 1 and the rest of the genotypes was less than 0.74, while the similarity among genotypes of the second group was more than 0.74. Bands of molecular weight 124.195, 120.422 bp with primer BARC066, 199.732 bp with primer BARC078, and 268.085bp with primer BARC010 are valuable to distinguish Sahel 1 from the rest of studied genotype. The second group was divided into two subgroups, the first subgroup separated Line 5 from the second subgroup which contained the six other genotypes (Line 1 , Line 2, Line 3, Line 4, Gemmeiza 9 and Sids 1). Bands of molecular weight 301.471, 276.471 and 263.956 bp of primer BARC011 are valuable to distinguish Line 5 from the rest of group 2 genotypes. It could be concluded from the dendrogram that the highest genetic diversity among the different gremplasm was exhibited by Sahel 1 followed by Line 5. While, Line 4 and Sids 1 are closely related to each other (0. 93) than the rest of the studied genotypes. These results are in agreement with Zeb *et al.* (2009) and Gorji and Zolnoori (2011).

Coefficient among parental genetic distance (GD), heterosis over better parent and specific combing ability for yield, yield components and chemical traits:

Molecular markers display an important role and are considered as a complementary tool with conventional breeding for wheat improvement. The first step to design breeding program for useful trait is choosing parental genotypes based on its genetic dissimilarity. An amplification products which were detected by the ten microsatellite markers were used to study the relationship of genetic diversity measured using SSR markers with the amount of heterosis over better parent and specific combining ability for yield and its component and chemical traits which computed for studied 28 hybrids combination at Gemmeiza location (L1) and Mataana location (L2) are given in Table (9).

Table (8): Genetic similarity estimates for eight genotypes based on 10 SSRs marker analysis

Parents	Sahel 1	Gemmeiza 9	Sids 1	Line 1	Line 2	Line 3	Line 4	Line 5
Sahel 1	1							
Gemmeiza 9	0.70	1						
Sids 1	0.64	0.84	1					
Line 1	0.62	0.87	0.81	1				
Line 2	0.65	0.85	0.88	0.86	1			
Line 3	0.73	0.86	0.80	0.83	0.81	1		
Line 4	0.65	0.91	0.93	0.87	0.85	0.86	1	
Line 5	0.67	0.75	0.77	0.75	0.74	0.83	0.74	1

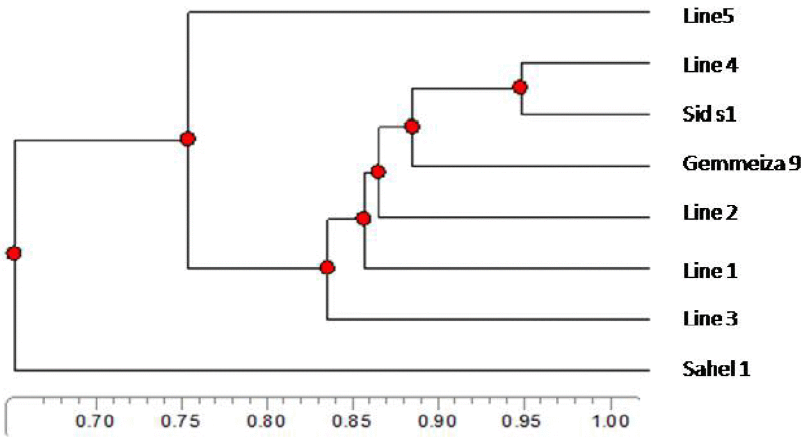

Fig. (1): Cluster analysis of genetic distance for eight genotypes.

Table (9): Correlation coefficient between genetic distance (GD) with studied materials with heterosis over better parent and specific combining ability (SCA) in yield, yield components and chemical traits.

Traits	Genetic distance (GD)			
	Heterosis over better parent		specific combining ability (SCA)	
	L1	L2	L1	L2
No. of spikes per plant	-0.031	-0.118	0.132	-0.018
1000- grain weight	0.209	-0.418*	0.310	-0.275
No. of kernels per spike	-0.144	-0.091	-0.006	-0.021
Grain yield/plant	0.128	-0.058	0.206	0.016
Protein percentage	-0.177	-0.173	-0.173	-0.189
Carbohydrate percentage	0.121	0.265	-0.061	0.167

The estimate value of correlation coefficient between genetic distance (GD) and heterosis over better parent showed that there is a negative significant correlation coefficient for 1000-grain weight and heterosis over better parent..

The correlation coefficient between GD and specific combining ability for all traits at L1 showed very low positive (r = 0.132, 0.206 and 0.310), for number of spikes per plant, grain yield per plant and 1000 -grain weight, respectively. There were negative correlation between GD and number of kernels per spike, Protein and Carbohydrate percentage (r=-0.006, -0.173 and-0.061), respectively. Also, the correlation coefficient among GD and specific combining ability for all traits under L2 showed very low positive value for grain yield per plant and Carbohydrate percentage (0.016 and 0.167), respectively. While, there were very low negative correlation among GD and number of spikes per plant, 1000 - grain weight, number of kernels per spike and protein percentage.

According to correlation analysis between genetic distances coefficient, heterosis over better parent and specific combining ability at L1 and L2 showed low correlation among most examined traits.

Sud *et al.* (2010) pointed out that the lack of association between heterosis and genetic dissimilarities for the methods that measure of measuring genetic diversity may be inherently different for different indices.

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توصيف وتقييم بعض التراكيب الوراثية في قمح الخبز باستخدام معلمات الميكروستاليت تحت ظروف حرارية متباينة

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الملخص العربى

أجريت هذه الدراسة خلال موسمين متتالين ٢٠٠٨/ ٢٠٠٩ و ٢٠٠٩/٢٠١٠ حيث استخدم لهذه الدراسة ثمانية تراكيب وراثية من قمح الخبز متباعدة المصدر منها خمسة سلالات بلدية قديمة وثلاث أصناف محلية, في موسم ٢٠٠٨/٢٠٠٩ تم التهجين بين هذه التراكيب الوراثية باستخدام طريقة التهجين التبادلي في اتجاه واحد في موسم ٢٠٠٩ /٢٠١٠ تم تقييم الآباء والهجن الناتجة منها في تجربتين مستقلتين ذات قطاعات كاملة العشوائية في ثلاث مكررات بكل من محطتي الجميزة (حرارة معتدلة) والمطاعنة (حرارة مرتفعة) . ولقد أجري هذا البحث بهدف :–

١–تقدير قوة الهجين و القدرة الخاصة على الائتلاف .

٢– استخدام المعلمات الجزئية الميكروستاليت لدراسة التنوع الوراثي بين التراكيب الوراثية للقمح المستخدمة في الدارسة.

٣–تقدير العلاقة بين قوة الهجين والقدرة الخاصة علي الائتلاف والتباعد الوراثي باستخدام الميكروستاليت.

وتم ذلك بتقدير عدد السنابل فى النبات, وزن الألف حبة (جم) , عدد الحبوب في السنبلة , محصول النبات الفردي من الحبوب (جم) , نسبة البروتين والكربوهيدرات. وفيما يلي ملخص لأهم النتائج المتحصل عليها:

١– كان التباين الراجع إلي المواقع معنويا لجميع الصفات المدروسة فيما عدا وزن الألف حبة و نسبة الكربوهيدرات .

٢– كانت قيم التباين الراجع إلى متوسط قوة الهجين عالية المعنوية وذلك لصفات نسبة البروتين والكربوهيدرات في موقعي الجميزة والمطاعنة والتحليل المشترك لهما و وزن الألف حبة والتحليل المشترك بينهما.

٣– أظهر الهجين سلالة ٤ × سلالة ٥ أهميته العملية في برامج تربية القمح وذلك بسبب تفوقه فى محصول الحبوب بالنبات واثنين من صفات مكونات المحصول كما أن قوة الهجين في صفة محصول الحبوب ترجع إلى قوة الهجين فى عدد السنابل في النبات ووزن الألف حبة.

٤– أظهرت الهجن : (سلالة ١ × سدس ١) ,(سلالة ٢ × سلالة ٥), (سلالة ٤ × سلالة ٥) قدرة خاصة على التآلف عالية المعنوية وذلك لصفة محصول النبات من الحبوب في موقعي الجميزة والمطاعنة والتحليل المشترك لهما.

٥– تم إجراء التحليل باستخدام عشرة بادئات SSR على عينات من الحمض النووي DNA تمثل ثمانية تراكيب وراثية من القمح. وقد تم الحصول على ٣٩ أليل التي تتراوح بين ٩٥.٤٧٥ إلى ٣٠١.٤٧١ زوج من القواعد .

٦– أظهر تحليل بيانات الـ SSR باستخدام مصفوفة تشابه وتقديرات المسافة الوراثية أو التباعد الوراثى أن معامل التشابه يتراوح بين ٦٢٪ إلى ٩٣٪ وكانت الأصناف والسلالات الأكثر تباعدا هي ساحل١ والسلاله١ بأقل معامل تشابه ٦٢%, بينما التراكيب الوراثية الأكثر تقاربا وراثيا كانتا السلاله٤ و سدس١ مع أعلى معامل تشابه ٩٣%.