

## SELECTION FOR PROMISING YELLOW RUST TOLERANT BREAD WHEAT GENOTYPES TO IN F<sub>2</sub> GENERATION

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### ABSTRACT

Recently, there are many several biometrical models for analysis of diallel data. This study was carried out to investigate the possibility of combining ability prediction from the relationship between biplot graph and Griffing analysis of half diallel data, and to identify superior genotypes. Six parental bread wheat cultivars and their half diallel hybrids (15 F<sub>2</sub> segregating populations) were evaluated during 2017/2018 season in the farm of Sakha Agricultural Research Station, ARC, Egypt in a randomized complete block design. The results reflected significant variances for both general (GCA) and specific combining ability (SCA) in most traits. Meanwhile, the SCA was higher than the GCA, indicating that the non-additive gene action is more important than additive one in controlling the studied traits. Simple correlation results showed that grain yield may be raised through selection for the highest number of spikes and lowest yellow rust susceptibility. Biplot graph and Griffing analyses exhibited equivalent results for GCA and SCA effects and are meaningful for identifying Sakha93 (P<sub>5</sub>) and Giza 168 (P<sub>6</sub>) as the best parents and Sakha94 x Giza 168 (H46), Misr 1 x Sakha93 (H15) and Misr 1 x Misr 2 (H12) as the best crosses. Biplot for diallel data was useful in estimation gene action and identifying the best crosses for breeding programs across all correlated traits (GT) and comparing genotypes based on multiple traits. Therefore, GT biplot data analysis was considered as good alternative analysis method for Griffing one, giving a complete picture about the interrelationships among genotypes and traits.

Key words: Biplot, Griffing, Diallel, Correlation, Combining ability.

### INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important cereal food commodities not only in Egypt but also all over the world. Currently, Egypt is the largest importer of wheat in the world where local consumption reached 18.6 million tons; meanwhile, total wheat production is not enough for local needs (Gomaa *et al* 2014). In addition to, yield as a complex trait was influenced by many biotic factors as rusts. Stripe or yellow rust of wheat caused by *Puccinias triiformis* f. *sp. tritici* is the most important rust in Egypt. The best approach towards breeding for resistance would be to identify the durable of the resistance and use it to be incorporated in a new cultivar (Johnson *et al* 1978). Genetic improvement of yield and rust-related traits and selection or hybridization breeding program depends on estimates of genetic components for the interested traits consisting of additive, dominance and non-allelic interaction effects, which may provide practical information to breeders during the development of rust-tolerant wheat varieties (Hussain *et al* 2008 and Dehghani and Moghaddam 2004).

Diallel mating design provides a very simple and convenient method for the estimation of genetic parameters (Sabaghnia *et al* 2010). The half

diallel analysis that usually done by Griffing's 1956 method have certain advantages, giving maximum information on the inheritance of quantitative traits to select the best parental combinations for crosses and to determine the heterotic responses are important tools in plant breeding programs (Griffing, 1956). Diallel crossing is a common tool in plant breeding for studying the inheritance of traits (Silva *et al* 2004, and Souza *et al* 2008). The application of principal component (PC) biplot techniques for diallel crosses were suggested by Yan and Hunt (2002). Biplot graphically displays a two-way data matrix (Gabriel, 1971). A modified biplot called GGE biplot was proposed by Yan *et al* (2000) for analysis of genotype by environment data matrix constructed from multi environment experiments. This method can be used for all types of two-way data such as diallel data (Yan, 2001 and Yan and Hunt, 2002) and also has been utilized remarkably in wheat breeding programs. Biplot approach based on diallel experimental data was used to estimate the general (GCA) and specific (SCA) combining ability and to identify potential heterotic relationships among different genotypes (Yan and Hunt, 2002). Then, this technique helps breeders for identifying superior hybrids (Yan and Kang, 2003). Two advantages of biplot analysis compared to other biometric diallel analysis are its graphical presentation and better interpretability of data, which greatly enhances the ability to understand the patterns of data. While the conventional method of diallel analysis was designed to describe the phenotypic performance of the crosses, the biplot approach tries to explain the phenotypic variation of the crosses by understanding the parents (Yan and Hunt, 2002). The biplot approach of diallel data analysis allows a much better understanding of parents. For a given set of data, the following information can be easily visualized: the GCA effects of each parent, the best crosses and genetic constitutions of parents with regard to the trait under investigation (Yan and Kang, 2003). Some of researchers used biplot techniques for analysis of diallel data in cereals to study the combining ability and distinguish the best general and specific combiners in bread wheat (Farshadfar and Hasheminasab 2012, Farshadfar *et al* 2012, Farshadfar and Hasheminasab 2013 and Mostafavi and Zabet 2013). Dehghani *et al* (2005) and (2013)

used biplot method for the analysis of diallel cross data for infection type of wheat stripe rust.

Correlation coefficient, measures only the degree (intensity) and nature (direction) of association among yield traits of wheat in several studies, but it provides only one-dimensional information neglecting the complex interrelationships among plant traits (Kang 1994).

The present study was undertaken to analyze diallel data using GGE (genotype + genotype-environment interaction) biplot model to gather information about genetic interrelationships among parents, crosses, general and specific combining ability and to identify combination for the important traits, namely, grain yield/plant and yellow rust-tolerance. Thus, the objectives of this study were 1) to evaluate the performance of the studied bread wheat diallel crosses, 2) to identify combining ability of parent's (GCA) and hybrid's (SCA), 3) to discuss whether genotype by trait (GT) biplot graph is possible to be a good alternative to the familiar procedure for diallel analysis to predict GCA and SCA effects and 4) to explain the possibility of biplot graph in interpretation of relationships among different genotypes and traits, showing the best crosses.

## **MATERIALS AND METHODS**

### **Genetic material**

The present experiment was carried out using twenty-one bread wheat genotypes (six commercial cultivars in Table (1) and 15 F<sub>2</sub> populations obtained according to a half-diallel design. Meanwhile, F<sub>1</sub> data was discussed in another work (Mohamed *et al* 2018) to study the disease reaction.

These genotypes were evaluated during 2017/2018 season in a randomized complete block design with three replications at the experimental farm of the Sakha Agricultural Research Station, Agricultural Research Center, Egypt.

### **Experimental procedure:**

The genotypes including six parents and 15F<sub>2</sub>'s were sown in a randomized complete block design with three replicates. Planting was done in rows; 3m long with 30 cm apart and plants within rows were spaced 10 cm.

**Table 1. Name, pedigree, selection history and infection type of six parental bread wheat genotypes.**

Parents	Pedigree and selection history	Yellow rust
Misir 1 (P <sub>1</sub> )	OASIS/KAUZ//4*BCN/3/2*PASTOR CMSS00Y01881T-050M-030Y-030M-030WGY- 33M-0Y-0S	MR †
Misir 2 (P <sub>2</sub> )	SKAUZ / BAV92 CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y- 0S	MR
Gemmeiza 11 (P <sub>3</sub> )	BOW"S"/KVZ"S"//7C/SER182/3/GIZA168/SAKH A 61 GM7892-2GM-1GM-2GM-1GM-0GM	S
Sakha 94 (P <sub>4</sub> )	OPATA/RAYON//KAUZ CMBW90Y3180-0TOPM-3Y-010M-010M-010Y- 10M-015Y-0Y-0AP-0S.	R
Sakha 93 (P <sub>5</sub> )	Sakha 92/TR 810328 S8871-1S-2S-13-0S.	S
Giza 168 (P <sub>6</sub> )	MRL / BUC // SERI CM93046-8M-0Y-0M-2Y-0B –OGZ.	S

†R= Resistant, MR = Moderately Resistant, MS= Moderately Susceptible and S= Susceptible.

Two rows were devoted to each parent, while 10 rows for each F<sub>2</sub> generation for each cross. After physiological maturity, data were recorded on 30 individual guarded plants of each of parents and 200 Plants of F<sub>2</sub>'s for plant height, number of spikes per plant, 100-kernel weight and grain yield per plant. Meanwhile, susceptibility to natural infection with wheat yellow rust (under the artificial infection of 2 spreaders around the experiment) was recorded at the time of disease onset.

#### **Disease infection and assessment under natural conditions**

The experiment was planted 15 days after the regular sowing date (the first half of December) to expose the plants to a suitable environment for rust infection. Wheat plants were exposed to the current recommended practices. Plots were surrounded by a spreader area planted with a mixture of highly susceptible wheat genotypes to rusts, i.e., Morocco and Max to spread rust inoculums. Rust disease spreader plants were inoculated by injection method twice in a week during the growing season to provide and

maintain the rust inoculum pressure in the experiment. Yellow rust was scored on the flag leaf of individual plants when the severity on the most susceptible parent was about 100%, i.e. most of the leaf surface was covered with uredinia. The modified Cobb scale Saari and Wilcoxson (1974) and Pathan and Park (2006) was used, multiplying of disease severity (DS) and constant values of infection type (IT). Disease severity and host response scores were multiplied together to give the coefficient of infection (C.I.) for data analysis.

#### **Biometrical analyses**

All data were subjected to analysis of variance. Data obtained from the 15 populations of F<sub>2</sub> and six parents were subjected to analysis by Griffing (1956) method II, model 1. The analysis of combining ability was performed. Simple correlation coefficients between all pairs of the studied traits were calculated based upon the method proposed Steel *et al* (1997).

#### **Model for GGE Biplot**

GGE (genotype main effect plus genotype-by-environment interaction) biplots are commonly used to analyze two-way data, where rows and columns represent different experimental units (Yan and Hunt 2002). Then, GGE biplot might be modified to GGT (genotype main effect plus genotype-by-trait interaction). Yan and Rajcan (2002) used the genotype by trait (GT) biplot, which is an application of the GGE biplot to study the genotype by trait data. Because the traits were measured in different units, the biplot procedure was generated using the standardized values of the trait means. All biplots presented in this paper were performed with the procedures of GenStat software package (2017).

### **RESULTS AND DISCUSSION**

The variability in populations is the basis of progress in the breeding program of certain crop traits when the desirable traits are heritable in this respect. However, the information of the genetic parameters for parents and their hybrids may be helpful for breeders to identify the best combiners which may be hybridized to build up favorable fixable genes. This information offers a great opportunity to improve yield and the rust resistance inheritance in bread wheat.

### Combining ability and genetic analysis

Analysis of variance showed significant mean squares due to genotypes in studied traits (Table 2). Mean performance of plant height, number of spikes per plant, 100-kernel weight, grain yield per plant and wheat yellow rust susceptibility, differed significantly among the six parental cultivars and 15 F<sub>2</sub> hybrids ( $P \leq 0.01$ ).

**Table 2. Mean squares and Griffing analysis of variance due to various studied traits in F<sub>2</sub>'s bread wheat.**

SOV	df	Plant height	100-kernel weight	Number of spikes/plant	Grain yield/plant	Yellow rust
Replications	2	5.22	0.64**	1.07	2.79	3.92
Genotypes	20	138.73**	0.55**	18.47**	70.74**	452.99**
Error	40	15.20	0.12	0.90	23.36	4.50
GCA	5	43.52**	0.13*	3.91**	12.73	256.97**
SCA	15	47.15**	0.20**	6.91**	27.20**	115.67**
Error	40	5.07	0.04	0.30	7.79	1.50
baker ratio		0.65	0.56	0.53	0.48	0.82

\* & \*\* significant at the 0.05 & 0.01 probability levels, respectively.

According to the above mentioned results, the detailed analysis of combining ability and type of gene action was therefore appropriate for estimating the traits investigated through this study. ANOVA of the diallel data set with respect to grain yield components and yellow rust traits revealed a highly significant general and specific combining ability (GCA and SCA) effects in most cases (Table 2). The GCA variance was significant for 100-kernel weight and highly significant for plant height, number of spikes per plant and yellow rust susceptibility, indicating the involvement of additive gene action in these traits. Meanwhile, SCA was highly significant (non-additive) for all traits as outlined by Griffing (1956). Hence, the significant estimates of both GCA and SCA variances suggested that both of additive and non-additive nature of gene action were involved in controlling these traits through all bread wheat genotypes. These results confirmed those findings by Farshadfar *et al* 2012 and Pagliosa *et al* 2017.

Both GCA and SCA were significant for plant height, number of spikes per plant, 100-kernel weight and yellow rust susceptibility, but GCA variance was not significant for the grain yield per plant. Mean square values were higher for GCA than SCA for yellow rust susceptibility; however, for plant height, number of spikes per plant, 100-kernel weight and grain yield per plant, the mean square of SCA was higher than the mean square of GCA, indicating that the non-additive gene effects are more important than additive ones. According to Baker (1978) ratio, when combining ability ratio approached near unity for yellow rust susceptibility (0.82), GCA alone can predict the performance of the parents. Thus, the GCA scores could not be used to predict the performance of the parents for other studied traits in the present study, because the value of Baker's ratio is much lower than the theoretical maximum of unity. Therefore, the low Baker's ratio emphasized the preponderant role of non-additive (dominance and/or epistatic) gene action in controlling most of the studied traits in bread wheat in comparison to additive one (Sadeghzadeh-Ahari *et al* 2014).

Performance of six parents and their respective crosses among F<sub>1</sub> (was discussed in the published paper of Mohamed *et al* 2018) and F<sub>2</sub> were presented in Table (3). Performance of second generation (F<sub>2</sub>) revealed best values compared with first generation (F<sub>1</sub>) values. The highest values for grain yield per plant were exhibited by P<sub>3</sub> (Gemmeiza11) and P<sub>5</sub> (Sakha 93) with (27.80g) and (24.89g), respectively. On the other side, the parent P<sub>5</sub> (Sakha 93) and P<sub>6</sub> (Giza 168) possessed the lowest value for yellow rust susceptibility with score of (0.20) and (3.23), respectively. Then, P<sub>5</sub> (Sakha 93) recorded the best performance for both relative scores of yellow rust susceptibility and grain yield per plant.

Crosses involving the previous highly yellow rust susceptibility parents recorded the highest value of resistance Sakha 93 (P<sub>5</sub>) x Giza 168(P<sub>6</sub>) with high grain yield and the highest Number of spikes/plant (0.01, 30.08g and 19.04, respectively) in F<sub>2</sub>'s. However, most crosses involving one of these parents exhibited high levels of resistance coupled with highest grain yield as Sakha 94 (P<sub>4</sub>) x Giza 168(P<sub>6</sub>), Misr 1 (P<sub>1</sub>) x Sakha 93 (P<sub>5</sub>) and Misr 2 (P<sub>2</sub>) x Sakha 93 (P<sub>5</sub>) with (10.04 and 33.20g - 2.29 and 32.69g – 7.00 and 29.05 g, respectively) in F<sub>2</sub>'s.

**Table 3. Mean performance of parents and their hybrids in the F<sub>1</sub> and F<sub>2</sub> generation for all studied traits.**

Genotypes	Plant height		100-kernel weight		No. of spikes/plant		Grain yield/plant		Yellow rust	
	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>
Misr 1 (P <sub>1</sub> )	76.50		4.12		9.70		14.98		30.00	
Misr 2(P <sub>2</sub> )	76.00		4.11		11.40		16.00		23.33	
Gemmeiza11 (P <sub>3</sub> )	91.00		4.59		13.10		27.80		14.67	
Sakha94 (P <sub>4</sub> )	86.50		3.94		12.10		22.03		53.33	
Sakha93 (P <sub>5</sub> )	85.00		4.44		14.70		24.89		0.20	
Giza 168 (P <sub>6</sub> )	90.00		4.14		12.30		21.82		3.23	
P <sub>1</sub> * P <sub>2</sub> (H12)	85.00	74.92	4.06	4.65	13.10	10.18	18.22	30.73	66.67	12.24
P <sub>1</sub> * P <sub>3</sub> (H13)	84.00	86.23	3.82	4.53	11.20	17.71	24.23	28.31	10.83	5.30
P <sub>1</sub> * P <sub>4</sub> (H14)	88.00	95.30	4.38	5.29	11.50	14.29	19.06	23.92	26.67	13.01
P <sub>1</sub> * P <sub>5</sub> (H15)	91.50	80.53	3.68	3.93	13.00	16.84	19.58	32.69	33.33	2.29
P <sub>1</sub> * P <sub>6</sub> (H16)	88.00	83.95	4.67	4.27	9.90	12.80	22.54	23.55	7.47	9.57
P <sub>2</sub> * P <sub>3</sub> (H23)	87.00	88.30	4.51	5.23	11.50	12.54	21.81	21.52	4.80	22.83
P <sub>2</sub> * P <sub>4</sub> (H24)	79.50	95.79	4.06	4.84	10.30	17.84	14.28	24.91	61.67	15.55
P <sub>2</sub> * P <sub>5</sub> (H25)	80.50	91.47	3.67	4.24	13.50	15.49	21.68	29.05	9.67	7.00
P <sub>2</sub> * P <sub>6</sub> (H26)	88.00	75.57	4.09	5.29	13.30	16.60	24.36	27.73	41.67	5.85
P <sub>3</sub> * P <sub>4</sub> (H34)	94.00	75.48	4.54	4.97	11.30	14.14	24.82	22.60	12.67	8.19
P <sub>3</sub> * P <sub>5</sub> (H35)	72.00	88.10	3.62	4.87	8.70	13.16	19.21	26.56	9.17	23.99
P <sub>3</sub> * P <sub>6</sub> (H36)	86.00	95.20	4.21	4.20	13.80	14.28	29.38	20.69	5.33	17.22
P <sub>4</sub> * P <sub>5</sub> (H45)	96.00	85.75	4.22	4.50	14.60	13.72	23.85	26.66	73.33	20.00
P <sub>4</sub> * P <sub>6</sub> (H46)	91.50	89.38	3.98	4.54	11.20	14.45	19.24	33.20	73.33	10.04
P <sub>5</sub> * P <sub>6</sub> (H56)	85.00	86.98	4.08	4.15	13.30	19.04	24.31	30.08	0.01	0.01
LSD (0.05)		6.43		0.85		3.12		19.81		10.42

H<sub>ij</sub>: hybrid female \* male.

From these findings may suggest that the above mentioned parents (Sakha 93 and Giza 168) and the F<sub>2</sub> crosses (Sakha 94 (P<sub>2</sub>) x Giza 168(P<sub>6</sub>), Misr 1 (P<sub>1</sub>) x Sakha 93 (P<sub>5</sub>) and Misr 2 (P<sub>2</sub>) x Sakha 93 (P<sub>5</sub>)) may be of value for improving grain yield of bread wheat through improvement of yellow rust resistance and rust disease. Similar results were obtained by Farshadfar and Hasheminasa (2013) and Abdelkhalik *et al* (2018) for grain yield and yellow rust susceptibility.



### Correlation studies

Adequate knowledge of the relationship that exists between grain yield and yield-related traits is essential for the identification of selection criteria to be used for yield improvement in wheat. Simple correlation coefficients for all comparisons among the wheat studied traits in F<sub>2</sub> generation are presented in Table (4). Results showed that there was a highly significant and positive correlation between grain yield and number of spikes/plant (0.547\*\*). This strong correlation suggested that grain yield may be raised through selection for the more spikes. However, non-significant and positive associations were obtained between grain yield and the Plant height and 100-kernel weight traits indicating that these traits may be independent in their genetic behavior under the tested genotypes. Meanwhile, the magnitude of the correlation coefficients among other traits was non-significant. These findings indicate that selection for number of spikes/plant would be accompanied by high yielding ability Baloch *et al* (2013), Abd El-Mohsen and Abd El-Shafi (2014), Iqbal *et al* (2017) and Gab Alla *et al* (2018).

On the other hand, yellow rust susceptibility correlated significantly and negatively with grain yield and number of spikes/plant (-0.507\*\* and -0.549\*\*, respectively).

**Table 4. Simple correlation coefficients for all comparisons among the wheat studied traits in F<sub>2</sub> generation.**

Traits	Plant height	100-kernel weight	Number of spikes/plant	Grain yield/plant
100-kernel weight	0.071			
Number of spikes/plant	0.322	0.117		
Grain yield/plant	0.123	0.102	0.547**	
Yellow rust	-0.002	-0.132	-0.549**	-0.507**

\* & \*\* significant at the 0.05 & significant at the 0.01 probability levels, respectively.

### **Combining ability**

The estimates of GCA effects for different genotypes which differed from one individual parent to another and from trait to trait (according to Griffing method), are listed in Table (5) and (Fig 1). The detailed analysis of combining ability and type of gene action was therefore appropriate for estimating the studied traits. General combining ability effects were found to be either significant or highly significant in some cases. Comparison between GCA effects associated with each parent revealed that the parental cultivar Sakha 93 (P<sub>5</sub>) was a good combiner for number of spikes per plant (1.11\*\*), grain yield per plant (2.28\*) and relative ranking scores of wheat yellow rust (-5.70\*\*). While, Giza 168(P<sub>6</sub>) had significant and positive GCA effects for number of spikes/plant and plant height (0.37\* and 1.47\*, respectively) and highly significant and negative GCA effect (-6.27\*\*) for yellow rust susceptibility.

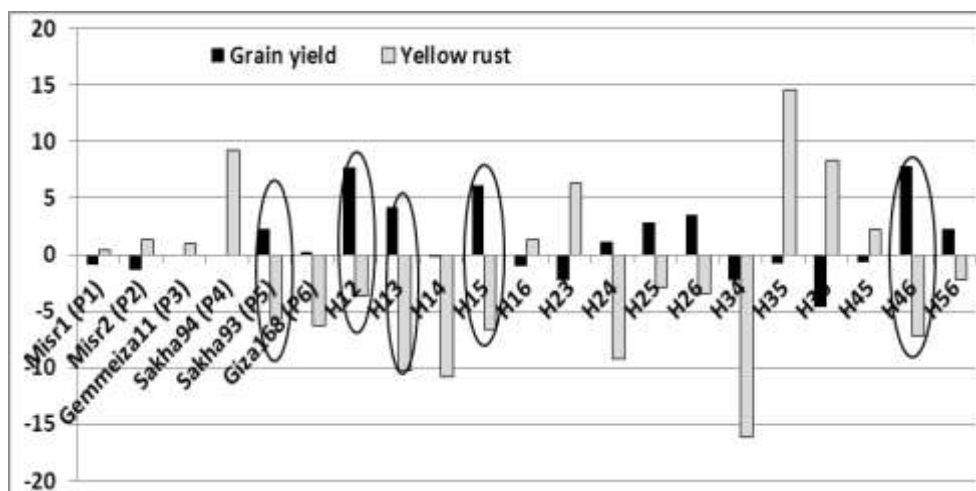
From above, it was mentioned that GCA effects associated with each parent revealed that the parental cultivar Sakha 93(P<sub>5</sub>) was a good combiner (Fig 1) for grain yield per plant (2.28\*) and yellow rust susceptibility (-5.70\*\*). Therefore, this parent could be considered as a good combiner for improving these studied traits, since it showed significant values, positive or negative according to the desirable trend of these traits.

The values of SCA effects are presented in Table (5). Six crosses (P<sub>1</sub>×P<sub>3</sub>, P<sub>1</sub>×P<sub>4</sub>, P<sub>1</sub>×P<sub>5</sub>, P<sub>2</sub>×P<sub>4</sub>, P<sub>2</sub>×P<sub>6</sub> and P<sub>5</sub>×P<sub>6</sub>) exhibited highly significant and positive SCA effects for number of spikes per plant. Four crosses (P<sub>1</sub>×P<sub>2</sub>, P<sub>1</sub>×P<sub>3</sub>, P<sub>1</sub>×P<sub>5</sub> and P<sub>4</sub>×P<sub>6</sub>) had significant and positive SCA effects for grain yield per plant. Meanwhile, ten crosses (P<sub>1</sub>×P<sub>2</sub>, P<sub>1</sub>×P<sub>3</sub>, P<sub>1</sub>×P<sub>4</sub>, P<sub>1</sub>×P<sub>5</sub>, P<sub>2</sub>×P<sub>4</sub>, P<sub>2</sub>×P<sub>5</sub>, P<sub>2</sub>×P<sub>6</sub>, P<sub>3</sub>×P<sub>4</sub>, P<sub>4</sub>×P<sub>6</sub> and P<sub>5</sub>×P<sub>6</sub>) showed significant and negative SCA effects for relative ranking scores of wheat yellow rust. Therefore, for general combining ability, the Sakha 93 (P<sub>5</sub>) can be considered as the most efficient cultivar based on its performance, and the four crosses (P<sub>1</sub>×P<sub>2</sub>, P<sub>1</sub>×P<sub>3</sub>, P<sub>1</sub>×P<sub>5</sub> and P<sub>4</sub>×P<sub>6</sub>) had high values for grain yield and wheat yellow rust susceptibility. These findings indicate that SCA for grain yield per plant may be influenced by SCA for yellow rust susceptibility.

**Table 5. Estimates of general (GCA) and specific (SCA) combining ability effects for studied traits in F2's bread wheat and its parents.**

Genotypes	Plant height	100-kernel weight	Number of spikes/plant	Grain yield/plant	Yellow rust
Misir 1 (P <sub>1</sub> )	-3.17**	-0.09	-0.95**	-0.93	0.39
Misir 2(P <sub>2</sub> )	-2.66**	0.11	-0.42*	-1.33	1.36**
Gemmeiza11 (P <sub>3</sub> )	2.00**	0.17*	-0.09	-0.16	0.95*
Sakha94 (P <sub>4</sub> )	1.92*	0.05	-0.02	-0.15	9.27**
Sakha93 (P <sub>5</sub> )	0.44	-0.13*	1.11**	2.28*	-5.70**
Giza 168 (P <sub>6</sub> )	1.47*	-0.11	0.37*	0.29	-6.27**
LSD g <sub>i</sub> 5%	1.47	0.13	0.36	1.82	0.80
LSD g <sub>i</sub> -g <sub>j</sub> 5%	4.03	0.36	0.98	5.00	2.19
P <sub>1</sub> * P <sub>2</sub> (H12)	-4.87**	0.11	-2.57**	7.76**	-3.69**
P <sub>1</sub> * P <sub>3</sub> (H13)	1.79	-0.06	4.64**	4.17*	-10.22**
P <sub>1</sub> * P <sub>4</sub> (H14)	10.93**	0.81**	1.14**	-0.22	-10.84**
P <sub>1</sub> * P <sub>5</sub> (H15)	-2.35	-0.37*	2.56**	6.11**	-6.58**
P <sub>1</sub> * P <sub>6</sub> (H16)	0.04	-0.04	-0.74	-1.03	1.26
P <sub>2</sub> * P <sub>3</sub> (H23)	3.34*	0.44**	-1.06*	-2.21	6.34**
P <sub>2</sub> * P <sub>4</sub> (H24)	10.91**	0.17	4.17**	1.17	-9.26**
P <sub>2</sub> * P <sub>5</sub> (H25)	8.07**	-0.25	0.69	2.87	-2.84**
P <sub>2</sub> * P <sub>6</sub> (H26)	-8.86**	0.78**	2.54**	3.54	-3.42**
P <sub>3</sub> * P <sub>4</sub> (H34)	-14.06**	0.23	0.14	-2.31	-16.21**
P <sub>3</sub> * P <sub>5</sub> (H35)	0.04	0.31*	-1.96**	-0.79	14.56**
P <sub>3</sub> * P <sub>6</sub> (H36)	6.11**	-0.38*	-0.11	-4.66*	8.35**
P <sub>4</sub> * P <sub>5</sub> (H45)	-2.23	0.06	-1.48**	-0.69	2.24*
P <sub>4</sub> * P <sub>6</sub> (H46)	0.37	0.08	-0.02	7.83**	-7.15**
P <sub>5</sub> * P <sub>6</sub> (H56)	-0.54	-0.13	3.45**	2.28	-2.20*
LSD S <sub>ij</sub> 5%	3.33	0.29	0.81	4.13	1.81
LSD S <sub>ij</sub> -S <sub>ik</sub> 5%	6.02	0.53	1.47	7.46	3.27
LSD S <sub>ij</sub> -S <sub>kl</sub> 5%	5.57	0.49	1.36	6.91	3.03

H<sub>ij</sub>: hybrid female \* male. \* & \*\* significant at the 0.05 & significant at the 0.01 probability levels, respectively.



**Fig 1. Estimates of general and specific combining ability effects (GCA and SCA) for grain yield and scores of yellow rust resistance.**

**Biplot graph to predict best GCA and SCA effects:**

Generally, the biplot graphs can be used to compare genotypes on the basis of multiple traits (Yan and Rajcan 2002 and Yan and Tinker 2005). The polygon view of a genotype by trait (GT) biplot graph is the best way to visualize the interaction patterns between genotypes and the correlated traits provided the biplot should explain a sufficient amount of the total variation of data, but what about the combining ability variation? As known, combining ability variation was the result of division product of total variation of data on replication number (Singh and Choudhary 1995). Then, the polygon biplot graph may explain the best general and specific combining ability for the correlated traits to identify genotypes that are particularly good in certain part or side and therefore could be nominated for selection and hybridization in wheat breeding program.

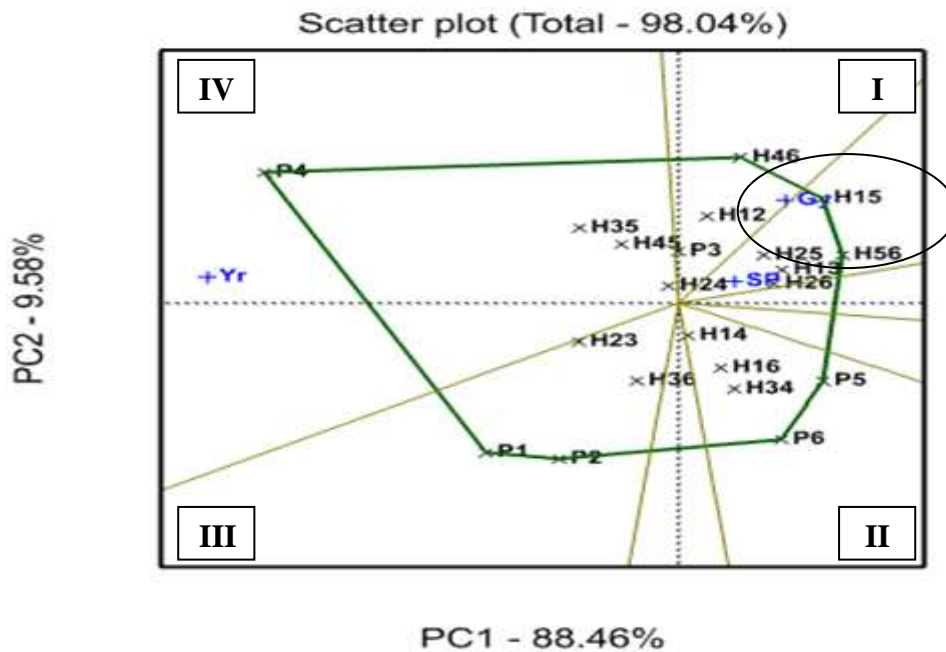
In this study, the application of biplot techniques for diallel crosses is sufficient to explain the whole performance variation of the parents and the hybrid combinations (Yan and Hunt 2002). Biplot approach based on diallel experimental data is used to plot the general combining ability

(GCA) and specific combining ability (SCA) among different genotypes (Yan and Hunt 2002). Biplot graph was used to compare genotypes on the basis of grain yield and its significant related traits (grain yield, number of spikes per plant and scores of yellow rust resistance) and to identify good genotypes to select via the best GCA and SCA effects in the studied  $F_2$  wheat populations, are shown in (Fig. 2).

Figure (2) showed the relationship among the studied wheat genotypes (crosses and its parents) using the grain yield and its related number of spikes per plant and yellow rust susceptibility. The GT biplot of the mean performance of these traits explained 98.04 % of the total variation of the standardized data. The first and two principal components (PC1 and PC2) explained 88.46% and 9.58%, respectively. This relatively high proportion reflects the complexity of the relationships among the genotypes and the measured correlated traits. The first two PC's result recorded high percent (more than 60 %) of the total variation, achieving the goodness of fit for GT biplot model (Yan and Kang 2003). Similar results were also found by Boćanski *et al* (2011) and Darwish *et al* (2019).

The graph of GT biplot showed that a vector is drawn from the biplot origin to each marker of the traits to visualize the relationships among these related traits (Yan and Tinker 2005).

Results revealed that grain yield (Gy) and number of spikes per plant (Sp) traits had acute angle ( $\theta < 90^\circ$ ) between their vectors, indicating to strong and positive correlation ( $r = \cos \theta : 0 < \cos \theta < 1$ ). Meanwhile; these traits (Gy and Sp) were strong and negatively correlated with yellow rust susceptibility (Yr) trait, because the angle between their Gy and Sp trait vectors and Yr trait vector was an obtuse angle ( $\theta > 90^\circ$ ), whereas ( $r = \cos \theta : -1 < \cos \theta < 0$ ). Therefore, the correlations among traits could be shown by the biplot graph (Yan and Kang 2003). In comparing, these association results in biplot graph would be confirmed by correlation coefficients between these traits (Table 4). These results agreed to those obtained by correlation matrix, indicating that the GT biplot graph is a good substitute procedure for correlation coefficients for interpreting the interrelationships among the studied traits.



Gy: grain yield, Sp: number of spikes per plant and Yr: yellow rust resistance.

**Fig. 2. Graphical-biplot for diallel data of grain yield and its significant related traits, showing the best genotypes in general and specific combining ability (GCA and SCA) effects in F<sub>2</sub>'s bread wheat.**

The polygon view of the biplot describes the interaction between the genotype and the traits (Fig. 2). This graph was drawn by joining the outermost genotypes, which become the vertices of the polygon, to the origin, showing that part (I) with axes (+, +) was the best and superior genotypes and resistance (top of the part). Meanwhile, part (II) with axes (+, -) concluded the preferred lowest susceptibility coupled with faint yield. On the other side, parts (III, IV) with axes (-, - and -, +) were considered as the worse for both yield and susceptibility. Perpendicular lines drawn from the origin to the sides of the polygon divide the diagram into different genotype and trait sectors. It was noticed, most crosses were concentrated on best preferred part (I) far from the parents located in another parts (II, III, IV). Therefore, the SCA was higher than the GCA, indicating the importance of

non-additive gene actions more than additive one in controlling the studied traits.

The polygon sides facilitate comparison between neighboring vertex genotypes. The parents Sakha-93 (P<sub>5</sub>) and Giza 168 (P<sub>6</sub>) are plotted on the positive end of the x-axis coordinate and negative y-axis (quarter II in Fig. 2), indicating that they had positive GCA effects for Gy and Sp trait and negative GCA effects for Yr trait to the improvement of their F<sub>2</sub> combinations (Yan and Hunt 2002). Meanwhile, the negative GCA effect values for Yr trait were higher than positive GCA ones for Gy trait. There is similarity between the Griffing results and GGE biplot analysis (Darvishzadeh *et al* 2009 and Boćanski *et al* 2011). On the other hand, H46, H15 and H12 crosses recorded the highest SCA estimates for both Gy and Yr trait. The SCA effects are associated with the parents instead of the F<sub>2</sub> combinations in the GGE biplot analysis (Rastogim *et al* 2011 and Shariff and Motlagh 2011), considering, the interaction between the genotype and the traits. Thus, emphasis should be placed on the crosses that have the parents Sakha-93 (P<sub>5</sub>) and Giza 168 (P<sub>6</sub>) because they have higher GCA and SCA estimates according to the GGE biplot and Griffing methods. These crosses were identified as having the best SCA effects based on the showing similarity among these methods.

Finally, the GT biplot graph is considered a successful and effective technique beside or instead of diallel analysis. Undoubtedly, GT biplot graph is preferred because it is easy to interpret and more informative. Therefore, GT biplot graph might be considered as the best alternative analysis method to predict combining ability and distinguished the best general and specific combiners across all studied traits in the present study.

### **CONCLUSION**

Analysis of variance showed significant differences in studied traits among the six parental cultivars and 15 F<sub>2</sub> hybrids, and then the detailed analysis of combining ability was estimated. Accurate GCA and SCA variance estimates can increase the breeding efficiency. Both additive and non-additive gene action were important, meanwhile, the non-additive more important one in controlling the studied traits through these bread wheat genotypes. Simple correlation results showed that grain yield may be raised

through selection for more spikes and low yellow rust susceptibility. GGE biplot graphical analysis provides information about the effect of the parents on the GCA and SCA, and the standard group of similar genotypes. However, the graphical display of the SCA effects to produce superior F<sub>2</sub> combinations in only certain crosses but not in all cases. Accordingly, the results revealed that the GCA and SCA effects and identified the best crosses, using the traditional Griffing method. The GT biplot of the correlated traits was used to compare the studied wheat genotypes (crosses and its parents). It is clear that the biplot method is a good tool compared with traditional Griffing method of data analysis, whereas; it has the many advantages: 1) it performs the parent's GCA, 2) it shows hybrid's SCA, 3) it identifies the best crosses, and 4) it is more interpretative and facilitates pair-wise genotype comparisons 5) it facilitates identification of possible genotypes or traits groups among gene action. Therefore, GT biplot approach gives a complete picture about the interrelationships among genotypes and traits.

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## انتخاب التراكيب الوراثية المباشرة من قمح الخبز للتحمل لمرض الصدا الناصفر في الجيل الثاني

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ظهرت العديد من النماذج البيومترية لتحليل بيانات الهجن الدائرية مؤخراً. أجريت هذه الدراسة بغرض معرفة مدى إمكانية التنبؤ بالقدرة على الإنتلاف، ودراسة العلاقة بين التحليل البياني ثنائي الاتجاه وتحليل Griffing للهجن النصف دائرية، والتعرف على التراكيب الوراثية المتفوقة. تم تقييم ستة أصناف قمح الخبز كآباء وهجنها النصف دائرية (١٥ عشيرة من الجيل الثاني) خلال موسم ٢٠١٧/٢٠١٨ في مزرعة محطة البحوث الزراعية بسخا، مركز البحوث الزراعية، مصر، في تصميم القطاعات الكاملة العشوائية. أظهرت النتائج تباينات واسعة لكل من القدرة العامة والخاصة على الإنتلاف في معظم الصفات؛ حيث سجلت القدرة الخاصة قيماً أعلى من العامة، مشيراً إلى أهمية الفعل الجيني غير المضيف أكثر من المضيف في التحكم في الصفات المدروسة. أظهرت نتائج الارتباط البسيط أن محصول الحبوب قد يزيد بالانتخاب لعدد السنابل الأعلى والحساسية المنخفضة للصدأ الأصفر. أظهر كلا من التحليل البياني ثنائي الاتجاه وتحليل Griffing نتائج متماثلة لقيم GCA و SCA حيث اجمعا على ان الصنفان سخا ٩٣ (P<sub>5</sub>) وجيزة ١٦٨ (P<sub>6</sub>) هما أفضل الأباء والهجن سخا ٩٤ × جيزة ١٦٨ (H46)، مصر ١ × سخا ٩٣ (H15) ومصر ١ × مصر ٢ (H12) هي الأكثر تفوقاً. إلا أن إجراء التحليل البياني ثنائي الاتجاه لبيانات الهجن الدائرية أوضح الفعل الجيني وأفضل الهجن المؤهلة لبرامج التربية لتحسين جميع الصفات المرتبطة (GT)، كما يمكن مقارنة التراكيب الوراثية بناءً على صفات متعددة. لذلك، يعتبر تحليل بيانات ثنائي الاتجاه GT أفضل طريقة تحليل بديلة لـ Griffing، لما تعطيه من صورة كاملة عن العلاقات المتبادلة بين التراكيب الوراثية والصفات.

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