RESULTS

Chapter I

1.Evaluation of the parental genotypes (Experiment I)

Separate analysis of variance was carried out for yield and yield components in each season under recommended conditions at Nubaria, Table (9). The analysis of variance indicated highly significant variation among genotypes which revealed differences for all studied characters in this experiment. Test of homogeneity of the error variance was insignificant. Thus, the hypothesis of homogenous error variances over the two seasons cannot be rejected.

Table (10) represents the mean and combined data over the two seasons of 1999/2000 and 2000/2001 of the ten genotypes for yield and its components. Data showed that the genotypes Sakha 93 and Gemmiza 7 were the most productive ones while, Line 8 resulted in poor yielding. The other genotypes showed different behavior and revealed variability between them under recommended conditions.

The average number of spikes per m^2 ranged from 202 for Line 8 which produced the smallest number of spikes per m^2 to 426 for Sakha 93 which showed the highest number of spikes per m^2. This range could revealed a high variability of spikes number among the ten genotypes.

Number of kernels per spike was varied from 32 for Line 6 to 47 for Gemmiza 7. However, all genotypes except Gemmiza 7 and

Line 6 are varied for number of kernels per spike under recommended conditions. Six were varied for number of kernels per spike under recommended conditions.

The mean of 1000-kernel weight varied from 55 gm for Gemmiza 7 to 41 gm for Line 2, Sakha 93 produced heavy kernels almost like Sids 6.

For leaf rust reaction, the monogenic lines (Line 1 and Line 2) showed a resistant type of reaction to leaf rust, while other genotypes revealed a susceptible type of reaction to leaf rust except Line 6 and Line 8 which showed moderate resistance and Sakha 61 showed a moderate susceptibility, Table (10).

Table (9). Mean square values of analysis of variance among parental genotypes for yield and its components (Mean of two years).

S.O.V.	D.F.	Mean.Square.				
		Grain Yield	Biological Yield	No. of spike/plant	No of kernels /spike	1000-kernel weight
Years	1	0.071	0.538	32109.06 **	0.816	26.93 *
Rep	2	0.007	0.036	4155.01 *	4.86	1.15
Genotypes	9	1.262 **	7.504 **	34558.3 **	117.42 **	124.02 **
Genotypes x Years	9	0.167 **	1.660 **	15064.4 **	13.85	20.94 **
Error	36	0.017	0.214	1223.15	10.129	4.808

*, ** significant at P< 0.05 and 0.01, respectively.

Table (10). Performance of parental genotypes means for yield and its components (Means of two years).

Genotype	Grain Yield Ardab/Fed.	Biological Yield Ton / Fed.	No. of Spike /m^2	No of kernels/ spike	1000-kernel weight	Leaf Rust Reaction
1- Gemmiza7	19.3 b	9.09 b	338 c	47 a	55 a	S
2- Sakha 61	13.1 d	6.75 c	327 cd	36 cd	47 cd	MS
3- Sakha 69	17.7 bc	8.45 b	381 b	40 bc	50 bc	S
4- Sids 6	14.9 d	6.71 c	264 ef	36 cd	52 b	S
5- Sakha 8	16.8 c	6.93 c	368 bc	42 b	47 cd	S
6- Sakha 93	21.4 a	9.55 a	426 a	43 b	52 b	S
7- Line 1	13.0 d	6.33 c	301 de	36 cd	42 e	R
8- Line 2	11.2 e	5.53 c	311 d	36 cd	41 e	R
9- Line 6	10.2 ef	5.40 d	244 f	32 e	47 d	MR
10- Line 8	9.3 f	5.12 d	202 g	38 cd	46 d	MR

Means with the same letter are not significant.& Ardab= 150 kg

1.1 Correlation Coefficient

Table (11) presents the phenotypic correlation between the studied traits under recommended conditions. With respect to the grain yield, it was noticed that the phenotypic correlation was positive and highly significant between this trait and each one of biological yield, number of spikes per m^2, number of kernels per spike and 1000-kernel weight.

The phenotypic correlation between biological yield and each one of grain yield, i.e., number of spikes per m^2, number of kernels per spike and 1000-kernel weight was positive and highly significant, Table (11). Highly significant positive correlation was noticed between number of spikes per m^2 and grain yield, biological yield and number of kernels per spike, While insignificant positive phenotypic correlation was detected between this trait and 1000-kernel weight.

The results indicated that the phenotypic correlation between number of kernels per spike and each one of grain yield, biological yield, number of spikes per m^2 and 1000-kernel weight was positive and highly significant.

Regarding to 1000-kernel weight, the phenotypic correlation was positive and highly significant between this trait and each of grain yield, biological yield and number of kernels per spike, while the correlation was insignificantly positive with number of spikes per m^2. Table (11).

Table (11). Phenotypic correlation between yield and its components in parental genotypes.

Trait	Grain Yield	Biological Yield	No. of spikes/plant	No. of kernels /plant	1000-kernel weight
Grain Yield	1.000	0.91**	0.53**	0.63**	0.46**
Biological Yield		1.000	0.52**	0.58**	0.46**
No. of spikes/plant			1.000	0.35**	0.17
No. of kernels /plant				1.000	0.39**
1000-kernel weight					1.000

*, ** significant at P< 0.05 and 0.01, respectively.

1.2 Path Coefficient analysis and Coefficient of Determination

Partitioning of simple correlation coefficient between grain yield and its components, i.e., number of spikes per m^2, number of kernels per spike, and 1000-kernel weight are presented in Table (12), Number of kernels per spike had the largest direct effect (0.38) followed by number of spikes per m^2 (0.34) and 1000-kernel weight (0.29), respectively.

The coefficient of determination were calculated for the direct and indirect effects of the three yield factors studied and transformed into percentage in order to evaluate these factors for their importance as sources of variation in grain yield. The components in percent for grain yield variation are presented in Table (13). The results indicated that the most important sources of variation in grain yield are the direct effect of number of kernels per spike followed by direct effect of number of spikes per m^2 and the direct effect of 1000-kernel weight. These three sources accounted for approximately 34.46 of grain yield variation. Indirect effects of yield components in grain yield revealed that the interaction between number of kernels per spike and number of spikes per m^2 was the first indirect effect followed by interaction between number of kernels per spike and 1000-kernel weight, while the interaction between number of spikes per m^2 and 1000-kernel weight was the last indirect effect in grain yield. These three sources accounted approximately 21.03 of indirect effects for grain yield variation.

Table (12). Path coefficient analysis for yield and its components in parents.

Traits	No. of spikes/ m^2	No. of kernels /spike	1000-kernel weight	Correlation
No. of spikes/m^2	0.34	0.133	0.058	0.53
No. of kernels /spike	0.133	0.38	0.115	0.63
1000-kernel weight	0.058	0.115	0.29	0.46

Table (13). Coefficient of determination for yield component and its contribution to grain yield in parents.

Trait	Coefficient of Determination	Contribution
No. of spikes/plant	0.116	11.6
No. of kernels /spike	0.144	14.4
1000-kernel weight	0.084	8.46
No. of spikes/plant X No. of kernels /spike	0.090	9.04
No. of spikes/plant X 1000-kernel weight	0.033	3.35
No. of Kernels/spike X 1000-kernel weight	0.086	8.64
Residual	0.446	44.6
Total	1	100

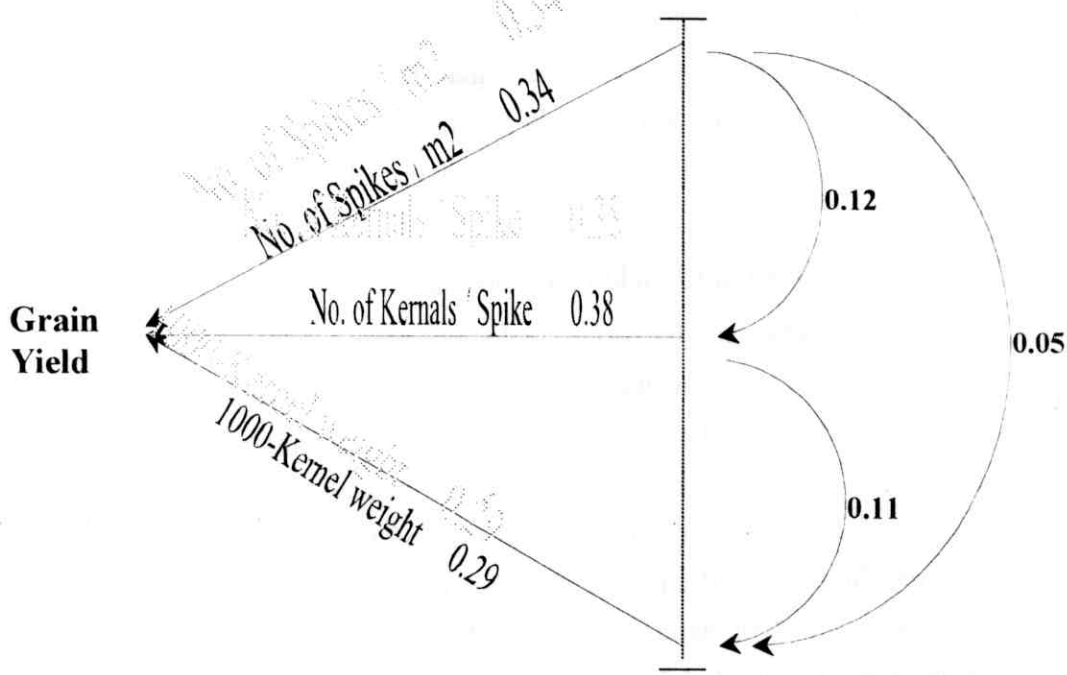


Figure (1). Sequential path analysis for grain yield and its components in parents generation

2. Estimation of Heterosis, Potence Ratio and Combining Ability (Experiment II)

2.1 Heterosis

The analysis of variance of diallel experiment indicated highly significant differences due to genotypes under recommended conditions for yield and its components, Table (14). Differences in the level of heterosis for all traits were detected among the 15 hybrids.

2.1.1 Yield and yield components:

The heterosis for grain yield per plant is presented in Table (15). The results indicated that positive heterosis was exhibited for 13 and 4 crosses, out of 15 crosses, over mid-parents (MP) and better parent (BP), respectively. The Eight crosses showed significant positive heterosis over mid-parents. Out of these eight hybrids, 6 F_1 showed highly significant positive heterosis and two crosses showed significant positive heterosis over MP. With regard to heterosis over better parent, out of 4 F_1 showed positive heterosis, only one hybrid, *i.e.* cross 15 (Line 1 x Line 2) showed highly significant positive heterosis and one cross, *i.e.* cross 2 (Gemmiza 7 x Sakha 93) showed significant positive heterosis. The two crosses, *i.e.* # 2 and 15 (Gemmiza 7 x Sakha 93 and Line 1 x Line 2) exhibited significant positive heterosis over both mid and better parent, Table (15).

With respect to heterosis for number of spikes per plant, Table (16), 9 F_1's showed positive heterosis over mid-parents, while 6 F_1's showed positive heterosis over better parent. From these nine crosses, 6 hybrids were highly significant positive heterosis over MP, while 2 crosses, *i.e.* # 3 and 8 (Gemmiza 7 x Sakha 8 and Sakha 69 x Line 1) showed highly significant positive heterosis and two crosses,

i.e. # 1 and 6 (Gemmiza 7 x Sakha 69 and Sakha 69 x Sakha 93) had significant positive heterosis over better-parent. Three crosses, i.e. # 1, 6 and 8 showed significant or highly significant positive heterosis over both mid and better parent.

Heterosis over MP for number of kernels per spike was generally positive, Table (17). Six crosses showed highly significant positive heterosis over mid-parent. The two crosses, *i.e.* # 13 and 15 (Sakha 8 x Line 1 and Line 1 x Line 2) were highly significany positive heterosis for both mid and better parent. Only one cross # 3 (Gemmiza 7 x Sakha 8) showed significant positive heterosis over better parent.

Heterosis for 1000-kernel weight as shown in Table (18) was positive over mid-parents except 4 crosses that showed negative heterosis. Out of these, 11 hybrid showed positive heterosis. However, 8 F_1's were highly significant positive heterosis over MP and two crosses had significant positive heterosis. Six crosses showed significant and highly significant over both mid and better parent, *i.e.* crosses # 5, 6, 10, 11, 12 and 14.

2.2 Type of Gene Action

As shown in Table (15), potence ratio was exceeding unity for some crosses, *i.e.* cross # 2, 3, 10 and 15, while it was less than unity for the other crosses, in case of grain yield per plant. Out of 15 hybrids for number of spikes per plant, seven hybrids were exceeding unity, *i.e.* cross # 1, 2, 3, 4, 6, 8 and 10 and the rest of crosses were less than unity, Table (16).

With regard to potence ratio for number of kernels per spike, Table (17), almost half of the fifteen hybrids were less than unity and

the other half crosses were exceeding unity. In case of 1000-kernel weight, Table (18), only three crosses were less than unity, *i.e.* cross # 1, 9 and 15 for potence ratio and 12 crosses were exceeding unity

Table (14). Mean square values of analysis of variance among genotypes (parents and F_1) for yield and yield components in diallel cross.

S.O.V	D.F	Traits			
		Grain Yield / Plant	No. of Spikes / Plant	No. of Kernels / Spike	1000-Kernel Weight
Blocks	2	51.52**	4.78*	34.47	26.21
Genotypes	20	42.69**	12.44**	110.41**	59.63**
GCA	5	44.50**	13.19**	119.17**	36.90
SCA	15	42.08**	12.19**	107.49**	67.20**
Error	40	2.81	0.46	4.18	6.42
GCA / SCA		1.05	1.08	1.11	0.55

*, ** significant at P< 0.05 and 0.01, respectively

Table (15). Heterosis and potence ratio for grain yield in F_1 by mid-parents (MP) and better parent (BP).

No.	Cross	Means			Heterosis	Potence	Heterosis
		MP	BP	F1	MP	Ratio	BP
1	(1 x 2)	19.75	24.7	17.4	-11.8 *	-0.47	-29.5 **
2	(1 x 3)	24.00	24.7	28.3	17.9 **	6.14	14.5 *
3	(1 x 4)	25.25	25.8	27.6	9.03 *	2.14	6.9
4	(1 x 5)	17.70	24.7	22.5	27.1 **	0.68	-8.9
5	(1 x 6)	16.55	24.7	23.0	38.9 **	0.78	-6.88
6	(2 x 3)	19.05	23.3	19.9	4.46	0.20	-14.5 **
7	(2 x 4)	20.30	25.8	25.3	24.6 **	0.90	-1.93
8	(2 x 5)	12.75	14.8	13.3	4.31	0.30	-10.1
9	(2 x 6)	11.60	14.8	12.4	6.8	0.20	-16.2 *
10	(3 x 4)	24.55	25.8	27.6	12.4 **	2.44	6.9
11	(3 x 5)	17.00	23.3	19.0	11.7 *	0.30	-18.4 **
12	(3 x 6)	15.85	23.3	15.1	-4.4	-0.10	-35.2 **
13	(4 x 5)	18.25	25.8	20.1	10.1	0.24	-22.0 **
14	(4 x 6)	17.10	25.8	18.0	5.2	0.10	-30.2 **
15	(5 x 6)	9.55	10.7	15.5	62.3 **	5.17	44.8 **
LSD 0.05					1.95		2.39
LSD 0.01					2.6		3.20

*, ** are significant and highly significant at 5% and 1%, respectively.

Table (16). Heterosis and Potence ratio for No. of spikes per plant in F_1 by Mid-Parents (MP) and Better-Parent (BP).

Cross No.	Mean			Heterosis	Potence	Heterosis
	MP	BP	F1	MP	Ration	BP
1 (1 x 2)	8.5	9.0	9.9	16.4 **	2.8	10.0 *
2 (1 x 3)	10.0	11.0	11.6	16.0 **	1.6	5.4
3 (1 x 4)	10.5	12.0	7.8	-25.7 **	-1.8	-35.0 **
4 (1 x 5)	8.0	9.0	9.7	21.2 **	1.7	7.7
5 (1 x 6)	7.0	9.0	8.5	21.4 **	0.75	-5.55
6 (2 x 3)	9.5	11.0	12.0	26.3 **	1.6	9.09 *
7 (2 x 4)	10.0	12.0	8.5	-15.0 **	-.75	-29.2 **
8 (2 x 5)	7.5	8.0	9.3	24.0 **	3.6	16.2 **
9 (2 x 6)	6.5	8.0	7.0	7.6	0.33	-12.5 *
10 (3 x 4)	11.5	12.0	8.0	-30.4 **	-7.0	-33.3 **
11 (3 x 5)	9.0	11.0	7.7	-14.4 **	-0.65	-30.0 **
12 (3 x 6)	8.0	11.0	7.3	-8.7	-0.23	-33.6 **
13 (4 x 5)	9.5	12.0	9.9	4.2	0.16	-17.5 **
14 (4 x 6)	8.5	12.0	8.0	-5.8	-0.14	-33.3 **
15 (5 x 6)	6.0	7.0	6.77	11.6	0.77	-4.28
LSD 0.05				0.79		0.96
LSD 0.01				1.05		1.29

*, ** are significant and highly significant at 5% and 1%, respectively.

Table (17). Heterosis and potence Ratio for No of kernels per spike in F_1 by Mid-Parents (MP) and Better-Parent (BP).

Cross No.	Mean			Heterosis	Potence	Heterosis
	MP	BP	F1	MP	Ratio	BP
1 (1 x 2)	43.5	47.0	44.8	2.9	0.37	-4.6
2 (1 x 3)	45.0	47.0	48.2	7.1 **	1.6	2.5
3 (1 x 4)	45.0	47.0	50.2	11.5 **	2.6	6.8 *
4 (1 x 5)	41.0	47.0	42.7	4.2	0.28	-9.1 **
5 (1 x 6)	42.0	47.0	38.3	-8.8 **	-0.74	-18.5 **
6 (2 x 3)	41.5	43.0	38.8	-6.5 *	-1.8	-9.7 **
7 (2 x 4)	41.5	43.0	43.7	5.3	1.4	1.6
8 (2 x 5)	37.5	40.0	35.7	-4.8	-0.72	-10.7 **
9 (2 x 6)	38.5	40.0	37.7	-2.1	-0.53	-5.7
10 (3 x 4)	43.0	43.0	44.9	4.4	3.8	4.4
11 (3 x 5)	39.0	43.0	42.5	8.9 **	0.87	-1.2
12 (3 x 6)	40.0	43.0	43.8	9.5 **	1.26	1.8
13 (4 x 5)	39.0	43.0	48.5	24.3 **	2.7	12.7 **
14 (4 x 6)	40.0	43.0	39.4	-1.5	-0.24	-8.3 *
15 (5 x 6)	36.0	37.0	41.2	14.4 **	5.2	11.3 **
LSD 0.05				2.38		2.9
LSD 0.01				3.18		3.9

*, ** are significant and highly significant at 5% and 1%, respectively.

Table (18). Heterosis and Potence Ratio for 1000-kernel weight in F_1 by Mid-Parents (MP) and Better-Parent (BP).

Cross No.	Mean			Heterosis	Potence Ratio	Heterosis
	MP	BP	F1	MP		BP
1 (1 x 2)	53.1	56.0	52.0	-2.1	-0.37	-7.1 *
2 (1 x 3)	51.6	56.0	57.7	11.8 **	1.4	3.0
3 (1 x 4)	54.2	56.0	56.6	4.4	1.3	1.1
4 (1 x 5)	51.8	56.0	56.8	9.6 **	1.2	1.4
5 (1 x 6)	47.5	56.0	59.5	25.3 **	1.4	6.3 *
6 (2 x 3)	48.7	50.2	61.8	26.8 **	9.03	23.1 **
7 (2 x 4)	51.3	52.5	54.3	5.8 *	2.6	3.4
8 (2 x 5)	48.9	50.2	46.2	-5.5	-2.2	-7.9 *
9 (2 x 6)	44.6	50.2	43.9	-1.5	-0.12	-12.5 **
10 (3 x 4)	49.9	52.5	65.4	31.0 **	5.9	24.5 **
11 (3 x 5)	47.5	47.7	58.0	22.1 **	52.5	21.5 **
12 (3 x 6)	43.2	47.3	59.6	37.9 **	4.0	26.0 **
13 (4 x 5)	50.1	52.5	53.9	7.5 *	1.58	2.6
14 (4 x 6)	45.8	52.5	56.0	22.2 **	1.5	6.6 *
15 (5 x 6)	43.4	47.7	42.9	-1.1	-0.11	-10.0 *
LSD 0.05				2.95		3.6
LSD 0.01				3.94		4.8

*, ** are significant and highly significant at 5% and 1%, respectively.

2.3 Combining ability

Analysis of variance for combining ability mean square for all traits are presented in Table (14). The analysis indicates that general

combining ability (GCA) mean square valueswere highly significant for yield and yield components, except 1000-kernel weight. Moreover, specific combining ability (SCA) mean square values were highly significant for yield and yield components, Table (14).

2.3.1 Yield and Yield Components

In relation to grain yield per plant, the general combining ability effects of parental means are listed in Table (19). All parents exhibited either negative or positive GCA effects estimated from F_1. except for the parents Gemmiza 7 and Line 2 which showed significant positive or negative GCA effects, respectively. Data shows that Gemmiza 7 gave the highest significant positive GCA effects (1.404) followed by Sakha 8 (0.352) and Sakha 93 (0.286). However, Line 2 revealed a significant negative combining ability (-2.586).

With regard to specific combining ability effects (SCA), all F_1 crosses exhibited either positive or negative SCA effects. Table (20) indicates that 3 crosses gave only significant positive SCA effects, these crosses resulted from a cross between parents with positive general combining ability effects (Gemmiza 7, Sakha 93 and Sakha 8). The crosses between best parental genotypes based on GCA effects (Gemmiza 7 and Sakha 93) and (Sakha 93 and Sakha 8) gave positive estimates (7.660 and 2.572, respectively), while (Gemmiza 7 and Sakha 8) gave a negative estimates (-3.879). The results showed that the cross between positive parent and negative parent (Gemmiza 7 and Line 6) and (Sakha 8 and Sakha 69) based on GCA effects, gave a significant positive SCA effect (3.932 and 5.843, respectively).

For number of spikes per plant, the GCA effects of parental means are listed in Table (19). All parents exhibited either positive or negative GCA effects estimated from F_1, except the parents Gemmiza 7 and Sakha 93 which are considered as a good combiner and exhibited significant positive GCA effects (0.443 and 0.973, respectively) and followed by Line 1 which had insignificant positive GCA effect (0.382). While Sakha 8 and Line 2 showed highly significant negative GCA effects and Sakha 69 was insignificant negative GCA effect.

Results of SCA effects on number of spikes per plant are shown in Table (20), all F_1 exhibited either positive or negative SCA effects. The cross between the two best parental genotypes based on their GCA effects (Gemmiza 7 and Sakha 93) gave a highly significant positive SCA estimated (2.608). While, the cross between one parent considered as a good combiner and parent as a bad combiner (Line 1 and Sakha 69) and (Sakha 93 and Line 2) gave a highly significant positive SCA effects (4.248 and 1.586, respectively). On the other hand, crosses (Sakha 93 and Sakha 8) and (Sakha 93 and Line 1) revealed highly significant negative SCA effects (-2.691 and -3.317), and the cross (Sakha 69 and Line 2) gave a highly significant negative SCA effect (-1.799).

In relation to number of kernels per spike trait, the GCA effects of parental means are listed in Table (19). Sakha 8 and Line 1 showed highly significant positive GCA effects (2.256 and 1.722 respectively) and were considered as best combiner parents. While, Sakha 69 had highly significant negative GCA effect (-3.944). The other parents showed insignificant either positive or negative GCA effect.

Table (20) shows results of specific combining ability (SCA) effects for number of kernels per spike. All F_1 exhibited either positive or negative SCA effects, 5 crosses revealed significant positive SCA effects and 3 crosses were highly significant negative SCA effects. The crosses between best parents Sakha 8 x Line 1 based on GCA effect had highly significant positive SCA effect (6.233) and significant positive SCA effect (3.908) for Sakha 8 x Sakha 93. The crosses which were highly significant positive SCA effect, only one of their parents was best or good combiner for GCA effect, Tables (19 and 20).

The GCA effects are listed in Table (19) for 1000-kernel weight, Two parents exhibited significant positive GCA effects (Gemmiza 7 and Sakha 93). Line 1 showed significant negative GCA effect (-1.799). All other parents showed either positive or negative GCA effects. Gemmiza 7 exhibited highly significant positive GCA and considered as a best combiner (2.272) followed by Sakha 93 exhibited significant GCA and considered as a good combiner (1.747) and Sakha 8 (0.943).

The results of SCA effects as shown in Table (20), indicated that four crosses gave highly significant positive SCA effects. Only one cross Sakha 93 x Sakha 8 resulted from a cross between parents has significant positive GCA effect (Sakha 93 and Sakha 8). Two crosses had significant positive SCA effect (4.774 for Line 2 x Gemmiza 7 and 4.354 for Sakha 8 x Sakha 69), one of their parents was a good combiner and the other parent was a bad combiner, while one cross (5.278) resulted from a cross between two bad combiner parents (Line 1 and Line 2). All other crosses exhibited either positive or negative SCA effects.

Table (19). Estimation of general combining ability (GCA) effects for yield and its components.

Genotype	Traits			
	Grain Yield/ Plant	No. of spikes/ plant	No. of kernels/spike	1000-kernel weight
1-Gemmiza 7	1.404 *	0.443 *	0.431	2.272 **
2-Sakha 69	-0.632	-0.062	-3.944 **	-0.081
3-Sakha 93	0.286	0.973 **	0.447	1.747 *
4-Sakha 8	0.352	-0.878 **	2.256 **	0.943
5-Line 1	-0.089	0.382	1.722 **	-1.799 *
6-Line 2	-2.586 **	-0.838 **	-0.911	-1.044
SE ±gi 0.05	1.09	0.44	1.33	1.65
SE ±gi 0.01	1.46	0.59	1.78	2.20

*, ** significant at P< 0.05 and 0.01, respectively.

Table (20). Estimation of specific combining ability (SCA) effects for yield and its components.

Crosses	Traits			
	Grain Yield/ Plant	No. of spikes/ plant	No. of kernels/ spike	1000-kernel weight
1 (1 x 2)	-3.149 *	-0.194	-3.008	-3.818
2 (1 x 3)	7.660 **	2.608 **	1.067	-2.551
3 (1 x 4)	-3.879 *	-0.376	2.192	-0.080
4 (1 x 5)	2.352	0.198	2.225	2.895
5 (1 x 6)	3.932 *	0.251	1.025	4.774 *
6 (2 x 3)	-2.924	0.575	-5.958 **	4.354 *
7 (2 x 4)	5.843 **	-0.260	7.067 **	-2.189
8 (2 x 5)	1.258	4.248 **	-10.400 **	0.420
9 (2 x 6)	0.731	-1.799 **	9.233 **	-0.601
10 (3 x 4)	2.572	-2.691 **	3.908 *	7.478 **
11 (3 x 5)	-3.113 *	-3.317 **	2.042	2.853
12 (3 x 6)	-2.083	1.586 *	6.042 **	3.632
13 (4 x 5)	-3.613 *	-1.035	6.233 **	-0.643
14 (4 x 6)	1.784	0.378	-6.200 **	0.670
15 (5 x 6)	0.725	-1.441 *	2.100	5.278 *
C.D.(Sij-Sik)	3.00	1.20	3.66	4.53
C.D.(Sij-Skl)	4.01	1.60	4.89	6.05

*, ** significant at P< 0.05 and 0.01, respectively.

3. Estimation of Cross Performance, Heritability, Correlation Coefficient and Path Coefficient in F_2 generation

3.1 Cross Performance in F_2:

Separate analysis of variance was carried out for yield and yield components in F_2 generation and under recommended conditions at Nubaria, Table (21). The analysis of variance indicated highly significant variation among genotypes for all studied characters in this experiment.

Table (22) represents the mean of the 15 segregant genotypes in F_2 for grain yield per plant. Table (22) shows that the genotypes # 2, 3, 6, 10 and 12 (Gemmiza 7 x Sakha 93, Gemmiza 7 x Sakha 8, Sakha 93 x Sakha 69 and Sakha 93 x Sakha 8) were the most productive, Meanwhile genotypes # 8 and 9 (Sakha 69 x Line 1 and Sakha 69 x Line 2) resulted in poor yielding. The other genotypes showed different behavior and revealed variability between them under recommended conditions.

The average number of spikes per plant varied among genotypes, Table (22) showed that genotypes # 6 (Sakha 93 x Sakha 69) produced the highest number of spikes per plant, followed by genotypes # 2, 10 and 4 (Gemmiza 7 x Sakha 93, Sakha 93 x Sakha 8 and Gemmiza 7 x Line 1) . On the other hand, the genotypes # 9 and 5 (Sakha 69 x Line 2 and Gemmiza 7 x Line 2) gave the smallest number of spikes per plant among all genotypes. This range revealed a high variability of spikes number among the 15 genotypes.

Number of kernels per spike varied from 32.6 for last genotype (Line 1 x Line 2) to 47.33 for the second genotype

(Gemmiza 7 x Sakha 93). However, all genotypes except genotype 2 and 15 (Gemmiza 7 x Sakha 93 and Line 1 x Line 2) were varied for number of kernels per spike under recommended conditions.

The mean of 1000-kernel weight varied from 58.36 gm for genotype # 13 (Sakha 8 x Line 1) to 43.6 gm for the last genotype (Line 1 x Line 2). All other genotypes revealed high variability of 1000-kernel weight, Table (22).

Table (21). Mean square values of analysis of variance among F_2 genotypes for yield and its components.

S.O.V.	D.F.	Mean.Square.			
		Grain Yield	**No. of spike/ Plant**	**No of kernels/ spike**	**1000-kernel weight**
Blocks	2	6.70	5.53*	5.59	16.34
Genotypes	14	34.66**	4.62**	46.40**	47.93**
Error	28	6.42	1.67	9.60	10.58

*, ** significant at P< 0.05 and 0.01, respectively.

Table (22). Means of F_2 populations for grain yield and its components

No.	Crosses	Grain Yield /Plant	No of spikes/plant	No of kernels / spike	1000-kernel weight
1	(1 x 2)	15.18 cde	8.86 abcd	41.43 bc	55.30 abc
2	(1 x 3)	23.68 a	10.5 ab	47.33 a	54.80 abcd
3	(1 x 4)	23.85 a	8.20 cde	40.20 bcd	55.46 abc
4	(1 x 5)	17.89 bcd	9.96 abc	40.10 bcd	57.10 ab
5	(1 x 6)	15.38 cde	6.73 de	39.93 bcd	48.36 ef
6	(2 x 3)	20.17 ab	10.6 a	42.46 abc	52.53 bcde
7	(2 x 4)	15.07 de	8.23 cde	42.03 bc	51.90 bcde
8	(2 x 5)	13.64 e	8.93 abc	43.60 ab	48.56 ef
9	(2 x 6)	13.41 e	6.53 e	33.63 ef	51.30 cde
10	(3 x 4)	20.12 ab	10.4 ab	43.73 ab	50.46 cde
11	(3 x 5)	15.43 cde	8.46 bcde	42.03 bc	49.40 de
12	(3 x 6)	20.21 ab	8.23 cde	35.76 def	50.50 cde
13	(4 x 5)	19.33 bc	8.90 abc	38.60 bcde	58.36 a
14	(4 x 6)	17.61 bcde	8.23 cde	38.03 cde	47.50 ef
15	(5 x 6)	14.77 de	8.56 abcde	32.60 f	43.60 f

3.2 Heritability Estimates

Heritability values in broad sense in F_2 generation for yield and its components estimated in 15 crosses are presented in Table (23). According to the results in Table (23), the highest value of heritability was estimated in F_2 generation for grain yield per plant trait (84%). The other traits showed value of 73% for number of spikes per plant, 82% for number of kernels per spike and 81% for 1000-kernel weight. The heritability value for each of number of spikes per plant, number of kernels per spike and 1000-kernel weight was nearby and was considered a medium values. These values of broad sense heritability could be over estimated due to the component of genetic variance especially dominant and additive by dominance variance.

3.3 Correlation Coefficient

Table (24) presents phenotypic correlation between each one of the character studied and traits under recommended conditions.

With respect to the grain yield per plant, it was noticed that the phenotypic correlation was positive highly significant between this trait and number of spikes per plant (0.367), while the correlation was positive significant with number of kernels per spike (0.259) and 1000-kernel weight (0.298). The phenotypic correlation between number of spikes per plant and number of kerneks per spike and grain yield was positive and highly significant, while was positive and insignificant with 1000-kernel weight, Table (24).

Highly significant positive correlation was noticed between number of kernels per spike with number of spikes per plant, while insignificant positive phenotypic correlation was detected between

this trait and 1000-kernel weight. Number of kernels per spike revealed positive significant correlation with grain yield, Table (24). Regarding to 1000-kernel weight, the phenotypic correlation was positive significant between this trait and grain yield, while the correlation was positive and insignificant with number of spike per plant and number of kernels per plant, Table (24).

Table (23). Heritability in broad sense for yield and its components in F2 generation.

	Grain Yield	No. of spike/ plant	No of kernels / spike	1000-kernel weight
$\delta^2 g$	34.66	4.62	46.40	47.93
$\delta^2 p$	41.08	6.29	56.00	58.50
h_b^2	0.84	0.73	0.82	0.81

Table (24). Phenotypic Correlation between yield and its components

Traits	Grain Yield	No. of spikes /plant	No. of kernels /plant	1000-kernel weight
Grain Yield	1.000	0.367**	0.259*	0.298*
No. of spikes/plant		1.000	0.388**	0.132
No. of kernels /plant			1.000	0.148
1000-kernel weight				1.000

*, ** significant at P< 0.05 and 0.01, respectively.

3.4 Path Coefficient Analysis and Coefficient of Determination

Partitioning of simple correlation coefficient between grain yield and its components i.e. number of spikes per plant, number of kernels per spike, and 1000-kernel weight are presented in Table (25). Number of spikes per plant had the largest direct effect (0.27) followed by 1000-kernel weight (0.23) and number of kernels per spike (0.16), respectively.

The coefficient of determination were calculated for the direct and indirect effects of the three studied yield factors and transformed into percentage in order to evaluate these factors for their importance as sources of variation in grain yield. The components in percent for grain yield variation are presented in Table (26). The results indicated that the most important sources of variation in grain yield are the direct effect of number of spikes per plant followed by direct effect of 1000-kernel weight and the direct effect of number of kernels per spike. These three sources account for approximately 15.0 of grain yield variation. Indirect effects of yield components in grain yield revealed that the interaction between number of kernels per spike and number of spikes per plant was the first indirect effect followed by interaction between number of spikes per plant and 1000-kernel weight, while the interaction between number of kernels per spike and 1000-kernel weight was the last indirect effect in grain yield. These three sources account of indirect effects for approximately 6.0 of grain yield variation.

Table (25). Path coefficient analysis for yield and its components in F_2 generation.

Traits	No. of spikes/ plant	No. of kernels /spike	1000-kernel weight	Correlation
No. of spikes/plant	0.27	0.062	0.043	0.37
No. of kernels /spike	0.066	0.16	0.033	0.26
1000-kernel weight	0.043	0.033	0.23	0.30

Table (26). Coefficient of determination for yield component and its contribution to grain yield in F_2 generation.

Trait	Coefficient of Determination	Contribution
No. of spikes/plant	0.07	7.0
No. of kernels /spike	0.03	3.0
1000-kernel weight	0.05	5.0
No. of spikes/plant X No. of kernels /spike	0.03	3.0
No. of spikes/plant X 1000-kernel weight	0.02	2.0
No. of Kernels/spike X 1000-kernel weight	0.01	1.0
Residual	0.79	79.0
Total	1	100

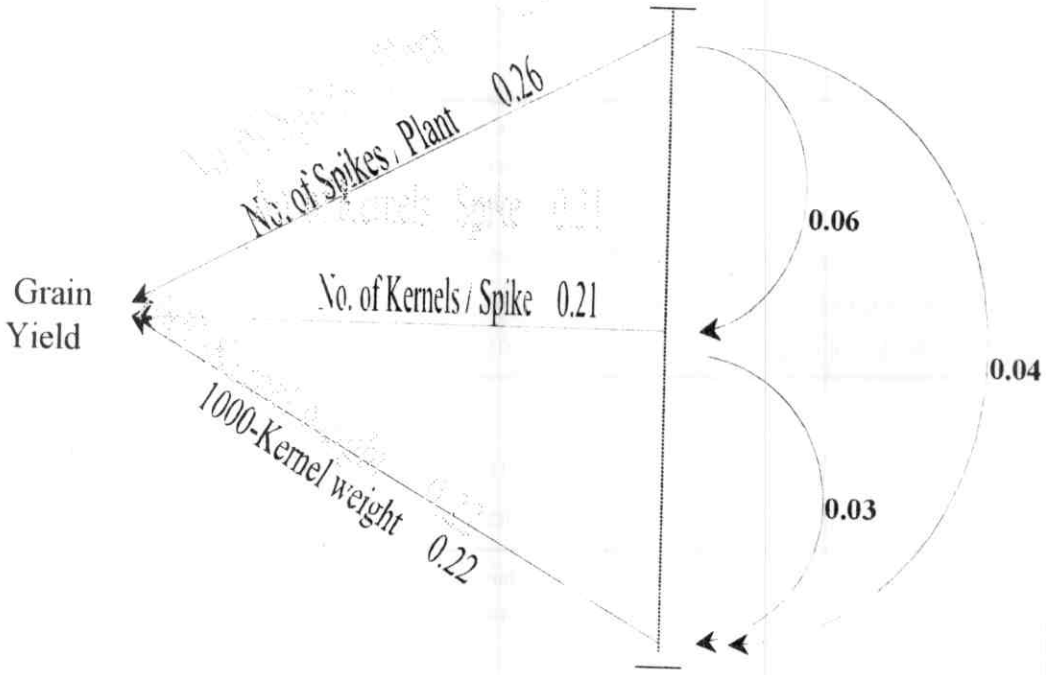


Figure (2). Sequential Path analysis for grain yield and its components in F_2 generation

4. Inheritance of Leaf Rust Resistance

In 2003/2004 season the parents, F_1's and F_2's of 15 cross combinations involving four susceptible parents to leaf rust disease caused by *Puccinia recondite* and two resistant parents to leaf rust were sown under field conditions at Nubaria Research Station. At the late tillering and beginning of booting stage, disease tests were carried using a mixture of the common races under the Nubaria conditions. At the same time, the experiment was surrounded by Sids 1 as spreader with highly susceptible wheat cultivars to leaf rust disease. The infection types 0, R, MR, M, MS and S were used to describe the disease reaction.

Table (27) shows the infection type frequency distribution of parents, F_1 and F_2 population of Gemmiza 7 X Line 1 cross at adult stage against leaf rust in the field. The infection type of Gemmiza 7 was S expressing the susceptibility to leaf rust and the infection type for Line 1 was R expressing resistance to leaf rust, while infection type of the 15 F_1 plants was Moderate Resistance (MR). The F2 infection types ranged from 0 to S, Table (27). Number of resistant and susceptible plants were 221 and 59, respectively. These frequencies fitted the theoretical expected ratio of 3:1 with P value=0.25 – 0.1 and obtained Chi-square was 2.30 as shown in Table (28).

Table (27). The infection type frequency distribution of parents, F_1 and F_2 population of Gemmiza 7 X Line 1 cross at adult stage against leaf rust in the field.

Cross name	No. of examined Plants	Types of infection					
		0	R	MR	M	MS	S
Gemmiza 7 X Line 1							
P_1	20						20
P_2	20		20				
F_1	15			15			
F_2	280	35	65	98	23	20	39

Table (28). Phenotypic classes of F_2 population of Gemmiza 7 X Line 1 cross inoculated with leaf rust at adult stage in the field.

Cross name	No. of plants	Reaction		Expected ratio	Chi-square	P. value
		R	S			
Gemmiza 7 X Line 1	280	221	59	3 : 1	2.30	0.25-0.1

Chapter II

1. Genetic Relationships

1.1 Genetic relationship using morphological traits

To find out the relationship among the ten wheat varieties under study, the Euclidean distance among the varieties was calculated. It was based on the parental phenotypic means of the two years.

1.1.1 Euclidean distance

Relationships among the ten wheat varieties based on standardized values of the quantitative morphological traits are presented in Table (29). The results showed that the dissimilarity matrix of the Euclidean distance using morphological traits between all pairs of varieties ranged from 1.04 between Sakha 93 and Sakha 8 to 9.97 between Sakha 61 and Sids 6. The average distance among varieties was 5.50.

1.1.2 Cluster analysis

The dissimilarity matrix was used to generate a phenogram of the ten varieties, Figure (3). The cluster diagram showed a complicated genetic variation pattern and the ten varieties formed three main clusters. The first cluster created two sub-clusters at a distance of about 25.0. The first sub-cluster included Line 1 and Line 2 at a distance of about 14.0, the second sub-cluster included Gemmiza 7 and Sakha 61 at a distance of about 15.0. The second main cluster included the varieties Sakha 69, Sakha 8 and Sids 6, which separated at distance of about 49.8. The third main cluster included an individual variety which was Line 8 at a distance of 49.8 and two varieties Sakha 93 and Line 6, which formed sub-cluster and

separated at a distance of 18.9. The differences between traits in groups led to formation of the three main clusters.

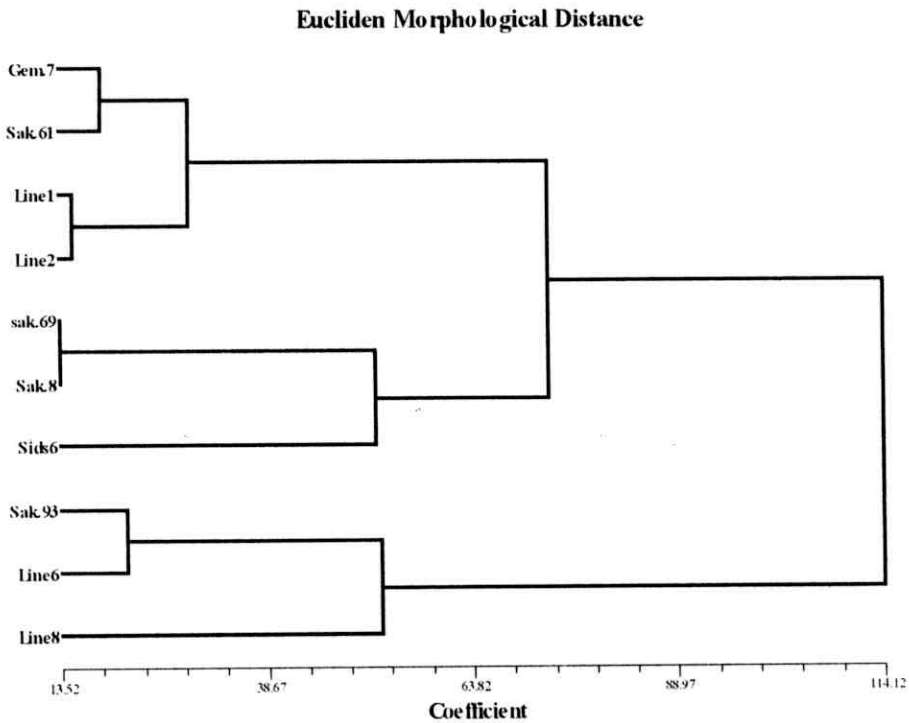


Figure (3). Dendrogram obtained from UPGMA cluster based on morphological data from the ten wheat genotypes.

Table (29). Euclidean Distance matrix of ten wheat genotypes using morphological traits.

	Gemmiza 7	Sakha 61	Sakha 69	Sakha 93	Sakha 8	Sids 6	Line 1	Line 2	Line 6	Line 8
Gemmiza 7	0.00									
Sakha 61	1.85	0.00								
Sakha 69	4.38	5.44	0.00							
Sakha 93	7.50	6.32	1.17	0.00						
Sakha 8	3.15	4.16	1.35	1.04	0.00					
Sids 6	8.81	9.97	4.52	1.62	5.84	0.00				
Line 1	3.92	2.64	8.02	3.70	6.75	1.25	0.00			
Line 2	3.33	1.71	7.09	4.84	5.78	1.16	1.49	0.00		
Line 6	9.59	8.35	1.37	2.15	1.24	1.82	5.74	6.73	0.00	
Line 8	1.36	1.22	1.79	6.25	1.66	2.24	9.92	1.09	4.24	0.00

1.2 Genetic relationship using simple sequence repeat

Microsatellites or Simple Sequence Repeats (SSRs) experiment was conducted using fifty SSR's primer pairs developed and provided by Dr. P. Cregan, USDA-ARS, Maryland, USA. These markers loci, Figure (4), were used to find out the genetic relationships between varieties and to create the molecular marker data. The Jaccard's similarity coefficient was calculated among the 10 wheat varieties.

1.2.1 Jaccard's similarity coefficient

Similarity between all pairs of varieties are illustrated in Table (30). This table showed that the similarity matrix of genetic distance ranged from 0.10 between Gemmiza 7 and Line 8 to 0.875 between Sakha 69 and Sakha 61. The other paris of varieties showed varied values of similarity ranges from 0.125 between Gemmiza 7 with each of Sakha 61 and Sakha 69 to 0.767 between Gemmiza 7 with Sids 6. The average similarity among varieties was 0.49.

1.2.2 Cluster analysis

Two hundred and twenty-five *Xbarc* loci assigned in linkage map both genetically and phiscally across 21 the chromosomes of bread wheat were downloaded from GrainGenes web site. Out of these 225 *Xbarc* loci, 50 SSR loci were used in this study, their mapping positions on the 21 chromosome of bread wheat are illustrated in Figure (4). Among these fifty SSR loci, ten microsatellite markers (20%) generated polymorphism between parents with a total of 92 fragments. Of the total scorable SSR bands

27 alleles were detected for polymorphism, Table (31). This represented an average of 2.7 alleles per locus with a range of two to five alleles detected by a single SSR locus. Nei's genetic distance (GD) was measured using the 27 polymorphic SSR alleles, Figures 6, 7, 8 and 9).

Nei's genetic distance, Figure (5) showed that the genetic distance for the different genotype combinations ranged from 0.27 to 0.72 and the studied varieties formed two main clusters. The first main cluster separated at genetic similarity about 0.38 and created two sub-clusters. The first sub-cluster included Gemmiza 7 and Sids 6 at a genetic similarity about 0.66. the second sub-cluster included Line 1 and Line 6 at a genetic similarity about 0.49. In relation to second main cluster, Figure (5) showed that this cluster formed two sub-clusters at a genetic similarity about 0.55. The first sub-cluster included Sakha 69 and Sakha 61 at a genetic similarity about 0.68 and Sakha 8 which represented an individual variety at a genetic similarity about 0.58. For the second sub-cluster, the results indicated that it included two varieties, Line 2 and Line 8, which separated at genetic similarity about 0.72. Table (31) showes the usefulness of SSR markers to detect the polymorphism among the parental genotypes based on the presence (+) and absence (-) for PCR-products.

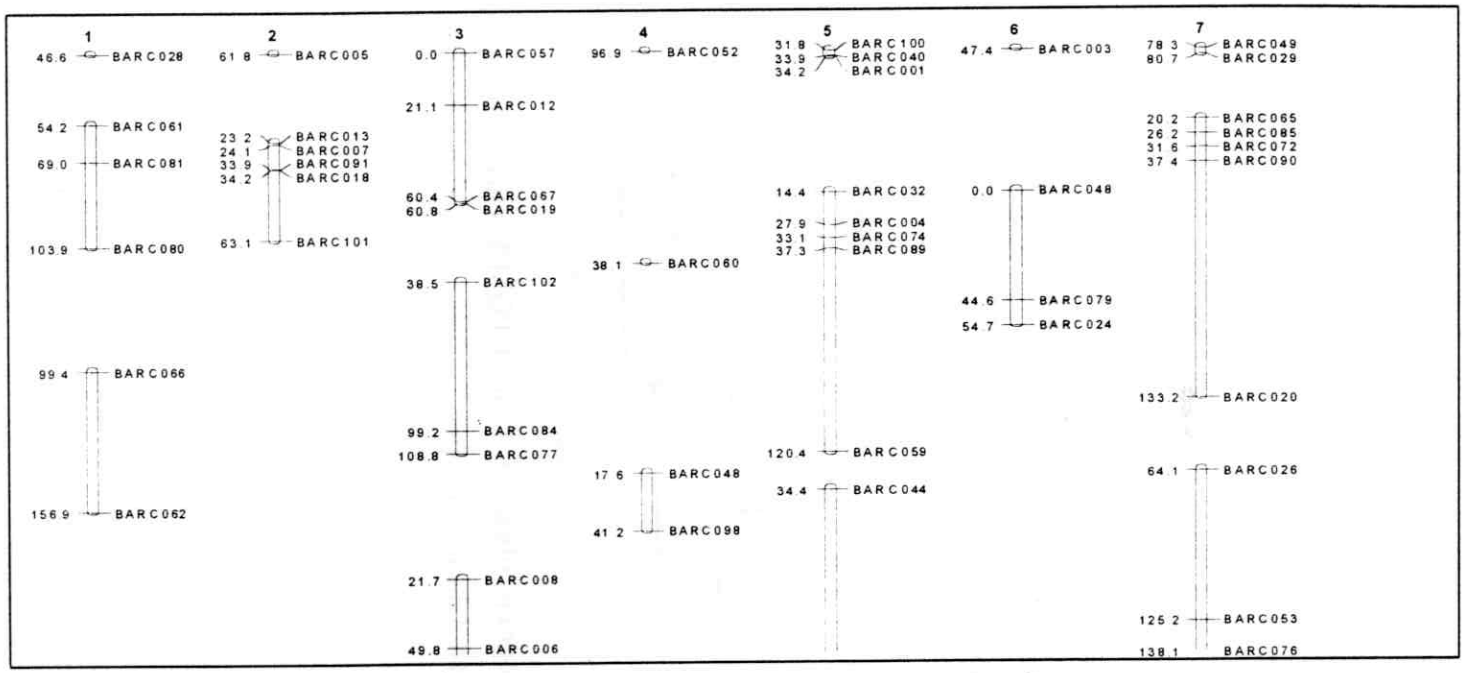


Figure (4). Genetic maps of 50 wheat Xbarc SSR loci produced by Joinmap 3.0 with 2 SSR markers.

www.scabusa.org/pdfs/BARC_SSRs_011101.xls

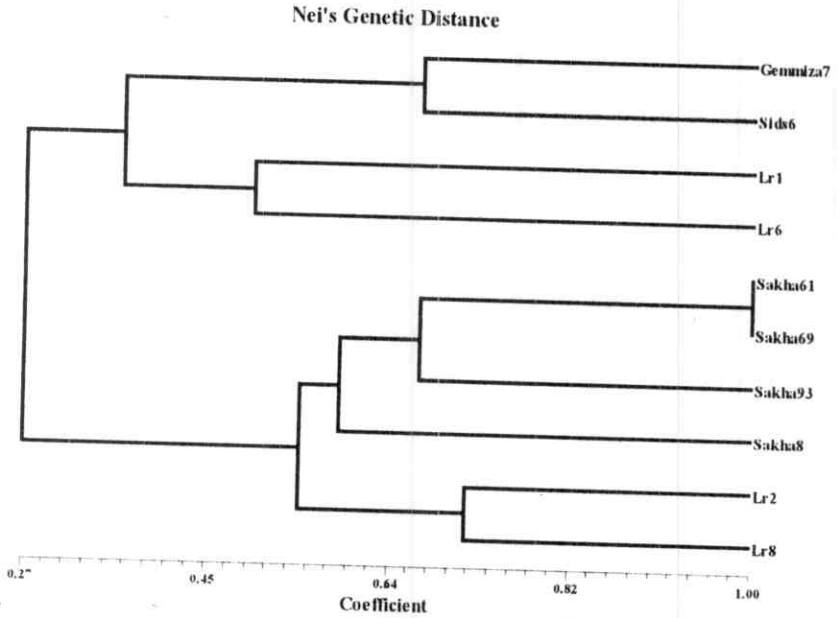
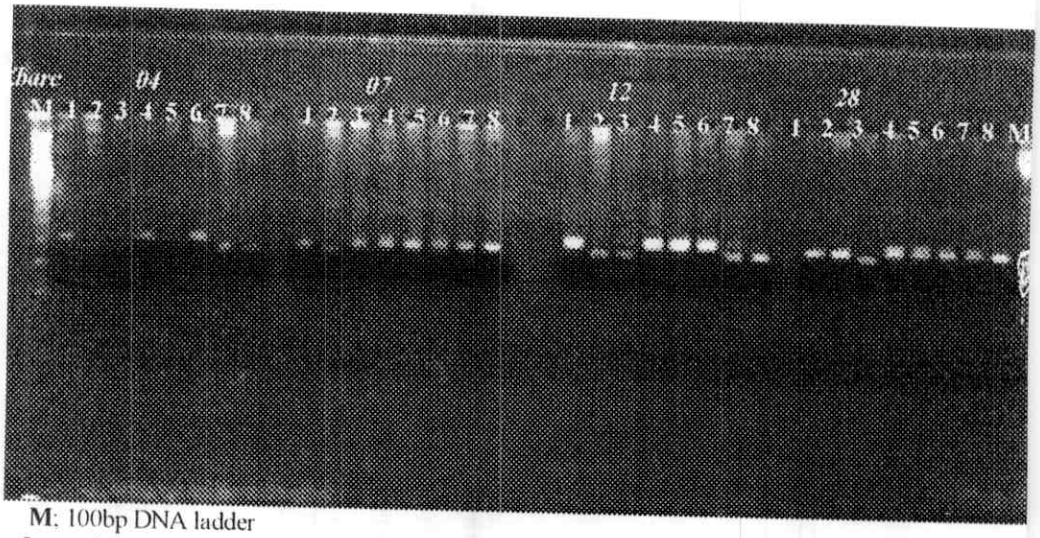


Figure (5). Dendrogram obtained from UPGMA cluster based on SSR data from the ten wheat genotypes.

Table (30). Similarity matrix for the ten wheat genotypes based on Jaccard's coefficient,using 10 SSR primers.

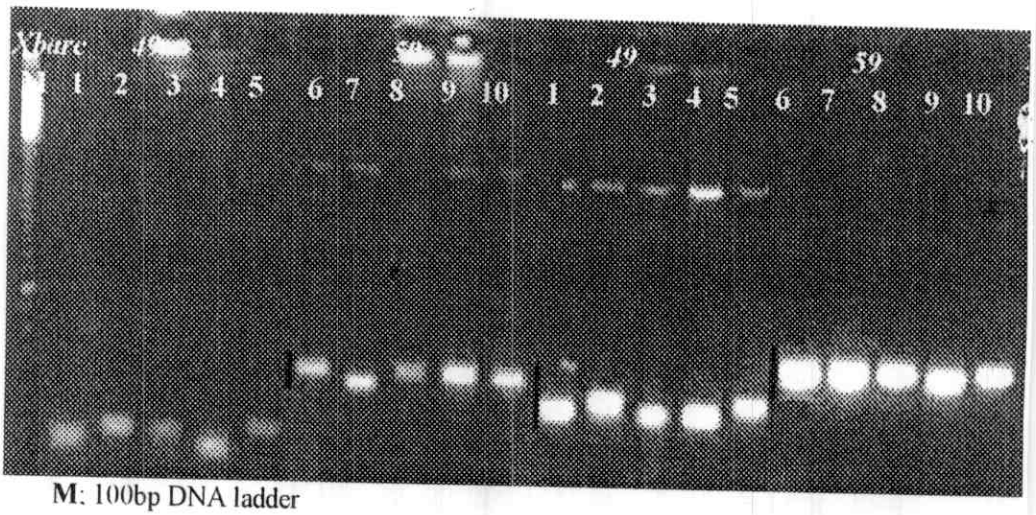
	Gemmiza 7	Sakha 61	Sakha 69	Sakha 93	Sakha 8	Sids 6	Line 1	Line 2	Line 6	Line 8
Gemmiza 7	1.000									
Sakha 61	0.125	1.000								
Sakha 69	0.125	0.875	1.000							
Sakha 93	0.270	0.675	0.667	1.000						
Sakha 8	0.372	0.521	0.537	0.500	1.000					
Sids 6	0.767	0.375	0.376	0.400	0.444	1.000				
Line 1	0.375	0.500	0.500	0.333	0.750	0.440	1.000			
Line 2	0.275	0.440	0.467	0.476	0.660	0.400	0.666	1.000		
Line 6	0.375	0.270	0.270	0.330	0.550	0.444	0.750	0.700	1.000	
Line 8	0.100	0.500	0.500	0.500	0.555	0.300	0.550	0.870	0.550	1.000



M: 100bp DNA ladder

Lane 1-8: wheat parental genotypes (Gemmiza7, Sakha61, Sakha69,Skha93, Sakha8, Sids6,Line 1 and Line 2)

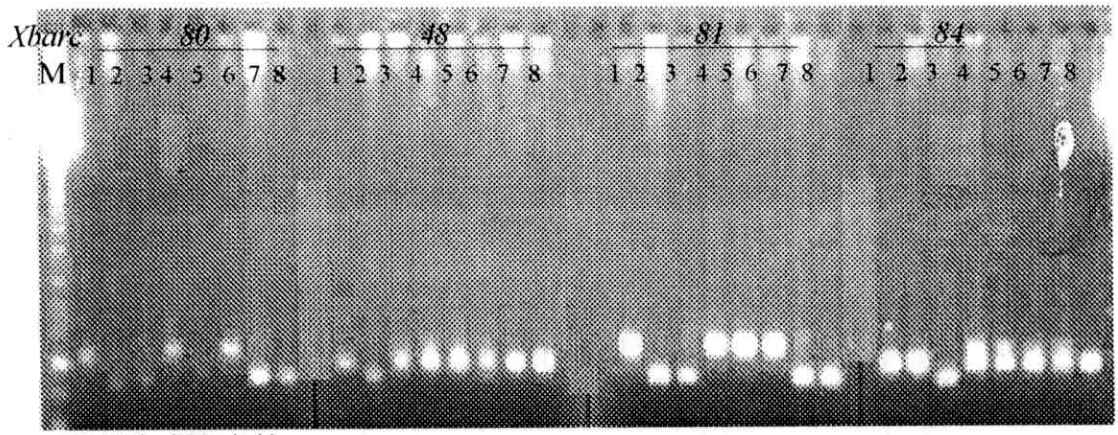
Figure (6). SSR patterns obtained with 4 different primers (*Xbarc 04, 07 07, 12 and28*).



M: 100bp DNA ladder

Lane 1-10: wheat parental genotypes ((Gemmiza7, Sakha61, Sakha69,Skha93, Sakha8, Sids6,Line 1, Line 2, Line 6 and Line 8)

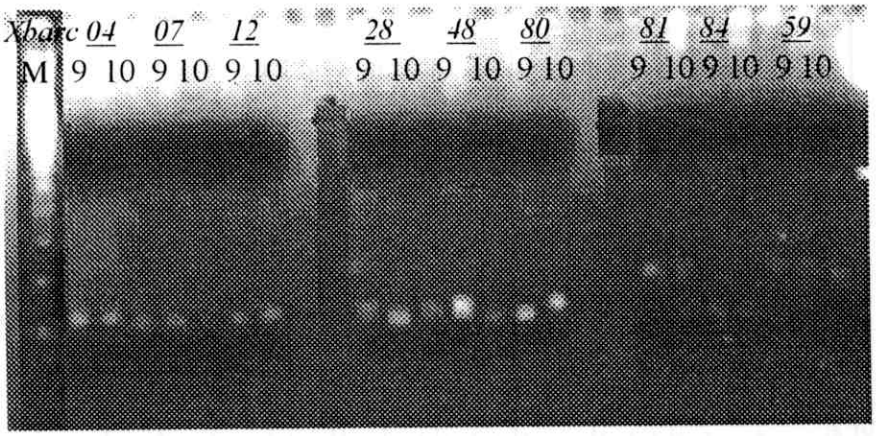
Figure (7). SSR patterns obtained with 2 different primers (*Xbarc 49, and 59*).



M: 100bp DNA ladder

Lane 1-8: wheat parental genotypes ((Gemmiza7,Sakha61, Sakha69,Skha93, Sakha8, Sids6,Line 1 and Line 2)

Figure (8). SSR patterns obtained with 4 different primers (*Xbarc 48, 80, 81 and 84*).



M: 100bp DNA ladder

Lane 9 and 10: wheat parental genotypes (Line 6 and Line 8)

Figure (9). SSR patterns obtained with 9 different primers (*Xbarc 04, 07,12, 28, 48, 59, 80, 81and 84*).

Table (31). Usefulness of SSR markers in different genetic background, tested on 10 wheat lines (+ presence of PCR products, - absence of of the PCR-products)

Marker	MW(bp)	Gemmiza7	Sakha 61	Sakha 69	Sakha 93	Sakha 8	Sids 6	Line 1	Line 2	Line 6	Line 8	BR	BS
Xbarc04	773	-	+	-	-	-	-	-	-	+	-	-	-
	791	-	-	-	-	-	-	+	-	-	+	-	-
	818	+	-	-	-	-	-	-	-	-	+	-	-
	827	-	-	-	+	-	-	-	-	+	-	-	-
	837	-	-	+	-	-	+	-	-	-	+	-	-
	877	-	-	-	-	+	-	-	-	-	-	-	-
Xbarc07	791	-	+	-	-	-	-	-	-	-	+	-	-
	809	+	-	-		-	-	-	-	-	-	-	-
	818	-	-	+	+	+	+	+	+	+	-	-	-
Xbarc12	791	-	-	-	-	-	-	+	+	-	-	-	-
	800	-	+	+	-	-	-	-	-	-	-	-	-
	846	+	-	-	+	+	+	-	-	+	-		
Xbarc28	791	-	+	-	-	-	-	-	-	-	-	-	-
	818	+	-	-	+	+	-	-	+	-	-	-	-
	827	-	-	+	-	-	+	+	-	-	-	-	-
Xbarc048	718	+	+	-	-	+	-	+	-	+	-	-	-
	726	-	-	+	+	-	+	-	+	-	-	-	-
Xbarc049	770	-	+	-	-	+	+	-	-	+	-	-	-
	810	+	-	+	+	-	-	-	+		+	-	-
Xbarc059	920	-	+	-	-	-	-	-	-	+	+	-	-
	990	+	-	+	+	+	+	+	-	-	+	-	-
Xbarc80	629	+	+	+	-	+	-	-	+	+	-	+	+
	700	-	-	-	+	-	+	-	-	-	-	+	-
Xbarc81	769	-	+	+	-	-	-	+	+	-	-	+	+
	824	+	-	-	+	+	+	-	-	-	-	+	-
Xbarc84	710	+	+	+	-	-	-	+	-	+	-	-	-
	730	-	-	-	+	+	+	-	+	-	-	-	-

1.3 The relationship of heterosis and specific combining ability with ith genetic distance based on SSR.

Predicting F_1 common wheat hybrid performance using DNA markers is one of the important applications of DNA markers, sence evaluation of hybrids for heterosis or combining ability in the field is expensive and time-consuming. For this reason, 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 specific combining ability and heterosis using the wheat genotypes under study, Figures (14 and 15). Table (32) reveals the relationship of heterosis and specific combining ability for yield and yield components with genetic distance, measured using 10 SSR markers, for the diallel.

Table (32) indicates that the amount of heterosis and specific combining ability were highly significantly correlated with Nei's genetic distance (GD) for grain yield per plant (0.60 and 0.49, respectively) as shown in Figures (10, 11, 12 and 13). Moreover, results showed that heterosis was significantly correlated with Nei's GD for number of spikes per plant (0.31), while SCA was significantly correlated with Nei's GD for 1000-kernel weight (0.40). On the other hand, all other traits revealed weak correlation between Nei's GD, heterosis and SCA. With regard to correlation of heterosis with SCA, heterosis was also significant or highly significant correlated with SCA for all traits under study and ranged from 0.60 for 1000-kernel weight to 0.43 for grain yield per plant, Table (32).

Table (32). Pearson Correlations among Nei' genetic distances (Nei' GD), Heterosis (H) and specific combing ability (SCA) for grain yield / plant, No. of spikes/plant, No. of kernels/spike, and 1000-kernel weight.

		Nei's GD	H	SCA
Nei's GD				
	Grain yield/plant			
	No.of spikes/plant	1.00		
	No.of kernels/spike			
	1000-kernel weight			
H				
	Grain yield/plant	0.60 **		
	No.of spikes/plant	0.31 *		
	No.of kernels/spike	0.13	1.00	
	1000-kernel weight	0.17		
SCA				
	Grain yield/plant	0.49 **	0.43 *	
	No.of spikes/plant	0.24	0.51 **	
	No.of kernels/spike	0.16	0.50 **	1.00
	1000-kernel weight	0.40 *	0.60 **	

** Correlation is highly significant at P = 0.01.

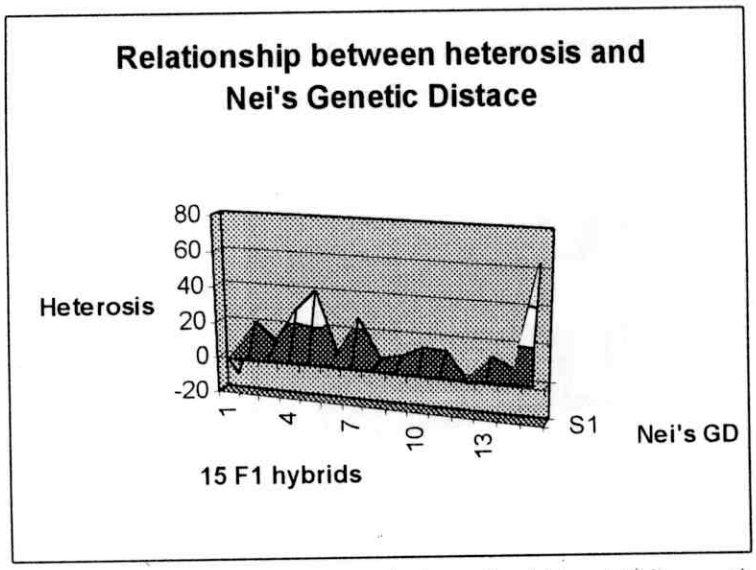


Figure (10). The relationship between heterosis for grain yield and Nei`s genetic distances in 15 F_1 hybrids.

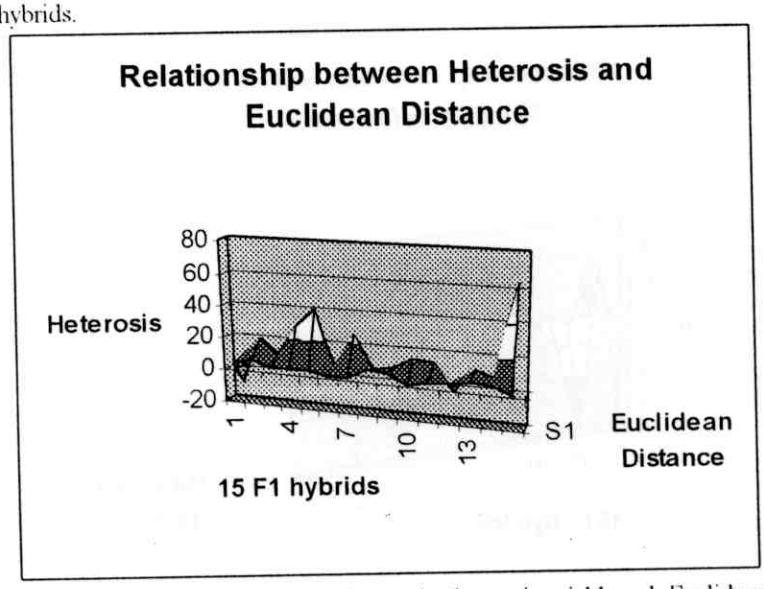


Figure (11). The relationship between heterosis for grain yield and Euclidean genetic distances in 15 F_1 hybrids.

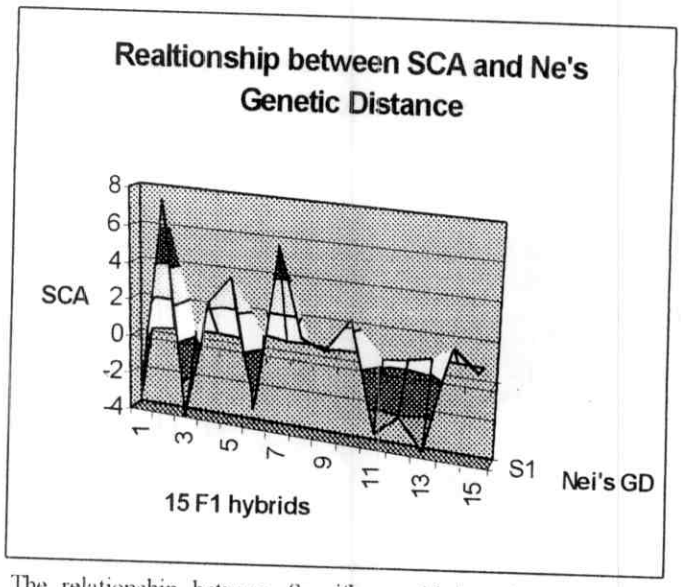


Figure (12). The relationship between Specific combining ability (SCA) for grain yield and Nei`s genetic distances in 15 F_1 hybrids.

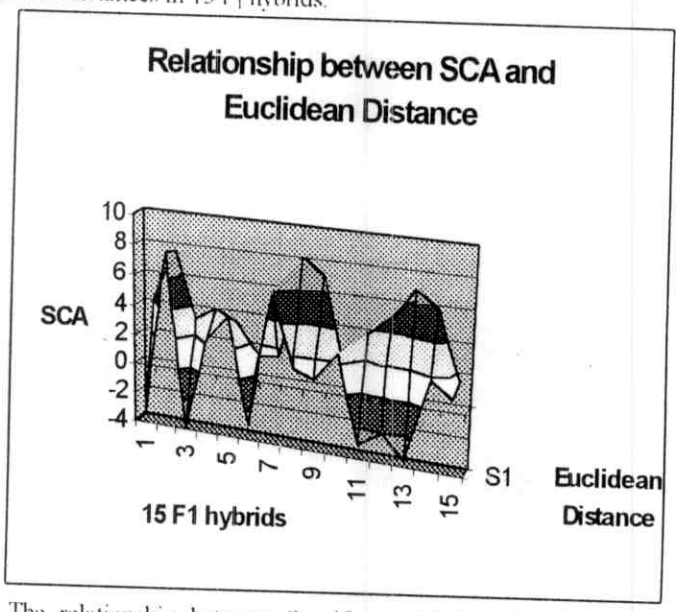


Figure (13). The relationship between Specific combining ability (SCA) for grain yield and Euclidean genetic distances in 15 F_1 hybrids.

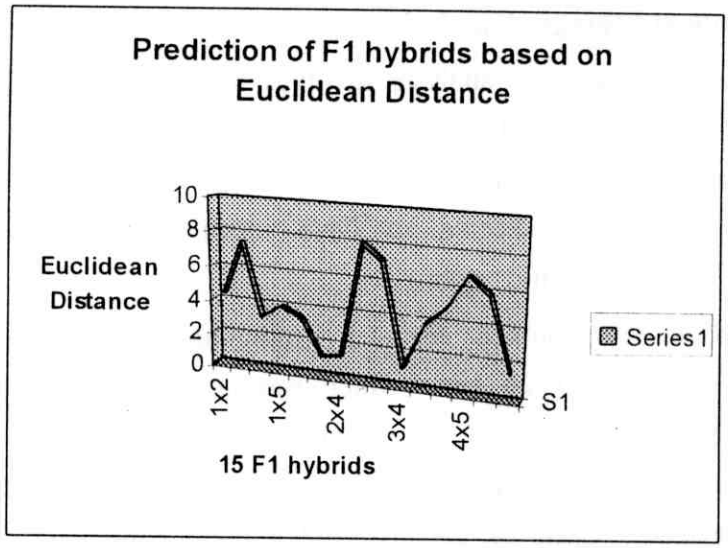


Figure (14). Prediction of F1 hybrids based on Euclidean genetic distances in 15 F_1 hybrids.

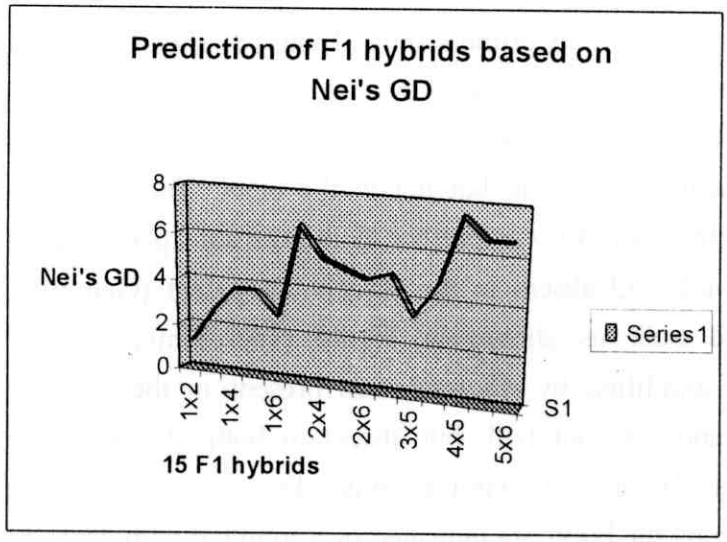
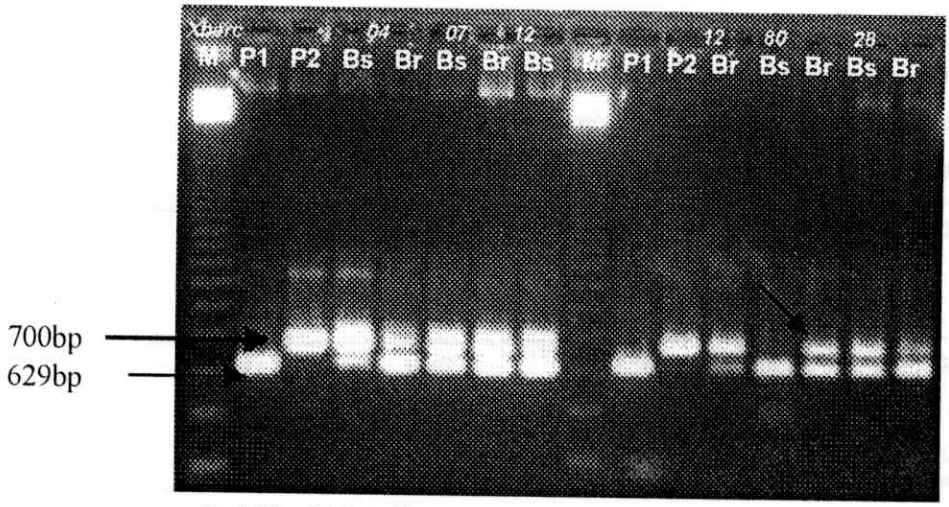


Figure (15). Prediction of F1 hybrids based on Nei's genetic distances in 15 F_1 hybrids.

1.4 Bulked Segregant analysis

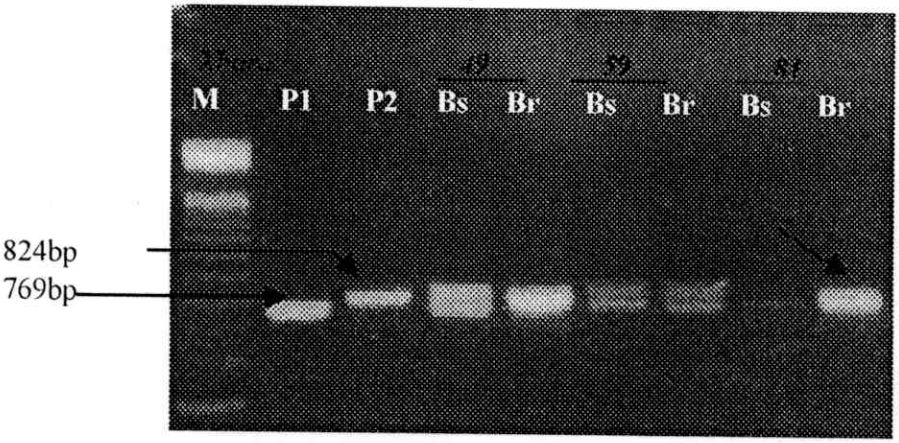
Bulked segregant analysis involves screening for differences between two pooled DNA samples derived from a segregating population that originated from a single cross. Each pool, or bulk, contains individuals selected to have identical genotypes for a particular trait or genomic region.

DNA was bulked from F_2 individuals homozygous for alternate alleles of *Lr26* gene which resulted from a single cross between Gemmiza 7 as a susceptible genotype and Line 1 as a resistant genotype (monogenic line carrying *Lr26* resistance gene) in the 33 progeny. Each of the two bulks were consisted of 10 F_2 homozygous individuals and were employed to identify SSR markers linked to *Lr26* by using 50 SSR primer pairs, Table (7). Out of the fifty SSR primers, ten primers only, Table (8) showed polymorphism among parental genotypes as shown in Figures (6, 7, 8, and 9). Two primers, *Xbarc80* and *Xbarc81*, generated amplification products that were present in one bulk but not in the other. The 700bp fragment, amplified by *Xbarc80* was present in the resistant parent (Line 1) and resistant bulk and absent in the susceptible parent (Gemmiza 7) and susceptible bulk as shown in Figure (16). Similarity, the 824bp fragment, amplified by *Xbarc81* was present in the resistant parent (Line 1) and resistant bulk but absent in both of susceptible parent (Gemmiza 7) and susceptible bulk, Figure (17). polymorphisms distinguishing the bulks are indicated by a solid bar with *Xbarc81*).



M; 100bp DNA ladder, **P1;** Gemmiza 7, **P2;** Line 1, **Bs;** Bulked susceptible, **Br;** Bulked resistance and different SSR primers (*Xbarc* 04, 07, 12, 28 and 80).

Figure (16). SSR markers detecting polymorphism between DNA Bulks (bulked resistance and bulked susceptible) by using different SSR primers (the polymorphism distinguishing the bulks are indicated by a solid bar with *Xbarc80*).



M; 100bp DNA ladder, **P1;** Gemmiza 7, **P2;** Line 1, **Bs;** Bulked susceptible, **Br;** Bulked resistance and different SSR primers (*Xbarc* 49,59 and 81).

Figure (17). SSR markers detecting polymorphism between DNA Bulks (bulked resistance and bulked susceptible) by using different SSR primers (the

Table (33). Chromosomal location and R^2 for microsatellite markers significantly associated with field Infection Type (IT) and Disease Severity recorded for leaf rust at adult plant stage in a single locus regression.

Marker	Chromosomal Location	Infection Type R^2 (%)	Disease Severity R^2 (%)
Xbarc80	1 BL	28 **	33 **
Xbarc81	1 BL	55 **	50 **
Xbarc80 * *Xbarc81*	1 BL	73 **	67 **

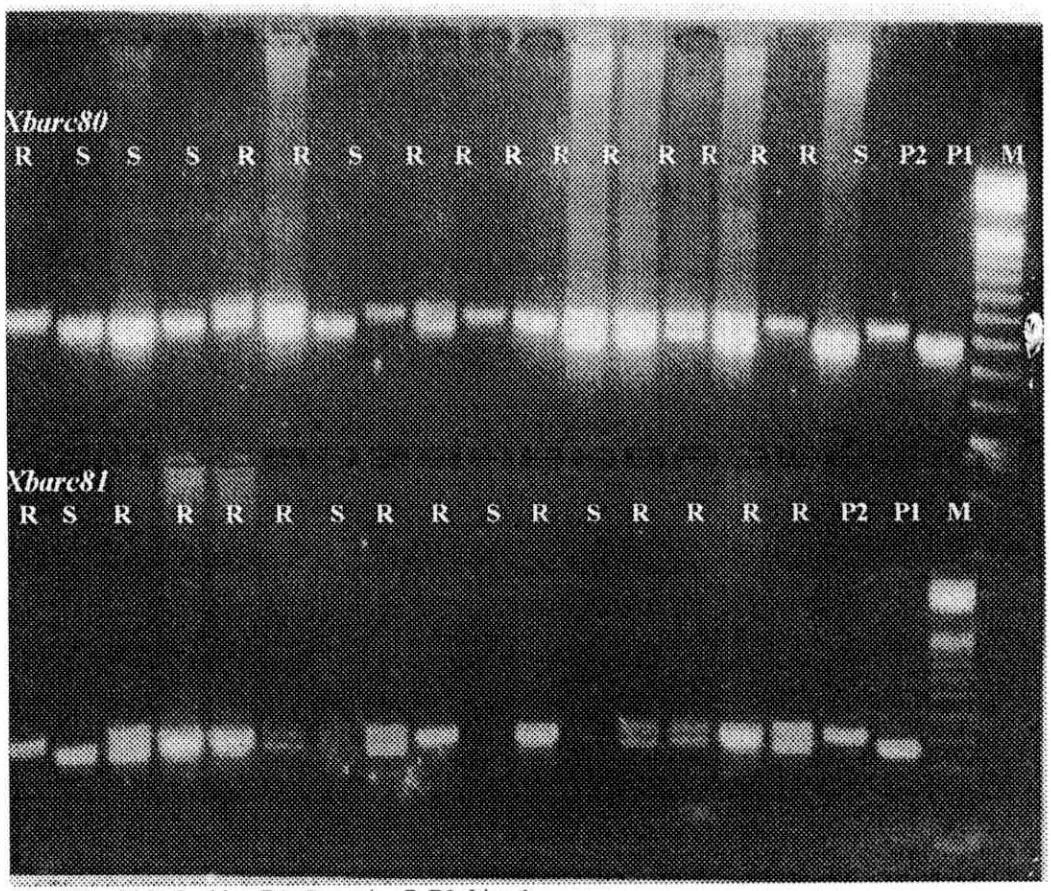
1.5 Identification of SSR markers linked to *Lr26*

Most wheats with *Lr26* are derived from wheat x rye hybridization. This gene was earlier localized on the long arm of chromosome 1B. Some wheats consist of both substitution and translocation biotypes 1B(1BL.1RS) or 1R(1B) and *Lr26* is completely linked with *Sr31* and *Yr9* (Zeller, 1973). In wheat, using molecular markers was necessary to identify the markers which are linked to leaf rust resistance genes and are simple to be used. In the cross between the resistant *Lr26* donor line (monogenic Line 1) and Gemmiza 7 as a susceptibleparent, F_2 segregating population was used to identify the SSR markers linked to leaf rust resistance genes. Bulked DNA from each of 10 F_2 individual plants resistant and susceptible were tested by using fifty SSR loci of known positions of on 21 wheat chromosomes. Primer pairs that gave clear, distinguishable and reproducible patterns were considered for analysis. Two primers (*Xbarc80* and *Xbarc81)* showed polymorphism between susceptible and resistant bulked DNA, Figures (16 and 17). The two SSR loci, *Xbarc80* and *Xbarc81*, were used to check their linkage to the *Lr26* using segregating F_2 plants (33 sample) of the cross between Line 1(monogenic carrying *Lr26*) and Gemmiza 7 (susceptible). Both primers could be analyzed as codominant markers and the results showed that 7 individuals were homozygous for the allele from resistance gene (RR), 17 individuals were heterozygous carrying both alleles (Rr) and 6 individuals were homozygous for the allele from susceptible parent (rr) with a 1:2:1 ratio (Chi-square=0.59, $p< 0.05$), Figure (18).

A regression analysis, Table (33) was performed to test the significance of the linkage between *Lr26* and the polymorphic markers. The results showed that the regression analysis for the markers *Xbarc80* and *Xbarc81* were significant. In relation to infection type, the calculated r^2 for *Xbarc80* and *Xbarc81* were 0.28 and 0.55, respectively. On the other hand, the calculated r^2 for *Xbarc80* and *Xbarc81* were 0.33 and 0.50 for disease severity, respectively.

1.6 Genetic mapping of *Lr26*

By the aid of MapMaker linkage analysis on F_2 population, a highly reliable linkage group consisting of two microsatellite loci and the leaf rust resistance gene *Lr26* was established from 50 microsatellite loci through the "map" command. The two closest microsatellite loci and the resistance gene *Lr26* were assigned to chromosome 1B. A standard maximium-likelihood technique was used to analyze the linkage between the two microsatellite loci and resistance gene *Lr26*. The map distance between *Lr26* and *Xbarc80* was 8.1 cM, Figure (19), while the distance between this resistance gene *Lr26* and *Xbarc81* was 18.5 cM, Figure (20). Lr26 was flanked on either side by *Xbarc80* and *Xbarc81*, with a total map length of 26.6 cM (Figure 21), with a LOD scores ranging from 10 to 18.6, respectively.



M: 100bp DNA Ladder, **P1**: Gemmiza 7, **P2**: Line 1
R: F_2 individual plant resistant
S: F_2 individual plant susceptible

Figure (18). SSR markers detecting polymorphism between P1(Gemmiza 7), Parent 2 (Line 1) and their F2 segregating population by using SSR primers (*Xbarc80 and Xbarc81*).

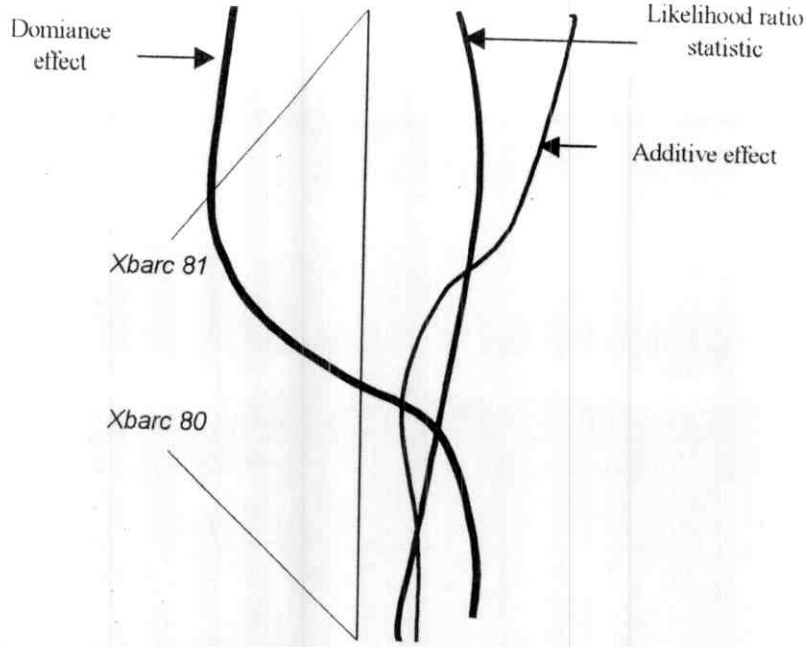


Figure (19). Interval mapping for *X*barc 80 SSR marker on chromosome 1B using Kosambi mapping function with 8.1 cM away from the resistance gene contributed by Line 1.

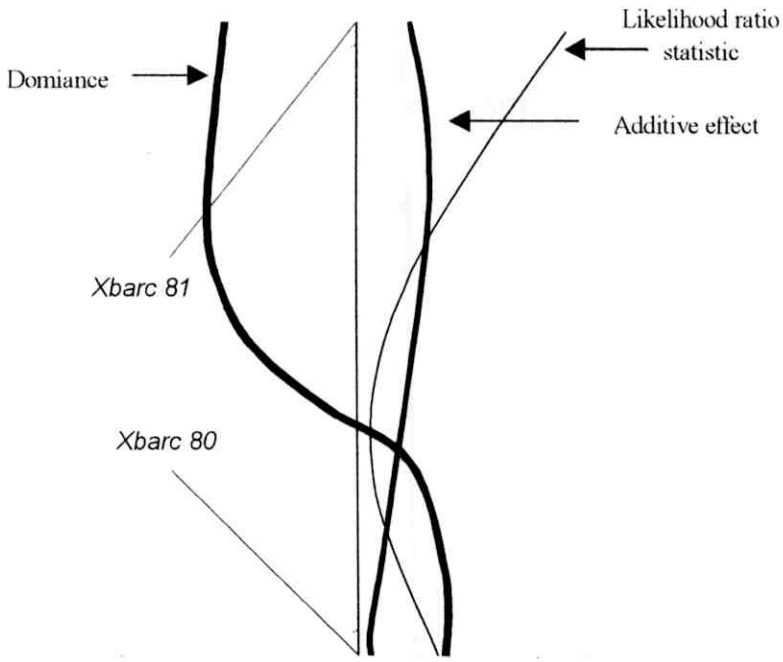


Figure (20). Interval mapping for *X*barc 81 SSR marker on chromosome 1B using Kosambi mapping function with 18.5 cM away from the resistance gene contributed by Line 1.

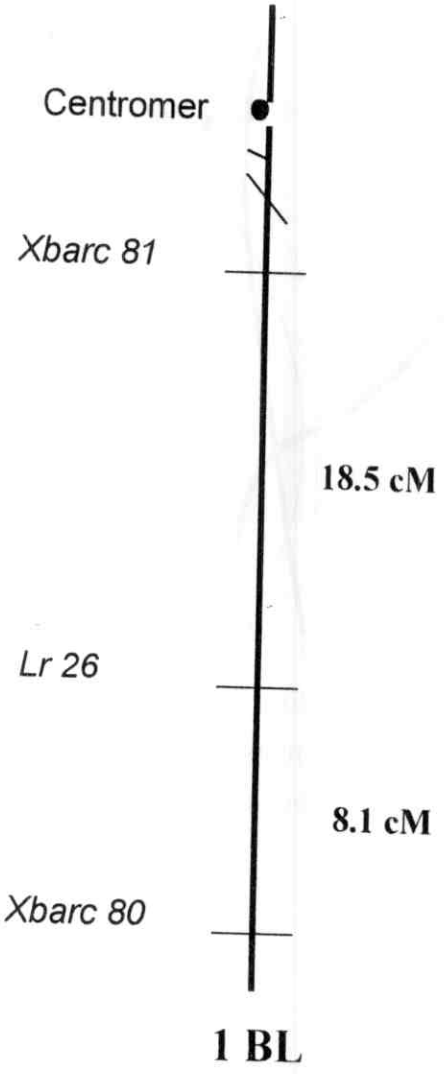


Figure (21). Linkage map showing the region near the Lr 26 gene, all distances are given in centiMorgan using Kosambi mapping function.