DIALLEL ANALYSIS FOR GRAIN YIELD AND RESISTANCE TO DOWNY MILDEW DISEASE IN MAIZE

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ABSTRACT

Sorghum downy mildew (SDM) is a damaging disease of sorghum and maize crops and considered to be highly important in terms of their geographical distribution and potential ability to cause significant yield reduction. Half-diallel matting system among 9 yellow inbred lines was done at Sakha Station during summer 2008. Combining abilities of the resulting 36 F_1's were estimated for grain yield and yield components across three locations (Sakha, Sids and Mallawy) in 2009 growing season. Furthermore, the same 36 F_1's were tested at Sakha Research Station in the field of downy mildew disease nursery in 2009 season to study the mode of gene effect which controls the resistance of downy mildew disease. Both additive and non-additive gene effects played an important role in the inheritance of all studied traits. However, the additive type of gene effect was predominant and of higher magnitude than non-additive gene effect for all studied traits. On the other side, the additive type of gene effects was more interacted and sensitive to change of environmental conditions for all studied traits than non-additive gene effects except for PH. Inbred lines Gz653 and Sk6001 were identified as good general combiners for yielding ability, prolificacy and resistance to SDM disease. Crosses Sk5008 × Sk6001 and Sk5008 × Sk6154 showed significant positive SCA effects for grain yield and positive effects for RSLM. Moreover, 4 single crosses (Sk9215 × Gz653, Sk10 × Gz653, Gz653 × Sk6001 and Gz653 × Sk5027) increased (but not significantly) in grain yield than the two checks and had high resistance to downy mildew disease, indicating that these promising single crosses could be considered valuable in the future maize program for high yielding ability with resistance to this disease.

Key words: *Maize, Grain yield, Downy mildew resistance, Gene action.*

INTRODUCTION

Breeding for high yielding ability and resistance to main diseases especially downy mildew disease are considered among the main targets of national maize breeding program to minimize the application of fungicides in view of the possible environmental hazards and that chemical disease control in maize is very difficult with high susceptible varieties. Whereas, among the various pathogens affecting maize (*Zea mays* L.) production and productivity worldwide, the downy mildews are considered to be highly important in terms of their geographical distribution and potential ability to cause significant yield reductions. Sorghum downy mildew (SDM) caused by *Peronosclerospora sorghi* [(Weston & Uppal) C.G. Shaw] is a destructive disease of sorghum and maize, and can cause severe yield loss (Williams, 1984). In Egypt, SDM has been considered as a major disease of

maize, where sorghum is grown as a forage crop (Nazim *et al* 1995). Germplasm less than 5 percent infection may be considered highly resistant; 5-10% as resistant; 10-20% as moderately resistant; 20-30% moderately susceptible and more than 30% as susceptible to highly susceptible (Gowda *et al* 1989).

Carangal *et al* (1970), Jinahyon (1973), Kaneko and Aday (1980), El-Shenawy (1995), Motawei and Ebrahim (2005) and Nair *et al* (2005) found that the resistance to sorghum downy mildew is controlled mainly by additive genetic effect. While, El-Shenawy *et al* (2005) and Mosa *et al* (2009) reported that the non-additive type of gene effect was more important in controlling the behavior of resistance to downy mildew disease than additive type of gene effect. Moreover, Mochizuki *et al* (1974), Frederiksen and Ullstrup (1975), Yamada and Aday (1977) and Singburaudom and Renfro (1982) concluded that the resistance to downy mildew was controlled by dominant gene effect and that level of dominance was in the range of partial to over-dominance. On the other hand, numerous investigators among of them Zhang *et al* (2000), Kalla *et al* (2001), Wu *et al* (2003), Yu *et al* (2003) and Mosa (2010) for days to mid-silk, plant height, ear position%, ear length, rows/ear and grain yield; El-Hosary (1988), Farshadfar *et al* (2002) and Motawei (2005) for no. of ears/100 plant reported that both additive and non-additive gene effects played an important role in the inheritance of these traits however, the additive type predominated and had higher magnitude than the non-additive gene effect.

The main target of this investigation was to study the mode of gene effect controlling resistance to SDM, grain yield and their related traits and to identify the best hybrid combinations which characterizes by high SDM resistance and yielding ability.

MATERIALS AND METHODS

Nine elite inbred lines of yellow maize (Sk10, Sk9215, Gz653, Sk5008, Sk5026, Sk5027, Sk6001, Sk6054 and Sk7078) were crossed in a 9×9 half-diallel mating system at Sakha Station in the 2008 growing season. In the next season, 36 F_1 single crosses along with two checks (SC162 and SC166) were evaluated at three locations (Sakha, Sids and Mallawy). A randomized complete block design (RCBD) with 4 replications was used. Plot size was 1 row, 6 m long, 80 cm width and 25cm between hills. Cultural practices were done as recommended. The following traits were recorded: no. of days to mid-silk (DS), plant height (PH) in cm, ear position% (EP%), no. of ears/100 plant (E/100PL), ear length (EL) in cm, no. of rows/ear (R/E), no. of kernels/row (K/R) and grain yield (GY) ard/fed (corrected at 15.5% grain moisture content). Furthermore, the same 36 F_1 hybrids along with the checks SC162 and SC166 were evaluated under three levels of nitrogen fertilizer i.e. 60, 120, and 180 kg N/fed (separate

experiments) in the disease nursery o: downy mildew disease at Sakha Station during July 2009, which was previously planted by Sudan gras; as a source of infection with downy mild(w disease. Sudan grass was also planted alternatively with maize rows with a ratio of 1: 3, respectively. This experiment was arranged in RCBD with four replications. The plot size was one row, 2 m long, 80 cm width and 2(cm between hills. Two seeds were sown per each hill and left without thinr ing. Each level of nitrogen fertilizer was divided into two parts where, the first dose was added before sowing irrigation as activating dose and the otl er dose was supplemented with the first irrigation i.e. after 21 days from sowing. The inoculated plants were recorded after 35 days from planting date and adjusted into percentage of resistance to downy mildew (RSDM%). The data were transformed by using arcsine scale according to Snedecor and Cochran (1980).

Combined analysis across the three locations for grain yield and its related traits and across three nitrogen levels for RSDM% was done after testing the homogeneity of error mean squares. Method 4, Model-1 (fixed model) according to Griffing (1956) was applied for combining ability analysis.

RESULTS AND DISCUSSION

Combined analysis of variance for grain yield and its related traits across three locations (Sakha, Sids and Mallawy) is shown in Table (1). Highly significant differences were detected among locations (L) for all studied traits except for R/E, meaning that markedly variation was observed among the three locations Sakha, Sids and Mallawy. Mean squares due to genotypes (G), F_1 crosses (C) and their interactions by locations were significant for all studied traits. While, mean squares due to checks (CH), C vs. CH and their interaction by locations were significant only for CH of PH, C vs. CH of DS and R/E and C vs. CH × L of PH, EP%, E/100PL, EL and K/R.

Table 1. Analysis of variance of 36 F_1 and two checks for grain yield
and its related traits across three locations.

SOV	df	Mean squares							
		DS	PH	EP%	E/100PL	EL	R/E	K/R	GY
Locations (L)	2	4409.76**	315761.6**	2868.91**	15155.11**	334.06*	72.26	567.53**	14903.62**
R/L	9	9.02**	468.32	19.51	48.11	55.27	29.11	58.66	135.22
Genotypes(G)	37	46.42**	1571.95**	57.55**	1426.13**	22.45**	6.56**	49.848**	147.07**
F₁Crosses(C)	35	40.56**	1451.72**	50.56**	1506.86**	16.123**	6.096**	40.196**	150.40**
Checks(CH)	1	6.000**	4004.17*	4.312	20.499	19.44	2.667	19.44	15.53
C vs. CH	1	291.94**	3347.8	355.33	6.211	246.91	26.62*	418.08	162.06
G × L	74	4.48**	178.74*	15.094**	318.36**	3.48**	2.217**	9.674*	29.10**
C × L	70	4.49**	169.73*	14.691**	322.10**	2.897**	2.309**	9.211*	29.11**
CH × L	2	7.13	74.04	0.891	31.51	0.155	0.542	12.62	26.56
C vs.CH× L	2	1.48	598.79*	43.402**	474.31*	27.21**	0.672	22.933*	31.29
Error	333	2.71	130.16	8.33	122.73	1.60	1.522	7.034	13.18
C.V%		2.58	4.69	5.29	10.08	6.50	8.02	6.42	12.57

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

41

Highly significant mean squares due to nitrogen levels (N) were found (Table 2), indicating that the mean of resistance to downy mildew disease was affected by nitrogen levels, whereas the optimum nitrogen dose (120kg N/fed) exhibited the highest value (95.5%) followed by low level (60 kg N/fed) 92.5% and high level (180 kg N/fed) 90.9% (not shown). Furthermore, mean squares due to genotypes (G), crosses (C) and their interactions with nitrogen levels showed highly significant differences. Also, C vs. CH mean squares were found significant.

Table 2. Analysis of variance for resistance to SDM% over three levels of nitrogen fertilizer.

SOV	df	Mean squares (RSDM%)
Nitrogen levels (N)	2	808.977**
Rep/N	9	62.93
Genotypes (G)	37	893.395**
F1 Crosses (C)	35	897.35**
Checks (CH)	1	12.47
C vs. CH	1	1635.89*
G × N	74	134.513**
C × N	70	137.79**
CH × N	2	88.60
C vs. CH × N	2	65.73
Error	333	73.899
C.V%		10.8

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

General and specific combining ability (GCA and SCA) mean squares and their interactions with locations for grain yield and its components are presented in Table (3). All traits under study exhibited highly significant GCA and SCA mean squares except for SCA of EP%, indicating that both additive and non-additive gene effects contributed in the inheritance of these traits with the additive type of gene effects being predominant and of higher magnitude than non-additive gene effects for all studied traits, where the ratio of GCA/SCA mean squares increased than the unity (Table 3). Many investigators reported that both additive and non-additive gene effects contributed to the expression of grain yield and its components but the additive effect played an important role; among of them Zhang *et al* (2000), Kalla *et al* (2001), Wu *et al* (2003), Yu *et al* (2003) and Mosa (2010) for days to mid-silk, plant height, ear position%, ear length, rows/ear and grain yield; El-Hosary (1988), Farshadfar *et al* (2002) and Motawei (2005) for no. of ears/100 plant.

Table 3. General and specific combining ability mean squares and their interaction with locations for grain yield and its components.

SOV	df	Mean squares							
		DS	PH	EP%	1/100PL	EL	R/E	K/R	GY
GCA	8	162.23**	4927.95**	181.922**	4419.54**	43.695**	11.46**	86.25**	355.06**
SCA	27	4.51**	421.73**	11.638	143.84**	7.953**	4.507**	26.55**	89.76**
GCA×L	16	11.29**	112.92	31.57**	44.10**	6.682**	3.640**	15.07**	41.77**
SCA×L	54	2.49	186.56*	9.690	97.07**	1.776	1.915	7.48	25.36**
Error	333	2.71	130.16	8.33	122.73	1.60	1.522	7.034	13.18
GCA / SCA		35.96	11.69	15.63	6.86	5.49	2.54	3.25	3.96
GCA×L/SCA×L		4.53	0.61	3.26	3.78	3.76	1.90	2.02	1.65

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

Regarding the interactions of GCA and SCA by locations (Table 3), the results revealed that highly significant GCA × L interaction was obtained for all studied traits except of PH. Meanwhile, mean squares due to SCA × L interaction were significant only for PH, E/100PL and GY traits. The results also showed that additive type of gene effect was more sensitive to change of environmental conditions than that of non-additive gene effect (ratio of GCA × L / SCA × L exceeded unity) for all studied traits except of PH (Table 3). As similar trend was reported by Mosa 2003 and Motawei 2005 for grain yield, rows/ear and plant height and El-Shenawy 2005 and Motawei 2006 for ear length and no. of ears/100 plant.

In relation to GCA and SCA mean squares and their interactions with nitrogen fertilizers for resistance to SDM (Table 4), highly significant mean squares were detected due to both the two types of gene effects (GCA and SCA) and their interactions by nitrogen levels. This means that the two types of gene effects operated but the additive type represented the effective portion in the inheritance of resistance to this disease. However, the additive type of gene effects was more influenced by nitrogen levels than non-additive type. Kaneko and Aday (1980), El-Shenawy (1995), Yen *et al* (2001), Nair *et al* (2005), and Motawei and Ebrahim (2005) reported that the additive gene effects played an important role in the inheritance of resistance to downy mildew disease.

Table 4. General and specific combining ability mean squares and their interactions with nitrogen fertilizer for resistance to SDM%.

SOV	df	Mean squares (RSDM%)
GCA	8	2674.11**
SCA	27	370.90**
GCA × N	16	214.749**
SCA × N	54	114.982*
Error	333	73.899
GCA / SCA		7.21
GCA × L / SCA × L		1.87

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

Mean performance of grain yield and its related traits across three locations and resistance to SDM% across three levels of nitrogen fertilizer is presented in Table (5). Means of DS ranged from 60.9 (Sk5008 × Sk7078) to 67.5 days (Sk9215 × Gz653) with an average 63.9 days. Moreover, 28 out of 36 F_1s were earlier than the two checks. Plant height means ranged from 222.4 cm (Sk9215 × Sk6054) to 265.5 cm (Gz653 × Sk5026) with an average of 243.1 cm. Six F_1 crosses were shorter than the short check (SC166) as well as SC162. Ear position % ranged from 48.2% (Sk10 × Sk7078) to 55.5% (Gz653 × Sk5027) with an average of 54.6%. All F_1 crosses had better ear position than the best check SC166. Ears/100 plants ranged from 94.8 ears (Sk5008 × Sk7078) to 137.9 ears (Sk9215 × Gz653) with an average of 110 ears/100 plant. Four single crosses i.e. Sk9215 × Gz653, Sk9215 × Sk6001, Sk6001 × Sk6054 and Sk9215 × Sk5026 increased significantly in number of ears/100 plant from the best check SC166 and surpassed it by 27, 22.8, 22.7 and 18.6 ears/100 plant, respectively.

With respect of means of grain yield and its components, ear length ranged from 17.48 to 22.31cm; rows/ear from 14.0 to 16.9 row; kernels/row from 37.5 to 45.3 kernel and grain yield from 17.94 to 34.2 ard/fed. Eleven out of 36 F_1's increased significantly than the best check SC166 toward increase of rows/ear. However, 5 F_1's [Sk9215 × Gz653 (34.20 ard/fed), G653 × Sk5026 (33.66 ard/fed), Sk10 × Gz653 (32.71 ard/fed), Gz653 × Sk6001 (32.59 ard/fed) and Gz653 × Sk5027 (32.56 ard/fed)] increased in grain yield but with no significant differences from the two checks.

Means of resistance to SDM ranged from 61.1% (Sk5027 × Sk7078) to 99.4% (Sk5008 × Sk5054) with an average of 92.9%. As outlined of Gowda et al (1989) scale, we could classify the genotypes into four classes i.e. 18 F_1's and the two checks showed high resistance (HR); 12 resistance (R); 4 moderately resistance (MR) and only two F_1's were susceptible (S). In general, these results indicated that 4 F's resulting from crossing the inbred line Gz653 with each of Sk10, Sk5027, Sk6001 and Sk9215 increased grain yield over the two checks and had high resistance to downy mildew disease. Therefore, these promising single crosses could be considered as valuable genotypes in future maize breeding program to realize high yielding hybrids and resistance to downy mildew disease

Estimates of GCA effects of nine parental lines for grain yield, its related traits and RSDM% are presented in Table (6). Inbred lines Sk10 and Sk7078 were good general combiners towards earliness, short plant and of ideal ear position. While, inbred lines Gz653 and Sk5026 had favorable alleles and were good combiners for grain yield and most yield components (no. of ears/100plant, ear length and no. of kernels/row). On the other hand, the inbred line Sk6001 was characterized as good general combiner for ears

44

Table 5. Mean performance of 36 F_1's and two checks for grain yield and its related traits across three locations and resistance to SDM% across three levels of nitrogen fertilizer.

Genotypes	DS	PH (cm)	EP%	E/100 plant	EL (cm)	R/E	K/R	GY (ard/fed)	RSDM%
Sk10 ×Sk9215	63.3	232.7	52.3	106.7	19.43	15.1	40.8	30.82	97.1
Sk10 × Gz653	65.08	259.5	50.9	107.0	22.31	14.6	44.6	32.71	98.2
Sk10 × Sk5008	61.3	226.9	49.9	98.1	17.48	14.0	37.5	17.94	92.3
Sk10 × Sk5026	62.0	249.0	49.7	111.4	20.65	15.3	41.8	30.48	90.1
Sk10 × Sk5027	63.2	239.8	51.3	101.2	19.83	16.0	40.0	26.19	90.0
Sk10 × Sk6001	62.8	240.7	51.4	106.4	18.80	15.4	41.0	31.56	98.4
Sk10 × sk6054	62.3	246.1	50.0	102.1	20.01	16.9	42.8	28.65	97.6
Sk10 × Sk7078	62.1	230.3	48.2	100.4	18.28	15.6	39.7	25.77	96.2
Sk9215×Gz653	67.5	256.7	53.0	137.5	20.83	14.8	41.9	34.20	98.6
Sk9215×Sk5008	61.9	238.7	54.2	102.8	19.30	15.7	40.4	28.08	97.4
Sk9215×Sk5026	63.7	240.6	53.5	129.4	18.48	13.9	40.3	31.08	90.6
Sk9215×Sk5027	65.0	229.6	55.3	105.4	19.26	15.8	40.4	30.38	92.5
Sk9215×Sk6001	64.6	239.6	54.4	133.7	18.40	15.0	39.8	29.90	97.7
Sk9215×Sk6054	64.9	222.4	53.6	110.0	17.56	16.0	39.4	26.29	98.8
Sk9215×Sk7078	63.3	243.5	49.9	98.8	19.80	15.2	43.7	27.76	94.8
Gz653×Sk5008	63.2	247.8	55.3	119.8	18.61	15.0	38.0	27.84	92.8
Gz653×Sk5026	65.5	265.5	53.8	121.2	21.13	14.7	44.2	33.66	92.9
Gz653×Sk5027	67.4	262.5	55.5	105.4	20.96	15.0	42.5	32.56	96.6
Gz653× Sk6001	66.4	258.6	52.5	116.2	19.31	14.9	40.8	32.59	98.9
Gz653× Sk6054	67.2	258.8	52.9	111.9	19.25	15.6	41.6	29.41	97.3
Gz653× Sk7078	65.9	254.3	51.4	100.8	21.31	16.2	45.3	31.90	88.9
Sk5008×Sk5026	61.2	255.0	51.4	98.6	19.70	14.4	40.2	28.96	91.0
Sk5008×Sk5027	62.0	231.7	55.1	106.2	19.23	15.7	41.5	26.60	86.0
Sk5008×Sk6001	61.2	239.1	54.0	116.7	18.30	15.4	39.4	31.86	98.0
Sk5008×sk6054	62.6	238.7	50.2	104.7	18.35	16.5	40.2	31.49	99.4
Sk5008×Sk7078	60.9	232.8	50.9	94.8	17.56	15.0	38.5	23.60	94.4
Sk5026×Sk5027	63.9	250.0	52.4	107.6	20.00	14.9	41.7	27.50	62.4
Sk5026×Sk6001	62.7	242.3	52.4	122.0	18.83	14.7	41.5	30.20	95.5
Sk5026×sk6054	64.0	241.2	50.2	110.5	18.76	16.1	41.0	27.29	83.9
Sk5026×Sk7078	63.0	245.9	50.3	99.2	20.85	14.9	44.3	30.53	84.9
Sk5027×Sk6001	63.8	240.7	55.2	123.4	19.13	15.4	40.5	28.46	91.8
Sk5027×Sk6054	66.4	229.3	55.2	99.6	18.30	16.2	39.1	20.60	97.8
Sk5027×Sk7078	62.7	235.4	52.5	101.4	18.81	16.0	40.2	25.87	61.1
Sk6001×Sk6054	62.5	238.2	54.1	133.6	17.58	16.2	39.5	29.51	98.8
Sk6001×Sk7078	62.1	229.5	51.1	107.0	18.83	15.3	40.9	29.03	94.6
Sk6054×Sk7078	63.0	233.1	49.1	101.2	19.06	16.7	43.0	23.14	96.7
Check SC 162	67.7	267.5	55.8	109.7	23.48	14.0	46.2	30.44	98.5
Check SC 166	66.7	241.6	56.7	110.9	21.68	14.6	44.4	32.27	99.2
LSD 0.05	1.70	3.10	3.10	14.40	1.50	1.20	2.51	4.36	9.38
LSD 0.01	2.30	4.2	4.2	19.10	1.99	1.59	3.33	5.77	12.41

45

Table 6. General combining ability effects of 9 inbred lines for grain yield, its components and RSDM% traits across different environments.

Inbred		DS	PH	EP%	E/100PL	EL	R/E	K/R	GY	RSDM%
Sk10		-1.000*	-2.225*	-2.131**	-6.362*	0.358	-0.032	-0.026	-0.821	2.899**
Sk9215		0.750	-5.073**	1.096	6.640*	-1.175**	-0.244	-0.252	1.233	4.354**
Gz653		2.738	17.784**	0.967	6.002*	1.348**	-0.327	1.491**	3.573**	3.700**
Sk5008		-2.095**	-4.073**	0.372	-5.194	-0.823**	-0.196	-1.816**	-1.929*	0.289
Sk5026		-0.441	7.189**	-0.672	3.056	0.587*	-0.606**	0.927*	1.409*	-8.11**
Sk5027		0.774*	-2.882*	2.037**	-4.093	0.177	0.266	-0.369	-1.674*	-8.408**
Sk6001		-0.417	-1.513	0.981	11.45**	-0.730*	-0.129	-0.719	1.892*	5.061**
Sk6054		0.548	-4.489**	-0.478	-0.656	0.032	1.002**	-0.261	-1.926**	5.181**
Sk7078		-0.857*	-4.918**	-2.172**	-10.713**	0.564	0.266	1.024*	-1.752*	-4.968**
LSD g_i	0.05	0.733	2.317	1.225	5.949	0.776	0.416	0.847	1.409	1.875
	0.01	1.009	3.236	1.688	8.153	0.845	0.573	1.166	1.941	2.582
LSD g_i-g_j	0.05	1.099	3.476	1.838	8.923	1.165	0.624	1.269	2.114	2.812
	0.01	1.514	4.788	2.531	12.290	1.605	0.859	1.749	2.911	3.873

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

/100PL and GY traits. Five inbred lines (Sk10, Sk9215, Sk6001, Gz653 and Sk6054) were identified as good general combiners toward resistance to SDM disease. These results revealed that inbred lines Gz653 and Sk6001 would be very useful in future maize breeding programs as good combiners for yielding ability, prolificacy and resistance to SDM disease.

Estimates of SCA effects of 36 F_1's for all studied traits are presented in Table (7). Single crosses Sk10 × Sk6054, Gz653 × Sk5008, Sk5027 × Sk7078 and Sk6001 × Sk6054 for days to mid-silk; Sk10 × Sk5008 and Sk9215 × Sk6054 for plant height and Sk653 × Sk6001 and Sk5008 × Sk6054 for ear position% exhibited significant negative values of SCA effects toward earliness, short plant and good ear position, respectively. On the other side, five single crosses (Sk10 × Sk7078, Sk9215 × Gz653, Sk9215 × Sk5056, Gz653 × Sk5008, and Sk6001 × Sk6054) exhibited positive and significant estimates of SCA effects toward prolificacy.

With respect of SCA effects for grain yield, EL, R/E and K/R traits (Table 7), the best single crosses which had positive and significant estimates of SCA effects were achieved by Sk10 × Gz653, Sk10 × Sk6054, Sk9215 × Sk5008 and Sk5026 × Sk7078 for EL; Sk9215 × Sk5008, Gz653 × Sk7078 for R/E; Sk10 × Gz653, Sk10 × Sk6054, Sk9215 × Sk7078, Gz653 × Sk7078 and Sk5008 × Sk5027 for K/R and Sk10 × Sk6054, Sk5008 × Sk6001 and Sk5008 × Sk6054 for GY. These results revealed that Sk10 × Sk6054 had favorable estimates for earliness, EL, K/R and GY followed by Sk5008 × Sk6054 for good ear position and high yielding ability. Moreover, estimates of SCA effects for RSDM% trait helped to identify the crosses Sk10 × Sk7078, Gz653 × Sk5026, Gz653 × Sk5027 and Sk5027 × Sk6054 that have significant positive SCA effects (favorable) for resistance to SDM disease.

46

Table7. Specific combining ability effects of 36 F₁'s for 9 studied traits of 36 single crosses across environments.

Crosses		DS	PH	EP%	E.100 plant	EL	R/E	K/R	GY	RSDM%
Sk10×Sk9215		-0.083	-2.60	1.01	-1.4	-0.04	-0.06	0.07	1.68	-2.09
Sk10×Gz653		-0.321	1.38	-0.28	-1.94	1.32**	-0.46	2.09**	1.23	1.73
Sk10×Sk5008		0.762	-9.43**	-0.60	-0.08	-1.34**	-1.15**	-1.69*	-8.05**	-5.44*
Sk10×Sk5026		-0.226	1.47	0.17	4.82	0.42	0.57	-0.15	1.17	1.32
Sk10×Sk5027		-0.190	2.29	-0.95	1.95	0.010	0.37	-0.67	-0.05	2.08
Sk10×Sk6001		0.583	1.84	0.21	-8.37*	-0.12	0.18	0.699	1.75	-0.85
Sk10×Sk6054		-0.881*	10.23**	0.31	-4.74	1.14**	0.53	1.99**	2.67*	-3.13
Sk10×Sk7078		0.357	-5.17	0.13	7.77*	-1.40**	0.02	-2.34**	-0.39	6.38**
Sk9215×Gz653		0.429	1.59	-1.33	15.39**	0.37	0.01	-0.42	0.66	0.57
Sk9215×Sk5008		-0.405	5.45	0.36	-8.37*	1.01**	0.72*	1.37	0.04	1.34
Sk9215×Sk5026		-0.226	-3.90	0.79	9.52**	-1.22**	-0.67	-1.45*	-0.29	-1.15
Sk9215×Sk5027		-0.107	-4.83	-0.20	-7.02	-0.02	0.35	-0.06	2.09	2.35
Sk9215×Sk6001		0.667	3.64	0.04	5.70	0.02	0.01	-0.26	-1.96	-2.40
Sk9215×Sk6054		-0.048	-10.47**	0.64	-5.24	-0.77*	-0.14	-1.10	-1.75	-0.71
Sk9215×Sk7078		-0.226	11.13**	-1.32	-4.97	0.66	-0.22	1.85**	-0.45	2.08
Gz653×Sk5008		-1.060**	-8.33*	1.66*	9.23*	-1.20**	0.17	-2.70**	-2.54*	-6.51
Gz653×Sk5026		-0.381	-1.92	1.18	2.35	-0.09	0.25	0.69	-0.05	4.99*
Gz653×Sk5027		0.238	5.23	0.20	-4.39	0.15	-0.32	0.300	1.93	9.26**
Gz653×Sk6001		0.429	-0.05	-1.73*	-11.04**	-0.59	-0.03	-1.00	-1.60	0.07
Gz653×Sk6054		0.298	3.09	0.06	-3.26	-0.61	-0.51	-0.71	-0.97	-3.51
Gz653×Sk7078		0.369	-0.98	0.24	-4.35	0.65	0.88*	1.76*	1.34	-6.60**
Sk5008×Sk5026		0.119	9.52**	-0.58	-8.98*	0.65	-0.18	0.01	0.75	3.75
Sk5008×Sk5027		-0.262	-3.74	0.40	5.79	0.59	0.27	2.66**	1.47	-2.64
Sk5008×Sk6001		0.095	2.30	0.33	0.64	0.56	0.29	0.84	3.16*	1.30
Sk5008×Sk6054		0.548	4.86	-1.97*	0.78	0.66	0.30	1.23	6.62**	3.92
Sk5008×Sk7078		0.202	-0.63	0.40	0.98	-0.93*	-0.42	-1.72*	-1.45	4.28
Sk5026×Sk5027		-0.083	3.33	-1.24	-1.16	-0.05	-0.16	0.08	-0.96	-7.85**
Sk5026×Sk6001		-0.060	-5.79	-0.17	-7.29	-0.31	0.003	0.25	-1.83	3.34
Sk5026×Sk6054		0.226	-3.90	-0.99	-1.71	-0.34	0.36	-0.73	-0.93	-8.01
Sk5026×Sk7078		0.631	1.20	0.84	-2.95	0.94**	-0.18	1.30	2.14	3.60
Sk5027×Sk6001		-0.190	2.70	0.13	6.08	0.40	-0.14	0.53	-0.49	-0.03
Sk5027×Sk6054		1.429**	-5.74	1.33	-4.54	-0.39	-0.47	-1.30	-4.53**	10.36**
Sk5027×Sk7078		-0.833*	0.77	0.33	6.31	-0.68*	0.10	-1.54*	0.56	-13.54**
Sk6001×Sk6054		-1.298**	1.80	1.23	12.00**	-0.20	-0.10	-0.57	0.81	-2.07
Sk6001×Sk7078		-0.226	-6.43	-0.04	-3.61	0.24	-0.22	-0.49	0.16	0.64
Sk6054×Sk7078		-0.274	0.13	-0.59	2.82	0.52	0.03	1.18	-1.91	3.15
LSD S₁ⱼ	0.05	0.796	6.898	1.572	7.09	0.672	0.698	1.381	2.543	4.341
	0.01	1.061	9.185	2.093	9.44	0.896	0.930	1.839	3.386	5.781
LSD S₁ⱼ -S₁ₖ	0.05	1.205	10.428	2.377	10.718	1.017	1.056	2.07	3.845	6.563
	0.01	1.604	13.887	3.165	14.272	1.355	1.407	2.781	5.120	8.740
LSD S₁ⱼ -S₁ₗ	0.05	1.099	9.520	2.169	9.784	0.928	0.964	1.906	3.509	5.991
	0.01	1.465	12.677	2.889	13.03	1.237	1.284	2.538	4.674	7.979

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

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تحليل الهجن التبادلية لمحصول الحبوب ومقاومة مرض البياض الزغبى

فى اذرة الشامية

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يعتبر مرض البياض الزغبى ذو اهمية كبيرة من حيث انتشاره الجغرافى الواسع وقدرتة الكبيرة على احداث خسارة ونقص معنوى لمحصولى الذرة الشامية والذرة الرفيعة.

تم عمل ثهجن التبادلية فى اتجاه واحد بين تسعة سلالات مختلفة من الذرة الشامية الصفراء بمحطة البحوث الزراعية بسخا خلال صيف ٢٠٠٨.

تم تقييم الـ ٣٦ هجين فردى الناتجة للذرة للعلمة والخاصة على التآلف لصفات المحصول ومكوناتة تحت ثلاثة بيئات مختلفة هى سخا – سدس – ملوى خلال موسم نمو ٢٠٠٩. وتم اختبار نفس الـ ٣٦ هجين فردى بحقل العدوى لمرض البياض الزغبى بمحطة بحوث سخا لدراسة نوع الفعل الجينى المتحكم فى صفة المقاومة لهذا المرض ويمكن تلخيص أهم للنتائج فيما يلى:-

١- لعب الفعل الجينى المضيف والغير مضيف دورا هاما فى وراثة كل الصفات المدروسة ومع ذلك أظهر الفعل الورائى المضيف اهمية اعلى من الفعل الورائى غير المضيف فى وراثة كل الصفات المدروسة. ومن ناحية اخرى اشارت النتائج ان الفعل الورائى المضيف كان اكثر تأثراً وحساسية للتغيرات فى الظروف البيئية عن الفعل الورائى الغير مضيف لكل الصفات المدروسة.

٢- أظهرت السلالتين جيزة ٦٥٣ وسخا ٦٠٠١ قدرة عامة جيدة على التآلف للقدرة المحصولية وتعدد الكيزان و مقاومة مرض البياض الزغبى بينما اظهر الهجينان الفرديان (سخا ٥٠٠٨ × سخا ٦٠٠١) و(سخا ٥٠٠٨ × سخا ٦٠٥٤) قدرة خاصة على التآلف موجبة ومعنوية لصفة المحصول وكذلك قيم موجبة فى اتجاه المقاومة لمرض البياض الزغبى.

٣- أظهرت أربعة هجن فردية وهى سخا ٩٢١٥ × جيزة ٦٥٣، سخا ١٠ × جيزة ٦٥٣، جيزة ٦٥٣ × سخا ٦٠٠١، جيزة ٦٥٣ × سخا ٥٠٢٧ زياده غير معنوية فى صفة محصول الحبوب عن هجينى المقارنة وكذلك تميزوا بالمقاومة العالية لمرض البياض الزغبى مما يشير الى أن هذه الهجن الجديدة ستكون قيمة ذات قيمة فى برنامج تربية الذرة الشامية للمحصول العالى والمقاومة لمرض البياض الزغبى.