

## DIALLEL CROSS ANALYSIS FOR EARLINESS, YIELD, ITS COMPONENTS AND RESISTANCE TO LATE WILT IN MAIZE

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### ABSTRACT

A half diallel set of crosses involved eight yellow maize inbred lines were evaluated in normal and artificial infection by late wilt environments at the Agricultural Research and Experiment Center, Faculty of Agriculture, Benha University, Egypt. To estimate combining ability, improve productivity of maize and resistant to late wilt in Egypt. Mean squares of environments, genotypes and its fractions as well as general and specific combining abilities (GCA and SCA) reached the significance level of probability for all traits. High GCA/SCA ratios exceeded than unity were obtained for days to 50% silking and resistance to late wilt% in artificial infection environment and across environments. For remain cases, non-additive type of gene action seemed to be more prevalent. Ten crosses in both and across experiments, gave significant superiority over SC 168. The useful superiority over SC 168 ranged from 10.02 to 33.59 %. Two crosses  $P_1 \times P_2$  and  $P_2 \times P_3$  in both and across experiments had significant superiority over the best check hybrid Hytech 2055 by 14.68 and 15.49% in the combined analysis. The parental inbred line  $P_2$  exhibited the most accurate general combiner for earliness and grain yield plant<sup>-1</sup>. The cross  $P_2 \times P_3$  was contain most desirable inter and intra-allelic interactions for most traits.

**KEYWORDS:** Combining Ability, Diallel Analysis, Yellow Maize, Resistant to Late Wilt

**Received:** Nov 05, 2015; **Accepted:** Nov 14, 2015; **Published:** Nov 19, 2015; **Paper Id.:** IJASRDEC201527

### INTRODUCTION

Great efforts are devoted to increase maize productivity with a high resistance to disease and pests. Several diseases attack maize fields. One of the most destructive diseases in maize growing areas in lower and Upper Egypt is late wilt. It is caused by fungi called *Cephalosporium maydis*. The degree of lose may be up to 80% in fields. Late wilt disease is wide spread and serious. Therefore, breeding new resistance hybrids is practical, inexpensive and effective for controlling this disease.

Several methods are available to study the inheritance yield productivity and disease resistance. One of the common use in this respect is the diallel cross methodology for its power and versatility. Different approaches to the diallel analysis for estimating certain genetic parameters in terms of gene models have been developed. Total genetic variation is portioned into the effects of general (GCA) and specific (SCA) combining ability. In this context, GCA is the average performance of an inbred line in hybrid combinations and as such it is primarily recognized as a measure of additive gene action. SCA indicates non-additive gene action and it desirable those instances in which certain hybrid combinations perform relatively desirable than would be expected on the mean performance of inbred lines involved (Sprague and Tatum 1942).

The objective of the present investigation is to evaluate eight maize inbred lines and their  $F_1$  hybrid

according to general and specific combining ability for earliness, grain yield, its components and resistance to late wilt disease.

## MATERIALS AND METHODS

Eight yellow maize inbred lines i.e. M-201(P<sub>1</sub>), M-202(P<sub>2</sub>), M-203(P<sub>3</sub>), M-204 (P<sub>4</sub>), M-241(P<sub>5</sub>), M-224(P<sub>6</sub>), M-228(P<sub>7</sub>) and M-524(P<sub>8</sub>) were sown in two different sowing dates (2<sup>nd</sup> and 12<sup>th</sup> May 2013) in order to make half diallel crosses by hand pollination giving a total of 28 hybrids.

In the 2013 season, two experiments were carried out. The first was a normal trial and the second involved artificial infection with late wilt disease. The inoculum was prepared by growing the fungus (*Cephalosporium maydis*) isolates in sterilized milk bottles containing wet cracked grain sorghum kept at room temperature for 45 days. The infection in the field was made according to **Shafshak et al. (1986)**. Each experiment contained 28 crosses and their parents along with single crosses SC 168 and Hytech 2055 (check hybrids) were grown in a randomized complete block design with three replications at the Agricultural Research and Experiment Center, Faculty of Agriculture, Benha University, Egypt. The sowing of the two experiments was on 6<sup>th</sup> June 2014. Each plot consisted of two ridges, 70-cm between ridges. The long of ridge was 6-m. Three kernels per hill were sown in one side of the ridge with 25-cm spacing between hills. Normal cultural practices were followed for maize growing in the area.

The traits studied were: days to 50% silking, plant height, resistance to late wilt disease% (percent of resistant plants in each plot following 105 days from sowing) according to **Sabet et al. (1961)**, number of kernels row<sup>-1</sup>, number of rows ear<sup>-1</sup>, 100-kernel weight and grain yield plant<sup>-1</sup> adjusted to 15.5% grain moisture. Fifteen guarded plants from each plot were randomly taken as samples tested for the previous traits except days to 50% silking where; the mean basis of plot was used.

Statistical analysis was done according to **Steel and Torri (1980)**. Relative superiority of grain yield was estimated for each cross as the percentage deviation of F<sub>1</sub> mean performance from check variety SC Hytech 2055 average value. Genetic analysis was done as described by **Griffing (1956)** for method 2 model 1. The combined analysis across the two experiments was carried out according to **(Gomez and Gomez, 1984)** whenever, homogeneity of error variance was found.

## RESULTS AND DISCUSSIONS

The results obtained from parental inbred lines and their F<sub>1</sub>'s for all traits studied in each and across, the two experiments were first subjected to an ordinary analysis of variance as presented in Table 1. The mean squares due to environments were significant for all studied traits except for days to 50% silking and No. of rows ear<sup>-1</sup>. These results are indicated that the plants generally remained symptomless until flowering stage. Also, the number of rows ear<sup>-1</sup> was formed in the ear before the flowering agrees with the findings of **Mostafa et al. (1996)**, **Vivek et al. (2010)** and **El-Gonemy (2015)**. Genotype mean squares were highly significant for all traits studied. Its fractions i.e. parents, crosses and parent vs crosses reached significant levels in most cases.

Appreciable genotypes by environment interaction were detected for all traits except for No. of rows ear<sup>-1</sup> and 100-kernel weight indicating that the genotypes behaved rather differently from normal environment to late wilt infection environment. For the exceptional traits, insignificant genotype by environment was detected revealing that the genotypes were suspected to environmental changes by nearly similar magnitudes. Insignificant interactions between parental inbred

lines and environments were detected in all traits except plant height. This may reveal the high repeatability of the parental inbred lines under different environments. Significant interaction between F1 hybrids and environment were detected for days to 50% silking, No of kernels row<sup>-1</sup>, late wilt resistance% and grain yield plant<sup>-1</sup>, indicating that these crosses behave differently from environment to another. Insignificant interactions occurred between parent vs hybrids and environment for all studied traits except for grain yield plant<sup>-1</sup> revealing that average of heterosis over all crosses was influence by environmental changes.

### Mean Performance and Superiority

The mean performances of tested the eight inbred lines and the 28 hybrids across environments for all traits as well as grain yield plant<sup>-1</sup> and resistance to late wilt % in normal and infection environment and across them and superiority over both checks (SC 168 and Hytech 2055) are presented in Tables (2 a and b). For days to 50% silking date, the inbred line No. 2 gave the earliest parents. However, inbred line P7 gave the lateness one. Days to 50% silking for crosses, ranged from 57.42 for cross P<sub>4</sub>xP<sub>8</sub> to 63.92 for cross P<sub>3</sub>xP<sub>6</sub> while all crosses were earliest than both check hybrids. For plant height (cm), means ranged from 248.75 for cross P<sub>4</sub>xP<sub>6</sub> to 290.54 for cross P<sub>3</sub>xP<sub>5</sub>. The results indicate that most crosses were shorter than the two check hybrids, for No of rows ear<sup>-1</sup>, means ranged from 8.9 for P<sub>2</sub> to 14.55 for P<sub>6</sub>, while, ranged from 11.93 for cross P<sub>5</sub>xP<sub>6</sub> to 15.47 for cross P<sub>1</sub>xP<sub>6</sub>. Most crosses gave higher No. of rows ear<sup>-1</sup> compared with the two check hybrids. The parental inbred lines P7 gave the lowest number of kernels row<sup>-1</sup>. However, the parent inbred line P<sub>1</sub> gave the highest one for this trait. The two crosses P<sub>1</sub>xP<sub>2</sub> and P<sub>1</sub>xP<sub>3</sub> gave the highest number of kernels row<sup>-1</sup> and significant differences from two check hybrids. However cross P<sub>4</sub>xP<sub>5</sub> gave the lowest ones, but without significant difference from check hybrids. The inbred lines P<sub>1</sub> and P<sub>5</sub> recorded heavier 100-kernel weight. On the other hand, the parental inbred line P<sub>7</sub> gave the lowest one for this trait. For the 100-kernel weight (g) means of crosses ranged from 31.0 for P<sub>1</sub>xP<sub>6</sub> to 45.67 for cross P<sub>2</sub>xP<sub>3</sub>. For resistance to late wilt disease, means ranged from 76.67 for cross P<sub>6</sub>xP<sub>8</sub> to 100.00 for P<sub>1</sub>, P<sub>5</sub>, P<sub>2</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>6</sub>, P<sub>3</sub>xP<sub>8</sub>, P<sub>5</sub>xP<sub>6</sub>, P<sub>5</sub>xP<sub>7</sub> and P<sub>5</sub>xP<sub>8</sub> at normal condition, Means ranged from 58.33 for P<sub>3</sub> to 100% for P<sub>1</sub>, P<sub>5</sub>, P<sub>1</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>6</sub>, P<sub>5</sub>xP<sub>7</sub> at infection trial. However, means ranged from 68.33 for P<sub>3</sub> to 100% for P<sub>1</sub>, P<sub>5</sub>, P<sub>1</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>6</sub> and P<sub>5</sub>xP<sub>7</sub> in the combined analysis.

For grain yield plant<sup>-1</sup>, the two crosses P<sub>1</sub>xP<sub>2</sub> and P<sub>2</sub>xP<sub>3</sub> in both experiments as well as the combined analysis had significant superiority over the best check hybrid Hytech 2055 by 14.68 and 15.49% in the combined analysis.

The ten crosses of P<sub>1</sub>xP<sub>2</sub>, P<sub>1</sub>xP<sub>3</sub>, P<sub>1</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>3</sub>, P<sub>2</sub>xP<sub>5</sub>, P<sub>3</sub>xP<sub>8</sub>, P<sub>4</sub>xP<sub>6</sub>, P<sub>4</sub>xP<sub>7</sub>, P<sub>4</sub>xP<sub>8</sub> and P<sub>5</sub>xP<sub>7</sub>, in both and across experiments and the combined analysis, gave significant superiority over SC 168 by 33.59, 23.63, 17.62, 34.54, 14.25, 16.23, 11.66, 16.32 and 10.02%, respectively. In addition, the crosses P<sub>1</sub>xP<sub>5</sub> and P<sub>5</sub>xP<sub>7</sub> gave the highest grain yield with resistance to late wilt. Hence, it could be concluded that these crosses offer possibility for improving grain yield in maize. These crosses may be released as commercial hybrids after further testing and evaluation. The previous crosses exhibited significant increase of two or more of traits contributing to grain yield plant<sup>-1</sup>. The fluctuation of hybrids from normal and infection environments was detected for most traits.

The mean squares associated with general and specific combining abilities were highly significant in all studied traits (Table 1). To get an idea about the produced performance of single-cross progeny in each case, the relative size of general to specific combining ability mean squares may be helpful. High ratios which largely exceeded the unity were obtained for days to 50% silking in both and across environments and resistance to late wilt% in artificial infection environment as well as the combined analysis. This indicates that the largest part of the total genetic variability was

associated with those traits giving additive and additive by additive gene action. For remain cases, non-additive type of gene action seemed to be more prevalent. The genetic variance reported by **El-Rouby *et al.* (1973)**, **El-Hosry, (1989)** and **El-Hosary *et al.* (2006)** to be mostly due to additive type of gene action for earliness. The non-additive genetic variance was reported by **Singh and Roy (2007)**, **Osman *et al.* (2012)**, **Zare *et al.* (2011)**, **Gouda *et al.* (2013)**, **Abdel-Moneam *et al.* (2014)**, **El-Ghonemy (2015)** and **Kamara (2015)** to be most prevalent for grain yield and most of its components. However other researcher **Derera *et al.* (2008)**, **Vivek *et al.* (2010)**, **Sibiya *et al.* (2011)**, **Ibrahim (2012)**, **El-Hosary and Elgammaal (2013)** and **El-Hosary (2014)** found that the additive play the major role in inheritance of grain yield. **Akbar *et al.* (2008)** and **Hefny (2010)** reported that both additive and non-additive effects were equal in expression of genetic variability for the yield and its components traits in maize.

Significant GCA and SCA by environments mean squares were obtained for all studied traits except No. of rows ear<sup>-1</sup> and 100-kernel weight, indicating that the magnitude of GCA and SCA varied from one environment to another. These findings agree to a large extent with those obtained from the ordinary analysis of variance.

Tables (3a and 3b) illustrate the estimates of  $\hat{g}_i$  effects for individual parental inbred lines at the combined across environment. High positive values would be of interest under all studied traits except days to 50% silking and plant height where negative one would be useful from the breeder point of view for earliness and lodging resistance. General combining ability effects computed herein were significantly different from zero in all traits. Significant negative  $\hat{g}_i$  effects were detected by parental inbred lines P<sub>1</sub>, P<sub>4</sub> and P<sub>8</sub> for days to 50 % silking and P<sub>1</sub>, P<sub>4</sub>, P<sub>7</sub> and P<sub>8</sub> for plant height. Meanwhile, the significant positive  $\hat{g}_i$  effects were detected by parental inbred lines P<sub>1</sub>, P<sub>3</sub>, P<sub>6</sub> and P<sub>8</sub> for No of rows ear<sup>-1</sup>; P<sub>1</sub>, P<sub>2</sub> and P<sub>6</sub> for No of kernel row<sup>-1</sup>; P<sub>2</sub>, P<sub>3</sub>, P<sub>5</sub> and P<sub>8</sub> for 100- kernel weight; P<sub>1</sub> and P<sub>5</sub> for resistant to late wilt and P<sub>1</sub>, P<sub>2</sub>, P<sub>3</sub> and P<sub>6</sub> for grain yield plant<sup>-1</sup>.

The aforementioned inbred line which had high  $\hat{g}_i$  effects for grain yield plant<sup>-1</sup>, also, possessed one or more of the traits contributing to grain yield. It is of interest for plant breeders to ask whether the GCA for parental inbred lines agrees with its own performance or where some parents are more potent when crossed than would be expected from their own performance. The results show positive correlation coefficient between the parental performance and the corresponding  $\hat{g}_i$  effects obtained for all studied traits. Therefore, it could be concluded that the high performing hybrids could be reached except that crossing is carried out between parental inbred lines characterized by high mean performances. For grain yield plant<sup>-1</sup>, plant height and 100-kernel weight the insignificant correlation coefficients between  $\hat{g}_i$  effects and mean performance was detected. This disagreement suggests that hybrids characterized by these traits could be expected by crossing between inbred lines with a low performance for these characters. Also, it could be concluded that the GCA variance had been with dominance with effects to a certain degree (**Jinks 1955**). The parental inbred line P<sub>2</sub> exhibited the most accurate general combiner for earliness and grain yield plant<sup>-1</sup>.

The parental inbred lines combinations specific combining ability  $\hat{s}_{ij}$  effects for all studied traits across environments are presented in Tables (4 a-b). twenty two, zero, twenty, twenty, fifteen, nine and twenty two crosses give desirable  $\hat{s}_{ij}$  effects for days to 50% silking, plant height, no of rows ear<sup>-1</sup>, No of kernels row, 100- kernel weight, resistant to late wilt% and grain yield plant<sup>-1</sup>, respectively. The most desirable inter and intra-allelic interactions were represented;

by  $P_4 \times P_7$ ,  $P_4 \times P_8$ ,  $P_5 \times P_6$ ,  $P_5 \times P_8$ ,  $P_6 \times P_7$  and  $P_7 \times P_8$  for days to 50% silking,  $P_3 \times P_8$  and  $P_5 \times P_7$  for No of rows ear<sup>-1</sup>,  $P_1 \times P_3$  for No of kernels row<sup>-1</sup>,  $P_2 \times P_3$  for 100-kernel weight,  $P_2 \times P_3$ ,  $P_2 \times P_4$ ,  $P_2 \times P_6$  and  $P_3 \times P_6$  for resistant to late wilt% and  $P_1 \times P_2$  and  $P_2 \times P_3$  for grain yield plant<sup>-1</sup>. Such combinations may be of interest in breeding programs aimed at excellent hybrids since they surpassed the best performing for these traits or produce new inbred lines as most combinations involved at least one good combiner parent or produced synthetic varieties.

## CONCLUSIONS

The previous results could be showed that the parental inbred line  $P_1$  was the good general combiner for earliness, resistant to late wilt and grain yield plant<sup>-1</sup>. The crosses  $P_1 \times P_2$  and  $P_2 \times P_3$  had high productivity and these crosses were superior over the check hybrids. However, the cross  $P_2 \times P_3$  was contain most desirable inter and intra-allelic interactions for most traits.

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## APPENDICES

Table 1: Mean of squares from ordinary analysis for studied traits in normal environment, artificial infection by late wilt disease and across the previous environments.

SOV	df	Mean squares						
		Days to 50% silking	Plant height	No of Rows ear <sup>-1</sup>	No of kernels row <sup>-1</sup>	100-kernel kernel weight	Resistant to late wilt%	Grain yield plant <sup>-1</sup>
Normal environment								
Replication	2	4.97*	150.42*	0.79	0.56	1.00	25.93	38.03**
Genotype (G)	35	56.17**	4772.73**	9.33**	110.09**	54.42**	157.06**	7718.44
Parent (P)	7	43.41**	3757.87**	9.41**	108.43**	13.69**	178.57**	3798.95**
Crosses (F <sub>1</sub> )	27	10.80**	505.19**	2.88**	31.93**	28.82**	157.18**	2636.92**
P vs. F <sub>1</sub>	1	1370.48**	127100.42**	183.06**	2231.86**	1030.92**	3.24	172355.99**
Error	70	1.13	46.81	0.47	2.65	3.87	33.54	79.08
GCA	7	19.47**	215.26**	1.68**	21.73**	9.57**	41.09**	650.93**
SCA	28	18.54**	1934.82**	3.47**	40.44**	20.28**	55.17**	3053.28**
Error	70	0.38	15.60	0.16	0.88	1.29	11.18	26.36
GCA/SCA	-	1.05	0.11	0.48	0.54	0.47	0.74	0.21
Artificial infection environment by late wilt disease								
Replication	2	5.58**	94.02	1.74*	3.56	17.07*	31.84	82.12
Genotype (G)	35	55.16**	5469.70**	10.43**	97.43**	58.75**	344.29**	8779.67**
Parent (P)	7	28.06**	955.85**	11.13**	78.14**	23.23**	536.36**	2833.69**
Crosses (F <sub>1</sub> )	27	18.71**	446.66**	2.59**	31.64**	30.34**	304.35**	2564.60**
P vs. F <sub>1</sub>	1	1229.13**	172688.63**	217.00**	2008.83**	1074.47**	78.26	218208.26**
Error	70	0.72	94.49	0.38	1.55	3.53	31.27	75.67
GCA	7	21.39**	325.84**	1.89**	16.45**	10.09**	191.59**	425.35**
SCA	28	17.64**	2197.58**	3.87**	36.48**	21.96**	95.56**	3551.86**
Error	70	0.24	31.50	0.13	0.52	1.18	10.42	25.22
GCA/SCA	-	1.21	0.15	0.49	0.45	0.46	2.00	0.12
Combined across environment								
Environment (E)	1	0.49	11022.45**	0.07	10.67**	13.73**	2660.02**	289.14**
Rep/E	4	5.28**	122.22	1.27*	2.06	9.04*	28.88	60.08
Genotype (G)	35	108.92**	9991.20**	19.53**	199.86**	110.95**	435.71**	16330.73**
Parent (P)	7	69.79**	3861.48**	20.44**	184.13**	33.57**	656.27**	6574.85**
Crosses (F <sub>1</sub> )	27	26.89**	911.69**	5.23**	54.38**	57.15**	392.57**	5049.55**
P vs. F <sub>1</sub>	1	2597.69**	298045.79**	399.33**	4237.75**	2105.17**	56.68	389213.82**
G x E	35	2.42**	251.23**	0.23	7.66**	2.23	65.64**	167.37**
P x E	7	1.68	852.24**	0.10	2.44	3.35	58.65	57.78
F <sub>1</sub> x E	27	2.63**	40.15**	0.24	9.19**	2.02	68.96**	151.97**
P vs. F <sub>1</sub> x E	1	1.92	1743.26**	0.72	2.93	0.23	24.83	1350.43**
Error	140	0.93	70.65	0.43	2.10	3.70	32.41	77.38
GCA	7	39.42**	450.75**	3.52**	35.81**	19.06**	197.48**	1036.69**
SCA	28	35.53**	4050.31**	7.26**	74.32**	41.46**	132.18**	6545.30**
GCA x E	7	1.43**	90.35**	0.05	2.37**	0.60	35.20**	39.59
SCA x E	28	0.65**	82.09**	0.08	2.60**	0.78	18.55*	59.84**
Error	140	0.31	23.55	0.14	0.70	1.23	10.80	25.79
GCA/SCA	--	1.11	0.11	0.48	0.48	0.46	1.49	0.16

\* and \*\* indicate  $p < 0.05$  and  $p < 0.01$ , respectively.

Table 2a: Mean performance of all genotypes for earliness, plant height, no of rows ear<sup>-1</sup>, no of kernels row<sup>-1</sup> and 100-kernel weight at the combined analysis across the studied environments and resistance of genotypes to late wilt in both and across environments

Genotype	Days to 50% Silking	Plant Height	No of Rows Ear <sup>-1</sup>	No of Kernels Row <sup>-1</sup>	100-Kernel Weight	Resistance to Late Wilt %		
						N.	Inf.	Comb.
P <sub>1</sub>	72.00	156.25	11.45	35.85	34.50	100.00	100.00	100.00
P <sub>2</sub>	63.71	210.33	8.90	27.13	30.17	93.33	88.33	90.83
P <sub>3</sub>	65.83	203.17	9.48	18.63	30.50	78.33	58.33	68.33
P <sub>4</sub>	66.58	207.21	11.03	30.28	29.83	96.67	90.00	93.33
P <sub>5</sub>	72.42	144.33	10.37	26.05	34.33	100.00	100.00	100.00
P <sub>6</sub>	70.83	186.46	14.55	35.00	29.83	96.67	91.67	94.17
P <sub>7</sub>	72.63	165.63	11.53	25.28	28.33	96.67	91.67	94.17
P <sub>8</sub>	68.38	165.04	9.00	28.13	28.67	85.00	80.67	82.83
P <sub>1</sub> xP <sub>2</sub>	59.50	278.46	15.00	46.77	39.00	80.00	75.00	77.50
P <sub>1</sub> xP <sub>3</sub>	62.08	265.21	14.42	47.04	39.00	93.33	91.67	92.50
P <sub>1</sub> xP <sub>4</sub>	60.38	259.63	14.77	38.33	38.17	98.33	83.33	90.83
P <sub>1</sub> xP <sub>5</sub>	62.42	289.75	15.25	39.92	39.33	100.00	100.00	100.00
P <sub>1</sub> xP <sub>6</sub>	62.63	272.29	15.47	34.73	31.00	98.33	90.00	94.17
P <sub>1</sub> xP <sub>7</sub>	63.58	269.67	12.73	36.23	33.50	96.67	91.67	94.17
P <sub>1</sub> xP <sub>8</sub>	63.00	266.29	13.23	38.83	37.67	96.67	91.67	94.17
P <sub>2</sub> xP <sub>3</sub>	58.21	276.75	14.80	41.62	45.67	98.33	90.00	94.17
P <sub>2</sub> xP <sub>4</sub>	56.63	250.46	13.93	38.73	36.67	100.00	100.00	100.00
P <sub>2</sub> xP <sub>5</sub>	61.50	290.08	14.62	41.17	38.67	83.33	73.33	78.33
P <sub>2</sub> xP <sub>6</sub>	59.00	258.88	15.30	39.07	35.67	100.00	100.00	100.00
P <sub>2</sub> xP <sub>7</sub>	57.71	254.79	14.82	35.53	37.17	93.33	86.67	90.00
P <sub>2</sub> xP <sub>8</sub>	57.04	267.75	13.57	37.67	42.00	93.33	83.33	88.33
P <sub>3</sub> xP <sub>4</sub>	60.88	265.54	13.12	37.93	41.33	90.00	75.00	82.50
P <sub>3</sub> xP <sub>5</sub>	62.29	290.54	12.75	38.97	39.00	86.67	83.33	85.00
P <sub>3</sub> xP <sub>6</sub>	63.92	262.25	15.03	37.47	38.17	91.67	91.67	91.67
P <sub>3</sub> xP <sub>7</sub>	62.71	261.17	13.63	37.67	39.00	93.33	75.00	84.17
P <sub>3</sub> xP <sub>8</sub>	63.42	284.96	14.53	35.50	42.21	100.00	75.00	87.50
P <sub>4</sub> xP <sub>5</sub>	62.63	275.25	14.17	33.83	31.67	98.33	91.67	95.00
P <sub>4</sub> xP <sub>6</sub>	60.83	248.75	14.17	38.60	40.00	88.33	75.00	81.67
P <sub>4</sub> xP <sub>7</sub>	58.38	252.21	14.12	40.87	37.67	83.33	66.67	75.00
P <sub>4</sub> xP <sub>8</sub>	57.42	256.00	13.67	40.33	40.83	83.33	83.33	83.33
P <sub>5</sub> xP <sub>6</sub>	61.38	283.00	11.93	41.73	40.00	100.00	93.33	96.67
P <sub>5</sub> xP <sub>7</sub>	61.83	279.75	15.33	39.37	37.67	100.00	100.00	100.00
P <sub>5</sub> xP <sub>8</sub>	59.67	281.00	13.20	37.83	37.47	100.00	96.67	98.33
P <sub>6</sub> xP <sub>7</sub>	60.96	269.42	13.07	38.87	34.67	81.67	66.67	74.17
P <sub>6</sub> xP <sub>8</sub>	60.21	268.08	13.10	39.81	38.67	76.67	78.33	77.50
P <sub>7</sub> xP <sub>8</sub>	59.58	258.33	13.97	36.18	40.00	96.67	86.67	91.67
SC 168	65.00	290.00	12.00	32.40	34.00	97.00	86.00	91.50
SC Hytech 2055	69.00	302.00	12.13	43.20	48.33	98.00	93.00	95.50
mean of parent	69.05	179.80	10.79	28.30	30.77	93.33	87.58	90.46
mean of cross	60.71	269.15	14.06	38.95	38.28	93.23	85.86	89.54
mean of Genotype	62.79	251.75	13.27	36.65	36.85	93.25	86.18	89.71
L.S.D 5%	1.54	13.45	1.05	2.32	3.08	9.41	9.08	9.11
L.S.D 1%	2.02	17.64	1.37	3.04	4.04	12.48	12.04	11.95

N., Inf. and Comb. refer to normal, artificial infection by late wilt disease and combined analysis across the two environments, respectively.



Table 2b: Mean performance of all genotypes for grain yield plant<sup>-1</sup> and the yield superiority over SC 168 and SC Hytech 2055 at normal environment (n), infection by late wilt (inf.) and across the previous environments

Genotype	Grain Yield Plant <sup>-1</sup>			Relative Superiority (%)					
	N	Inf.	C.						
P <sub>1</sub>	140	132.33	136.17	Relative Superiority (%)					
P <sub>2</sub>	77.33	71.33	74.33						
P <sub>3</sub>	53	50.67	51.83						
P <sub>4</sub>	98.67	89	93.83						
P <sub>5</sub>	91.67	89	90.33						
P <sub>6</sub>	164.33	143.33	153.83						
P <sub>7</sub>	81.67	78.33	80	Over Single Cross 168			Over Single Cross Hytech 2055		
P <sub>8</sub>	102.33	98.67	100.5	N	Inf.	Comb.	N	Inf.	Comb.
P <sub>1</sub> xP <sub>2</sub>	260	255.67	257.83	33.33**	33.86**	33.59**	16.42**	12.96**	14.68**
P <sub>1</sub> xP <sub>3</sub>	236.9	240.33	238.62	21.49**	25.83**	23.63**	6.07	6.19	6.13
P <sub>1</sub> xP <sub>4</sub>	203	209.67	206.33	4.10	9.77*	6.91	-9.10**	-7.36*	-8.23**
P <sub>1</sub> xP <sub>5</sub>	221.67	232.33	227	13.68**	21.64**	17.62**	-0.75	2.65	0.96
P <sub>1</sub> xP <sub>6</sub>	163	158.67	160.83	-16.41**	-16.93**	-16.67**	-27.01**	-29.90**	-28.47**
P <sub>1</sub> xP <sub>7</sub>	137.33	149	143.17	-29.57**	-21.99**	-25.82**	-38.51**	-34.17**	-36.32**
P <sub>1</sub> xP <sub>8</sub>	166.33	178.67	172.5	-14.70**	-6.46	-10.62**	-25.52**	-21.06**	-23.28**
P <sub>2</sub> xP <sub>3</sub>	253.33	266	259.67	29.91**	39.27**	34.54**	13.43**	17.53**	15.49**
P <sub>2</sub> xP <sub>4</sub>	199.33	190.67	195	2.22	-0.17	1.04	-10.75**	-15.76**	-13.27**
P <sub>2</sub> xP <sub>5</sub>	220	221	220.5	12.82**	15.71**	14.25**	-1.49	-2.36	-1.93
P <sub>2</sub> xP <sub>6</sub>	206.67	208	207.33	5.98	8.90*	7.43*	-7.46*	-8.10*	-7.78*
P <sub>2</sub> xP <sub>7</sub>	180.6	188	184.3	-7.38	-1.57	-4.51	-19.13**	-16.94**	-18.03**
P <sub>2</sub> xP <sub>8</sub>	214	195	204.5	9.74*	2.09	5.96	-4.18	-13.84**	-9.04**
P <sub>3</sub> xP <sub>4</sub>	194	193.33	193.67	-0.51	1.22	0.35	-13.13**	-14.58**	-13.86**
P <sub>3</sub> xP <sub>5</sub>	187	185.67	186.33	-4.1	-2.79	-3.45	-16.27**	-17.97**	-17.12**
P <sub>3</sub> xP <sub>6</sub>	209	208	208.5	7.18	8.90*	8.03*	-6.42	-8.10*	-7.26*
P <sub>3</sub> xP <sub>7</sub>	185.67	198	191.83	-4.79	3.66	-0.6	-16.87**	-12.52**	-14.68**
P <sub>3</sub> xP <sub>8</sub>	215	233.67	224.33	10.26**	22.34**	16.23**	-3.73	3.24	-0.22
P <sub>4</sub> xP <sub>5</sub>	152.67	143.67	148.17	-21.71**	-24.78**	-23.23**	-31.64**	-36.52**	-34.10**
P <sub>4</sub> xP <sub>6</sub>	199.33	218.33	208.83	2.22	14.31**	8.20*	-10.75**	-3.53	-7.12*
P <sub>4</sub> xP <sub>7</sub>	218.33	212.67	215.5	11.97**	11.34**	11.66**	-2.24	-6.04	-4.15
P <sub>4</sub> xP <sub>8</sub>	222	227	224.5	13.85**	18.85**	16.32**	-0.6	0.29	-0.15
P <sub>5</sub> xP <sub>6</sub>	181.2	194.33	187.77	-7.08	1.75	-2.71	-18.87**	-14.14**	-16.49**
P <sub>5</sub> xP <sub>7</sub>	210	214.67	212.33	7.69*	12.39**	10.02**	-5.97	-5.15	-5.56
P <sub>5</sub> xP <sub>8</sub>	191.67	190.67	191.17	-1.71	-0.17	-0.95	-14.18**	-15.76**	-14.97**
P <sub>6</sub> xP <sub>7</sub>	157	167.67	162.33	-19.49**	-12.22**	-15.89**	-29.70**	-25.92**	-27.80**
P <sub>6</sub> xP <sub>8</sub>	162	185	173.5	-16.92**	-3.14	-10.10**	-27.46**	-18.26**	-22.83**
P <sub>7</sub> xP <sub>8</sub>	175	196	185.5	-10.26**	2.62	-3.89	-21.64**	-13.40**	-17.49**
SC 168	195	191	193						
SC Hytech 2055	223.33	226.33	224.83						
mean of parent	101.13	94.08	97.6						
mean of cross	197.22	202.2	199.71						
mean of Genotype	177.61	179.78	178.7						
L.S.D 5%	14.44	14.13	14.08						
L.S.D 1%	19.15	18.74	18.46						

\*and \*\* indicate  $p < 0.05$  and  $p < 0.01$ , respectively. N., Inf. and Comb. refer to normal, artificial infection by late wilt disease and combined analysis across the two environments, respectively.

Table 3a: GCA effects ( $\hat{g}_i$ ) of the studied parental inbred lines for earliness, plant height, no of rows ear<sup>-1</sup> and no of kernels row<sup>-1</sup> and 100-kernel weight across the two environments

Parents	Days to 50% Silking	Plant Height	No of Rows Ear <sup>-1</sup>	No of Kernels Row <sup>-1</sup>	100-Kernel Weight
P <sub>1</sub>	1.46**	-2.99**	0.38**	2.43**	-0.28*
P <sub>2</sub>	-2.60**	5.42**	-0.02	0.56**	0.57**
P <sub>3</sub>	0.21**	6.91**	-0.28**	-1.58**	1.59**
P <sub>4</sub>	-1.27**	-2.14**	0.00	0.00	-0.35**
P <sub>5</sub>	1.35**	3.44**	-0.20**	-0.43**	0.30*
P <sub>6</sub>	0.76**	-0.81	0.72**	1.10**	-1.17**
P <sub>7</sub>	0.70**	-6.71**	0.07	-1.40**	-1.32**
P <sub>8</sub>	-0.59**	-3.12**	-0.67**	-0.68**	0.67**
L.S.D(0.05) gi	0.13	1.12	0.09	0.19	0.26
L.S.D(0.01) gi	0.17	1.47	0.11	0.25	0.34
L.S.D(0.05) gi-gj	0.24	2.13	0.17	0.37	0.49
L.S.D(0.01) gi-gj	0.32	2.79	0.22	0.48	0.64
r	0.88**	0.42	0.86**	0.88**	0.15

\*and \*\* indicate  $p < 0.05$  and  $p < 0.01$ , respectively. r indicate the correlation coefficient between  $\hat{g}_i$  effects for parents and its mean performance

Table 3b: GCA effects ( $\hat{g}_i$ ) of the studied parental inbred lines for resistant to late wilt% and grain yield plant<sup>-1</sup> at both and across the studied environments

Parents	Resistant to Late Wilt %			Grain Yield Plant <sup>-1</sup>		
	N	Inf.	Comb.	N	Inf.	Comb.
P <sub>1</sub>	2.62**	4.94**	3.78**	8.55**	8.54**	8.54**
P <sub>2</sub>	-0.21	1.11	0.45	10.58**	6.34**	8.46**
P <sub>3</sub>	-2.71**	-7.56**	-5.13**	0.41	2.28	1.34*
P <sub>4</sub>	-0.21	-1.89	-1.05**	0.32	-3.03*	-1.35*
P <sub>5</sub>	3.12**	6.44**	4.78**	-3.52*	-4.32**	-3.92**
P <sub>6</sub>	-0.71	0.44	-0.13	2.41	2.31	2.36**
P <sub>7</sub>	0.12	-1.73	-0.80*	-15.55**	-12.09**	-13.82**
P <sub>8</sub>	-2.04*	-1.76	-1.90**	-3.21*	-0.02	-1.62**
L.S.D(0.05) gi	1.97	1.90	0.76	3.02	2.96	1.17
L.S.D(0.01) gi	2.61	2.52	1.00	4.01	3.92	1.54
L.S.D(0.05) gi-gj	2.98	2.87	1.44	4.57	4.47	2.23
L.S.D(0.01) gi-gj	3.95	3.81	1.89	6.06	5.93	2.92
r	0.85**	0.89**	0.88**	0.27	0.30	0.29

\* and \*\* indicate  $p < 0.05$  and  $p < 0.01$ , respectively. r indicate the correlation coefficient between ( $\hat{g}_i$ ) effects for parents and its mean performance. N., Inf. and Comb. refer to normal, artificial infection by late wilt disease and combined analysis across the two environments, respectively.

Table 4a: SCA effects  $\hat{S}_{ij}$  of the studied diallel crosses for earliness, plant height, no of rows ear<sup>-1</sup> and no of kernels row<sup>-1</sup> and 100-kernel weight across the two environments

Crosses	Days to 50% Silking	Plant Height	No of Rows Ear <sup>-1</sup>	No of Kernels Row <sup>-1</sup>	100-Kernel Weight
P <sub>1</sub> xP <sub>2</sub>	-1.91**	26.73**	1.31**	7.20**	2.11**
P <sub>1</sub> xP <sub>3</sub>	-2.14**	11.99**	0.98**	9.61**	1.08
P <sub>1</sub> xP <sub>4</sub>	-2.37**	15.46**	1.06**	-0.68	2.19**
P <sub>1</sub> xP <sub>5</sub>	-2.95**	40.00**	1.74**	1.34*	2.71**
P <sub>1</sub> xP <sub>6</sub>	-2.14**	26.79**	1.04**	-5.38**	-4.16**
P <sub>1</sub> xP <sub>7</sub>	-1.13**	30.07**	-1.05**	-1.38**	-1.51*
P <sub>1</sub> xP <sub>8</sub>	-0.42	23.10**	0.20	0.50	0.67
P <sub>2</sub> xP <sub>3</sub>	-1.96**	15.13**	1.76**	6.06**	6.90**
P <sub>2</sub> xP <sub>4</sub>	-2.06**	-2.11	0.162*	1.60**	-0.16
P <sub>2</sub> xP <sub>5</sub>	0.19	31.93**	1.50**	4.46**	1.19
P <sub>2</sub> xP <sub>6</sub>	-1.71**	4.97	1.27**	0.82	-0.34
P <sub>2</sub> xP <sub>7</sub>	-2.94**	6.79*	1.43**	-0.21	1.31
P <sub>2</sub> xP <sub>8</sub>	-2.32**	16.15**	0.92**	1.21*	4.15**
P <sub>3</sub> xP <sub>4</sub>	-0.62	11.48**	0.06	2.93**	3.48**
P <sub>3</sub> xP <sub>5</sub>	-1.83**	30.90**	-0.11	4.40**	0.50
P <sub>3</sub> xP <sub>6</sub>	0.39	6.85*	1.26**	1.36*	1.13
P <sub>3</sub> xP <sub>7</sub>	-0.76*	11.67**	0.50*	4.06**	2.12**
P <sub>3</sub> xP <sub>8</sub>	1.24**	31.87**	2.15**	1.18*	3.34**
P <sub>4</sub> xP <sub>5</sub>	-0.01	24.66**	1.04**	-2.31**	-4.89**
P <sub>4</sub> xP <sub>6</sub>	-1.21**	2.40	0.12	0.92	4.91**
P <sub>4</sub> xP <sub>7</sub>	-3.61**	11.76**	0.71**	5.68**	2.72**
P <sub>4</sub> xP <sub>8</sub>	-3.27**	11.96**	1.01**	4.44**	3.90**
P <sub>5</sub> xP <sub>6</sub>	-3.29**	31.07**	-1.92**	4.48**	4.26**
P <sub>5</sub> xP <sub>7</sub>	-2.77**	33.72**	2.13**	4.61**	2.08**
P <sub>5</sub> xP <sub>8</sub>	-3.65**	31.38**	0.74**	2.37**	-0.11
P <sub>6</sub> xP <sub>7</sub>	-3.05**	27.64**	-1.06**	2.58**	0.54
P <sub>6</sub> xP <sub>8</sub>	-2.51**	22.71**	-0.28	2.80**	2.55**
P <sub>7</sub> xP <sub>8</sub>	-3.08**	18.86**	1.23**	1.68**	4.04**
LSD5%(sij)	0.70	6.10	0.47	1.05	1.40
LSD1%(sij)	0.92	8.00	0.62	1.38	1.83
LSD5%(sij-sik)	1.03	9.02	0.70	1.56	2.07
LSD1%(sij-sik)	1.35	11.83	0.92	2.04	2.71
LSD5%(sij-skl)	0.34	3.01	0.23	0.52	0.69
LSD1%(sij-skl)	0.45	3.94	0.31	0.68	0.90

\* and \*\* indicate p&lt; 0.05 and p&lt; 0.01, respectively.

Table 4b: SCA effects ( $\hat{S}_{ij}$ ) of the studied diallel crosses for resistance to late wilt disease and grain yield plant<sup>-1</sup> in both and across the studied environments

Crosses	Resistance to Late Wilt%			Grain Yield Plant <sup>-1</sup>		
	N	inf.	Comb.	inf.	N	Comb.
P <sub>1</sub> xP <sub>2</sub>	-15.43**	-17.04**	-16.23**	65.01**	62.61**	63.81**
P <sub>1</sub> xP <sub>3</sub>	0.41	8.29**	4.35*	52.07**	51.34**	51.71**
P <sub>1</sub> xP <sub>4</sub>	2.91	-5.71	-1.40	18.27**	25.97**	22.12**
P <sub>1</sub> xP <sub>5</sub>	1.24	2.63	1.93	40.78**	49.94**	45.36**
P <sub>1</sub> xP <sub>6</sub>	3.41	-1.37	1.02	-23.82**	-30.36**	-27.09**
P <sub>1</sub> xP <sub>7</sub>	0.91	2.46	1.68	-31.53**	-25.63**	-28.58**
P <sub>1</sub> xP <sub>8</sub>	3.07	2.49	2.78	-14.87**	-8.03	-11.45**
P <sub>2</sub> xP <sub>3</sub>	8.24**	10.46**	9.35**	66.47**	79.21**	72.84**
P <sub>2</sub> xP <sub>4</sub>	7.41*	14.79**	11.10**	12.56**	9.17*	10.87**
P <sub>2</sub> xP <sub>5</sub>	-12.59**	-20.21**	-16.40**	37.08**	40.81**	38.94**
P <sub>2</sub> xP <sub>6</sub>	7.91*	12.46**	10.18**	17.81**	21.17**	19.49**
P <sub>2</sub> xP <sub>7</sub>	0.41	1.29	0.85	9.70*	15.57**	12.64**
P <sub>2</sub> xP <sub>8</sub>	2.57	-2.01	0.28	30.76**	10.51*	20.64**
P <sub>3</sub> xP <sub>4</sub>	-0.09	-1.54	-0.82	17.40**	15.91**	16.65**
P <sub>3</sub> xP <sub>5</sub>	-6.76*	-1.54	-4.15*	14.25**	9.54*	11.89**
P <sub>3</sub> xP <sub>6</sub>	2.07	12.79**	7.43**	30.31**	25.24**	27.78**
P <sub>3</sub> xP <sub>7</sub>	2.91	-1.71	0.60	24.94**	29.64**	27.29**
P <sub>3</sub> xP <sub>8</sub>	11.74**	-1.67	5.03*	41.93**	53.24**	47.59**
P <sub>4</sub> xP <sub>5</sub>	2.41	1.13	1.77	-20.00**	-27.16**	-23.58**
P <sub>4</sub> xP <sub>6</sub>	-3.76	-9.54**	-6.65**	20.74**	40.87**	30.81**
P <sub>4</sub> xP <sub>7</sub>	-9.59**	-15.71**	-12.65**	57.70**	49.61**	53.65**
P <sub>4</sub> xP <sub>8</sub>	-7.43*	0.99	-3.22	49.02**	51.87**	50.45**
P <sub>5</sub> xP <sub>6</sub>	4.57	0.46	2.52	6.45	18.17**	12.31**
P <sub>5</sub> xP <sub>7</sub>	3.74	9.29**	6.52**	53.21**	52.91**	53.06**
P <sub>5</sub> xP <sub>8</sub>	5.91	5.99*	5.95**	22.54**	16.84**	19.69**
P <sub>6</sub> xP <sub>7</sub>	-10.76**	-18.04**	-14.40**	-5.72	-0.73	-3.22
P <sub>6</sub> xP <sub>8</sub>	-13.59**	-6.34*	-9.97**	-13.06**	4.54	-4.26
P <sub>7</sub> xP <sub>8</sub>	5.57	4.16	4.87*	17.90**	29.94**	23.92**
LSD5%(sij)	6.03	5.83	4.13	9.26	9.06	6.38
LSD1%(sij)	8.00	7.73	5.42	12.29	12.02	8.37
LSD5%(sij-sik)	8.93	8.62	6.11	13.71	13.41	9.44
LSD1%(sij-sik)	11.84	11.44	8.01	18.18	17.79	12.38
LSD5%(sij-skl)	8.42	8.13	2.04	12.92	12.64	3.15
LSD1%(sij-skl)	11.17	10.78	2.67	17.14	16.77	4.13

\*and \*\* indicate  $p < 0.05$  and  $p < 0.01$ , respectively. N., Inf. and Comb. refer to normal, infection by late wilt disease and combined analysis across the two environments, respectively.