

USING BIPLLOT ANALYSIS OF F₁ FABA BEAN DIALLEL DATA TO PREDICT COMBINING ABILITY

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ABSTRACT

This study was carried out under insect cages during 2017/18 and 2018/19 seasons at Giza Research Station, ARC, Egypt to investigate the combining ability possibility prediction and relationship between biplot graph and Griffing of half diallel data, and to identify promising genotypes. Six parental faba bean genotypes and their half diallel crosses (15 F₁'s) were evaluated under a randomized complete block design in three replications. The results reflected significant differences for both GCA and SCA in most traits, indicating the important role of both additive and dominant components in the inheritance. Meanwhile, Baker's ratio emphasized the preponderant role of additive gene action in controlling the most studied traits. Simple correlation results showed that seed yield may be raised through selecting most pods and seeds per plant, which recorded the highest heritability in broad and narrow sense (h_b^2 and h_n^2 %) estimates coupled with highest genetic advance (GA %) in faba bean. Biplot graph (innovative) and Griffing (traditional) analysis exhibited equivalent results for gca and sca effects and are meaningful for identifying Giza 843 (P₁), Misr 1 (P₂) and Giza 40 (P₆) as the best parents and Giza 843 x Misr 1 (C12), Giza 843 x Nubaria 1 (C15), Misr 1 x Giza 3 (C24), Giza 716 x Nubaria 1 (C35) and Nubaria 1 x Giza 40 (C56) as promising five crosses. Then, GT-biplot method is considered as the best alternative analysis for giving a complete picture about the interrelationships among genotypes and traits (for relative comparing genotypes based on multiple traits). Hence, number of pods and seeds per plant traits could be used for the improvement of seed yield. Besides, five faba bean crosses were distinguished which possess genetic factors for high yield and highly promising to be employed in the development of high yielding populations of faba bean breeding programs.

Key words: GT-Biplot, Griffing, Diallel, Correlation, Combining ability, Promising, Heritability, Genetic advance.

INTRODUCTION

Faba bean (*Vicia faba* L.) is considered as the first food legume crop cultivated in Egypt, providing the main source of low cost protein with high nutritional value, for the majority of Egyptian population. Also, it can amend the Egyptian soil fertile by biological nitrogen fixation (Al-Ghamdi, 2007). The genetic improvement of crop desired traits depends on the nature and magnitude of genetic variability controlling the inheritance of these traits. It can be estimate using diallel cross technique, which provide early information on the genetic behavior of these traits in the first (F₁) generation (Chowdhry *et al* 1992).

Plant breeders consider the combining ability as important criteria, where it is useful in connection with testing procedures to study and compare the performance of hybrid combinations and the nature of gene action. So, the gene effect estimates were used to apply the most effective breeding procedure for improvement the desired traits (Bramawy and

Osman 2012). The total value of variances must be portioned into its genetic components for obtaining a clear picture of genetic mechanism of faba bean populations. Hence, the genetic components could be exploited in the improving yield potential and its components in faba bean plants, whereas, the superiority of crosses over parents for seed yield is associated with gene effects in important yield components. The important of gene action and heritability were previously discussed by El-Bramawy and Osman (2012), Ghareeb and Helal (2014) and Ghareeb and Fares (2015). Knowledge on genetic aspects, heritability and genetic advance is a basic step to identify the traits amenable to genetic improvement through selection. Bakheit *et al* (2011) and Fikreselassie and Seboka (2012) confirmed that considering genetic advance and the heritability values (h^2) would be practically useful in breeding program depending on phenotypic selection.

Diallel mating design provides a very simple and convenient method for the estimation of genetic parameters (Sadeghzadeh-Ahari *et al* 2014). The half diallel methods 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, Freitas Júnior *et al* 2006 and Abdalla *et al* 2017). Analysis of diallel data is usually done by Griffing (1956) method. The biplot GGE graphically technique helps breeders for generating superior hybrids (Yan and Kang 2003). This method has been utilized remarkably in faba bean breeding programs. A modified biplot GGE graphically method can be used as genotype-trait (GT-biplot) for all types of two-way data such as diallel data (Yan 2001 and Yan and Hunt 2002). Biplot approach based on diallel experimental data are used to estimate the general (GCA) and specific (SCA) combining ability and to identify potential heterotic relationships among different genotypes (Yan and Hunt 2002). For a given set of data, the following information can be easily visualized: the GCA effect 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 to study the combining ability and distinguished the best general and specific combiners

in faba bean (Sharifi 2018, Gurmu *et al.* 2012 and Yan and Hunt 2002) used biplot method for the analysis of genotypes and diallel cross data.

The objectives of this study were to 1) evaluate the performance of the studied faba bean diallel genotypes and the nature of gene action influencing seed yield components, 2) identify combining ability of parent's (GCA) and hybrid's (SCA), 3) discuss whether GT-biplot graph is possible to be a good alternative procedure for diallel analysis to predict GCA and SCA effects and 4) to explain the possibility of biplot graph in interpretation relationships among different genotypes and traits, showing the best crosses.

MATERIALS AND METHODS

The present investigation was conducted during the two growing seasons 2017/18 and 2018/19 under insect proof at Giza Research Station, ARC, Egypt. Six faba bean parental genotypes were selected on the basis of the presence of wide differences among them with respect to certain important traits (Table 1).

Table 1. Name, pedigree and special characteristics of six parental faba bean genotypes.

Parent	Pedigree	Seed type	Special remarks
Giza 843 (P ₁)	561/2076/85 × 461/845/83.	<i>Equina</i>	Resistant to <i>Orobanche</i> and foliar diseases.
Misir 1 (P ₂)	Derived from Giza3 × 123A/45/76	<i>Equina</i>	Tolerant to <i>Orobanche</i> .
Giza 716 (P ₃)	461/843/83 × 503/453/84.		Resistant to foliar diseases and early maturing.
Giza 3 (P ₄)	Cross (Giza 1 x Dutch Intr.).	<i>Equina</i>	Resistant to foliar disease and high yield.
Nubaria 1 (P ₅)	Single plant selection from Rina Blanca.	<i>Major</i>	Late mature, large seeded type and high resistant to foliar diseases.
Giza 40 (P ₆)	Derived from Rebaya 40.	<i>Equina</i>	Early mature and high susceptibility to foliar diseases.

The selected parents were crossed in a diallel model to obtain all possible combinations, excluding reciprocals during the first season of 2017/18, the parents and their respective F₁ hybrids (15 F₁ seeds) were sown during the second growing season (2018/2019). A randomized complete

block design (RCBD) with three replications was used. Each plot consisted of one ridge of 3m length and 60cm width. Hills were spaced 20cm with one seed by hill. Cultural practices were adopted as recommended for field beans production. At harvest, ten guarded plants were randomly sampled from each plot to provide measurements for plant height (cm), number of branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight (g) and seed yield per plant (g).

Statistical analysis

All data were subjected to analysis of variance. Data obtained from the 15 hybrids of F_1 and six parents were subjected to analysis by Griffing (1956) method II, model 1. The analysis of combining ability was performed to determine the combining ability to separate some components of genetic variance, such as additive and non-additive gene action under certain assumptions. Heritability and genetic parameters were determined through variance component method (Breese, 1972). Predicted genetic advance as mean percent from selection (GA %) was calculated according to Johanson *et al* (1955) at 5% selection intensity. Baker's ratio was used for approximate estimations of gene effects (Baker 1978).

Model for GGE Biplot

GGE (genotype main effect plus genotype-by-environments interaction) biplot are commonly used to analyze two-way data, where rows and columns represent different experimental units (Yan and Hunt, 2002). In addition, GGE biplot might be modified to GGT (genotype main effect plus genotype-by-traits interaction). Yan and Rajcan (2002) used the genotype by trait (GGT) 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 biplot presented in this paper were performed with the procedures of GenStat software package (18.0 version) by ICARDA.

RESULTS AND DISCUSSION

The variability among populations is the basis of progress in the breeding program of a certain crop traits in which the desirable traits are heritable. However, the information of the genetic parameters as parents and their crosses may be helpful to breeders in order to identify the best

combiners which may be hybridized to build up favorable fixable genes in Egypt. This information offers a great opportunity to improve yield and its traits inheritance in faba bean.

Combining ability and genetic analysis

The statistical analysis of variance revealed significant differences ($P \leq 0.01$) among all genotypes (parents and their possible F_1 's) for plant height, number of branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight and seed yield per plant traits (Table 2). These findings indicated the presence of high considerable amount of genetic variability among these genotypes, which may facilitate genetic improvement in faba bean. These results were in harmony with those reported by Bramawy and Osman (2012), Ghareeb and Helal (2014) and Ghareeb and Fares (2015).

Table 2. Mean squares and Griffing analysis of variance due to various studied traits in F_1 's faba bean.

SOV	df	Plant height	No. of branches/plant	No. of pods/plant	No. of seeds /plant	Seed yield/plant	100-seed weight
Replications	2	17.33	0.98	3.05	5.25	54.29	47.33
Genotypes	20	184.97**	3.29**	157.14**	1321.40**	1015.89**	413.80**
Error	40	28.7	0.863	8.398	39.48	27.85	35.52
GCA	5	97.24**	1.26**	35.17**	561.57**	356.87**	26.42
SCA	15	49.79**	1.04**	58.12**	400.10**	332.55**	175.10**
GCA/SCA		1.95	1.18	0.61	1.40	1.07	0.15
Baker ratio		0.80	0.71	0.55	0.74	0.68	0.23

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

Concerning combining ability and type of gene action in the above mentioned results in Table (2), the detailed analysis was appropriate for estimating the traits investigated through this study. ANOVA of the diallel data set with respect to seed yield and its components attributes revealed a highly significant general (GCA) and specific combining ability (SCA) for most traits. The GCA variance was significant or highly significant for plant height, number of branches per plant, number of pods per plant, number of seeds per plant and seed yield per plant traits, indicating the involvement of additive gene action in these traits. Meanwhile, SCA variance contains highly significant non-additive for all traits except for number of branches

per plant. The previous results of significant estimates of both GCA and SCA variances suggested that each of additive and non-additive nature of gene actions were involved in controlling these traits through all faba bean genotypes. These results are agree with those findings by Ibrahim (2010), El-Bramawy and Osman (2012), Ghareeb and Helal (2014), El-Harty (2016) and Abdalla *et al* (2017) who reported the significant genetic variation among faba bean genotypes in respect to yield and yield components.

Both GCA and SCA were significant for most traits. Mean square values were higher for GCA than SCA for plant height, number of branches per plant, number of seeds per plant and seed yield per plant in faba bean genotypes. There were higher than unity, indicating the importance of additive gene effects more than non-additive one in the genetic expressions, which controlling these traits (Abdalla *et al* 2017). Therefore, selection can be effective in the improvement through these faba bean materials. In contrast, non-additive gene action was found to be more important for number of pods per plant and 100-seed weight traits only.

According to Baker (1978) ratio, when combining ability ratio approached near unity for plant height, number of seeds per plant, number of branches per plant and seed yield per plant (0.80, 0.74, 0.71 and 0.68, respectively), 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 as number of pods per plant and 100-seed weight (0.55 and 0.23, respectively) in the present study, because the value of Baker's ratio is much lower than the unity. Therefore, the high Baker's ratio emphasized the preponderant role of additive gene action in controlling the most studied traits in faba bean in comparison to non-additive (dominance and/or epistatic) one. This state is due to the deferential parental ability to combine well with each other. These results were confirmed obviously by El-Bramawy and Osman (2012), Ghareeb and Helal (2014).

Mean performance of parents and their hybrids

Table (3) showed the mean performance of six parents and their respective crosses. The parent P₄ (Giza3) had the tallest plants (118.33cm) whereas F₁ crosses P₁×P₂ (Giza843× Misr 1) recorded the tallest cross (126.00cm).

Table 3. The genotypes mean performances for faba bean yield traits in the six parents and its F₁ crosses.

Genotypes	Plant height	No. of branches /plant	No. of pods/plant	No. of seeds/plant	Seed yield/plant	100-seed weight
P₁ Giza 843	101.67	5.33	16.00	66.00	53.00	83.33
P₁XP₂	126.00	5.67	37.33	104.33	82.57	79.17
P₁XP₃	119.00	5.33	23.67	78.50	79.27	100.77
P₁XP₄	119.00	4.00	23.00	84.67	73.33	93.43
P₁XP₅	110.33	5.00	34.33	101.67	81.93	81.13
P₁XP₆	113.00	6.33	22.33	67.00	76.87	114.67
P₂ Misr 1	113.33	5.33	16.33	66.67	51.67	79.67
P₂XP₃	105.33	5.67	22.67	66.00	58.83	89.00
P₂XP₄	106.67	5.33	31.33	94.00	87.00	92.13
P₂XP₅	107.00	5.00	21.33	78.33	73.33	93.00
P₂XP₆	112.67	5.00	20.00	67.00	69.33	104.33
P₃ Giza 716	96.67	4.33	12.33	35.00	29.67	84.00
P₃XP₄	104.00	4.00	17.00	45.00	39.67	87.17
P₃XP₅	104.67	4.33	20.33	85.67	69.83	81.67
P₃XP₆	100.67	6.00	20.67	62.17	60.50	92.67
P₄ Giza 3	118.33	4.00	12.67	35.00	40.00	86.67
P₄XP₅	117.00	3.00	26.67	58.33	39.53	66.67
P₄XP₆	115.67	5.33	16.00	55.67	59.43	105.00
P₅ Nubaria 1	96.67	6.33	9.50	33.00	33.67	101.67
P₅XP₆	114.00	5.00	24.67	85.67	84.67	97.00
P₆ Giza 40	108.33	4.00	27.33	75.00	50.00	68.33
Grand mean	110.00	4.96	21.69	68.79	61.62	89.59
LSD (5%)	8.84	1.60	4.78	10.37	8.71	9.83

The parental genotype P₅ (Nubaria 1) exhibited the highest number of branches per plant (6.00 branch) and 100-seed weight (101.67g), meanwhile crosses P₁×P₆ (Giza843×Giza40) recorded the highest values for these traits (6.33 branch and 114.67g, respectively). The parent P₆ (Giza40) showed the highest values for number of pods (27.33 pod) and number of seeds (75.00 seed), moreover F₁'s P₁×P₂ (Giza843× Misr 1) revealed the highest values for the same traits(37.33 pod and 104.33 seed, respectively).

Regarding to seed yield per plant, the highest values for parents were exhibited by P₁ (Giza 843) and P₂ (Misr 1) with (53.00g and (51.67g), respectively. On the other side, the cross P₂XP₄ (Misr 1×Giza3), P₅XP₆ (Nubaria 1× Giza 40), P₁×P₂ (Giza 843×Misr 1) and P₁×P₅ (Giza

843×Nubaria 1) possessed the highest value for seed yield with (87.00 g), (84.67 g), (82.57 g) and (81.93 g), respectively. Then, these four crosses (Misr 1×Giza3, (Nubaria 1× Giza 40), Giza 843×Misr 1 and Giza 843×Nubaria 1) recorded the best performance for both number of pods and number of seeds coupled with seed yield per plant. These results could confirm the possibility of selection for these traits through hybridization of respective parents with allowing plant breeders to build future breeding program for high potential yield in faba bean crop. Similar results were obtained by El-Bramawy and Osman (2012), Ghareeb and Helal (2014) and Abdalla *et al* (2017) with respect to seed yield development.

Genetic parameters

Genetic variability is very important for the improvement of faba bean crop. Significant differences were observed for all the studied traits, considering adequate variability provides a good chance for improvement in studied faba bean genotypes. Estimates of PCV and GCV coefficients of variation, heritability (in broad h_b^2 and narrow h_n^2 sense) and GA expected from selecting the superior genotypes for each trait computed using the variance components (σ_{ph}^2 , σ_g^2 and σ_A^2 one) based on the diallel analyses are shown in Table (4). In general, phenotypic variance (v_{ph}) was greater than the genotypic variance (v_g) for all studied traits. Therefore, phenotypic coefficient of variability (PCV %) was higher than corresponding genotypic (GCV %) ones for all traits, confirming the environmental effects upon the traits. The highest phenotypic and genotypic coefficient of variability were recorded for number of pods per plant (58.81 and 57.28%), number of seed per plant (53.36 and 52.58%) and seed yield (52.19 and 51.49 %), respectively. This indicates the presence of exploitable genetic variability for these traits. Similar results were obtained by Ghareeb and El-Emam (2013) and El-Harty (2016).

Heritability estimates and genetic advance provide information about the expected grain in the following generations. The most important function of heritability in the genetic studies of quantitative traits is their predictive role. Possible advance through selection based on phenotypic values can be predicted only from knowledge of the degree of correspondence between phenotypic and genotypic values.

Table 4. Estimates of genetic variances, heritability and genetic advance % of the some faba bean studied traits.

Genetic parameters		Plant height	No. of branches /plant	No. of pods /plant	No. of Seeds /plant	Seed yield /plant	100-seed weight
Variance	Phenotypic (σ^2_{ph})	204.1	3.87	162.74	1347.72	1034.45	437.48
	Genotypic (σ^2_g)	175.4	3.00	154.34	1308.24	1006.61	401.96
	Additive (σ^2_A)	71.44	2.01	40.34	395.85	107.50	73.47
Coefficient of variation	Phenotypic (PCV%)	12.99	39.71	58.81	53.36	52.19	23.35
	Genotypic (GCV%)	12.04	34.99	57.28	52.58	51.49	22.38
Heritability	Broad ($h_b^2\%$)	85.94	77.52	94.84	97.07	97.31	91.88
	Narrow ($h_n^2\%$)	21.97	63.21	66.73	74.24	11.06	29.65
Expected Genetic advanced	GA	25.29	3.15	24.92	73.41	64.47	39.59
	Percent mean GA%	22.99	63.53	114.91	106.71	104.62	44.19
	Maximum expected	135.29	8.10	46.61	142.20	126.10	129.18

Table (4) and Figure (1) revealed that heritability in broad sense (h_b^2 %) estimates were generally high for all studied traits and recorded values from 97.31% for seed yield per plant to 77.52 % for number of branches per plant. In general, the traits as seed yield per plant, number of seed per plant and number of pods per plant had higher heritable values. Hence it can be assumed that phenotypes of almost all the traits are mainly determined by their genotypes (Ghareeb and El-Emam 2013 and Ghareeb and Helal 2014). High heritability values coupled with high genetic advance were observed for these last traits. From the results, it can be concluded that all these traits are controlled by additive type of gene action as reported by other workers. Similar results were also obtained by El-Hady *et al.* (2009) and Ghareeb and El-Emam 2013 who reported high heritability coupled with high genetic advance for most of the quantitative characters.

Figure (1) revealed that higher estimates of expected genetic advance percent (GA%) were observed for number of pods per plant (114.91%), number of seeds per plant (106.71%) and seed yield per plant (104.62%). Based on this expected (GA %), the maximum expected value for these traits may be recorded values reach to 46.61 pods for number of pods per plant, giving 142.20 seeds and producing 126.10 g as seed yield per plant.

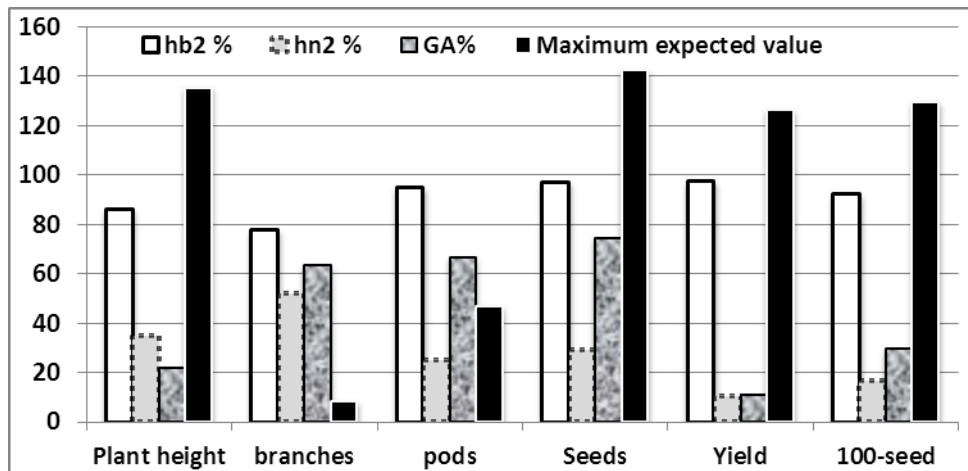


Fig. 1. Estimates of broad (h_b^2 %) and narrow (h_n^2 %) sense heritability, genetic advance % and maximum expected value of some faba bean studied traits.

Meanwhile, heritability in narrow sense (h_n^2 %) exhibited highest estimates for number of seeds per plant (74.24%), number of pods per plant (66.73%) and number of branches per plant (63.21%). High estimates of (h_n^2 %) heritability indicated that selection based on mean of number of seed per plant, number of pods per plant and number of branches per plant would be successful in faba bean improvement (Ghareeb and Helal 2014).

It is clear that a trait with high GCV and high heritability h_b^2 % will have high genetic advance. It can be stated that high heritability h_b^2 % for a trait does not necessarily mean that it will also show high genetic gain, unless it is coupled with high GCV. The heritability h_n^2 %, which is a ratio of genotypic and phenotypic variance, is mainly due to the additive gene effects in narrow sense, but in the broad sense h_b^2 % it includes both additive as well as non-additive gene effects. The heritability values estimated are expressed in broad sense, however, gives only a rough estimate. Moreover, broad sense heritability and narrow sense heritability are generally negatively correlated (Kempthorne 1957). Heritability h_n^2 % was mainly due to additive effects in number of pods and seeds per plant that would be associated with high genetic gain GA%. Meanwhile, high

genetic gain GA% value in seed yield per plant was due to non-additive effects (Panse 1957).

From previous results, improvement in these yield traits (number of pods per plant, number of seeds per plant and seed yield per plant) can be achieved through mass selection for recording high heritability and uppermost genetic advance (GA%), indicating positively of improvement of these traits by selection. In conclusion, the present results revealed that several of the obtained faba bean crosses are highly promising and can be used in breeding programs which possess genetic factors for high yield potentiality.

Correlation studies

Adequate knowledge of the relationship that exists between seed yield and yield-related traits is essential for the identification of selection criteria to be used for yield improvement in faba bean. Simple correlation coefficients for all comparisons among the faba bean studied traits in F₁ generation are presented in Table (5).

Table 5. Simple correlation coefficients for all comparisons among the faba bean studied traits in F₁ generation (n=63).

Character	Plant height	No. of branches	No. of pods/plant	No. of seeds/plant	100-seed weight
No. of branches/plant	-0.025				
No. of pods/plant	0.377**	0.131			
No. of seeds/plant	0.351**	0.234	0.844**		
100-seed weight(g)	-0.007	0.363**	-0.261*	-0.115	
Seed yield/plant(g)	0.354**	0.386**	0.683**	0.867**	0.394**

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

Results showed that there was a highly significant positive correlation between plant height, number of branches per plant, number of pods, number of seeds per plant and 100-seed weight (0.354**, 0.386**, 0.683**, 0.867** and 0.394**). This strong correlation suggested that seed yield may be raised through selection for the more branches, pods, seeds

and 100-seed weight. On the other hand, number of pods correlated significantly and negatively with 100-seed weight (-0.261^{*}). However, significant and negative associations were obtained between 100-seed weight and the number of seeds trait (-0.115), indicating that this trait may be independent in their genetic behavior under the tested genotypes. Meanwhile, the magnitude of the correlation coefficients among number of seeds per plant and number of pods per plant traits was highly significant. These findings indicate that selection for number of pods and seeds per plant in faba bean would be accompanied by high yielding ability. These findings are in agreement with those obtained by Alghamdi (2007), Tadesse *et al* (2011), Yamani *et al* (2012) and Osman *et al* (2013).

Combining ability

The estimates of GCA effects for different genotypes which differed from one individual parent to another and from trait to trait, are listed in Table (6). 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 variety Giza 843 (P₁) and Misr 1 (P₂) were good combiners for number of pods per plant (2.67^{**} and 1.75^{**}, respectively), number of seeds per plant (10.99^{**} and 7.85^{**}, respectively) and seed yield per plant (8.74^{**} and 5.55^{**}, respectively). Meanwhile, Giza 40 (P₆) showed significantly positive GCA values for seed yield per plant and 100-seed weight (2.60^{*} and 3.11^{**}). On other hand, Giza 716 (P₃) Giza 3 (P₄) and Nubaria1 (P₅) had highly significant negative GCA for seed yield per plant (-7.83^{**}, -6.38^{**} and -2.68^{**}, respectively).

From above, it was mentioned that GCA effects associated with each parent revealed that the parental genotypes Giza 843 (P₁), Misr 1 (P₂) and Giza 40 (P₆) were good combiners (Figure 2) for seed yield per plant (8.74^{**}, 5.55^{**} and 2.60^{**}). Therefore, these parents could be considered as good combiners for improving these studied traits, since they showed significant positive values according to the desirable trend of seed yield trait. These findings are relatively similar with those of Ibrahim (2010), El-Bramawy and Osman (2012), Ghareeb and Helal (2014), El-Harty (2016) and Abdalla *et al* (2017).

Table 6. Estimates of general and specific combining ability effects (GCA and SCA) for studied traits in F₁'s faba bean and its parents.

Genotypes	Plant height	No. of branches/plant	No. of pods/plant	No. of Seeds/plant	Seed yield/plant	100-seed /plant
Giza 843 (P ₁)	2.58*	0.33	2.67**	10.99**	8.74**	1.29
Misr 1 (P ₂)	1.79	0.38*	1.75**	7.85**	5.55**	-1.07
Giza 716 (P ₃)	-5.38**	-0.04	-2.79**	-9.11**	-7.83**	-0.78
Giza 3 (P ₄)	3.63**	-0.58**	-1.50**	-9.07**	-6.38**	-0.97
Nubaria1 (P ₅)	-2.96**	-0.25	-1.00	-1.57	-2.68**	-1.59
Giza 40 (P ₆)	0.33	0.17	0.88	0.91	2.60*	3.11**
S.E.(gi-gj)	1.55	0.28	0.84	1.81	1.52	1.72
C12	11.63**	0.05	11.30**	16.89**	6.85**	-10.42**
C 13	11.79**	0.14	2.17	8.01**	16.92**	10.90**
C 14	2.79	-0.65	0.21	14.14**	9.54**	3.75
C 15	0.71	0.01	11.05**	23.64**	14.43**	-7.93**
C 16	0.08	0.93*	-2.83*	-13.51**	4.10	20.91**
C 23	-1.08	0.43	2.09	-1.34	-0.32	1.49
C 24	-8.75**	0.64	9.46**	26.62**	26.40**	4.81
C 25	-1.83	-0.03	-1.04	3.45	9.03**	6.30*
C 26	0.54	-0.45	-4.24**	-10.36**	-0.24	12.94**
C 34	-4.25	-0.28	-0.33	-5.42*	-7.56**	-0.44
C 35	3.00	-0.28	2.51*	27.74**	18.90**	-5.32*
C 36	-4.29	0.97*	0.96	1.76	4.30	0.98
C 45	6.33**	-1.07*	7.55**	0.37	-12.84**	-20.13**
C 46	1.71	0.85*	-4.99**	-4.78	1.79	13.51**
C 56	6.63**	0.18	3.17*	17.72**	23.31**	6.13*
S.E.(Sij-Sik)	4.09	0.74	2.21	4.80	4.03	4.55

C_{ij}: Cross female * male.

Regarding to the values of SCA effects, Table (6) revealed that four crosses (P₁×P₂, P₁×P₃, P₄×P₅ and P₅×P₆) had highly significant positive SCA effects for plant height. In number of branches per plant, only three crosses (P₁×P₆, P₃×P₆ and P₄×P₆) recorded significant positive SCA effects. Six crosses (P₁×P₃, P₁×P₄, P₂×P₅, P₂×P₆, P₄×P₆ and P₅×P₆) exhibited four highly significant positive crosses and two significant crosses for 100-seed weight.

Concerning on pods and seeds number, and seed yield per plant, results in, Table (6) and Figure (2) showed that six crosses ($P_1 \times P_2$, $P_1 \times P_5$, $P_2 \times P_4$, $P_3 \times P_5$, $P_4 \times P_5$ and $P_5 \times P_6$) exhibited positive and significant or highly significant values for number of pods per plant. While, seven crosses ($P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_4$, $P_1 \times P_5$, $P_2 \times P_4$, $P_3 \times P_5$ and $P_5 \times P_6$) had highly significant positive SCA effects for number of seeds per plant. Thus, eight crosses ($P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_4$, $P_1 \times P_5$, $P_2 \times P_4$, $P_2 \times P_5$, $P_3 \times P_5$ and $P_5 \times P_6$) showed highly significant positive SCA effects for seed yield per plant. Therefore, five crosses ($P_1 \times P_2$, $P_1 \times P_5$, $P_2 \times P_4$, $P_3 \times P_5$ and $P_5 \times P_6$) had high values for number of pods, seeds and seed yield per plant. These findings are similar with those of Ibrahim (2010), El-Bramawy and Osman (2012), Ghareeb and Helal (2014) and Abdalla *et al* (2017).

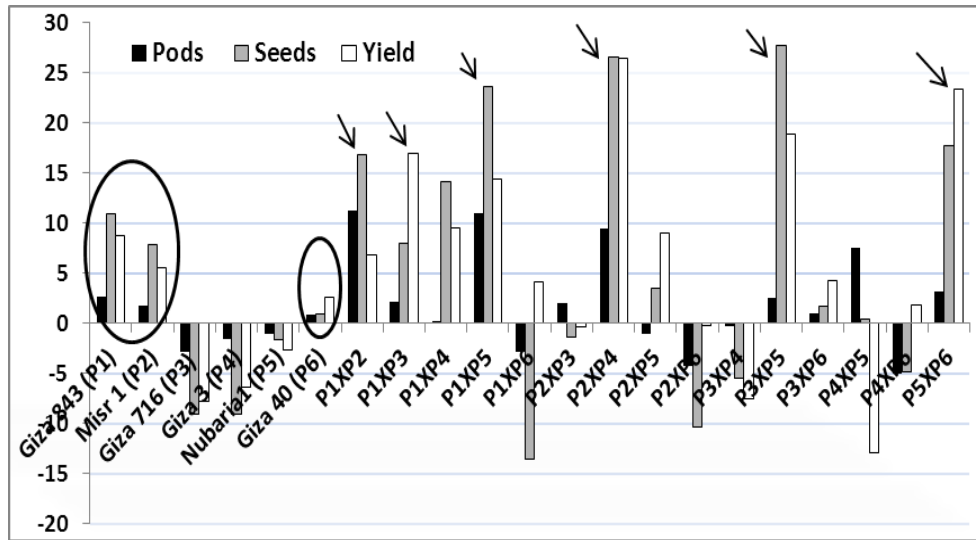


Fig. 2. Genotypes comparison for general and specific combining ability (GCA and SCA) effects of some important yield traits (number of pods, seeds and seed yield per plant).

Therefore, from obvious results, Giza 843 (P_1), Misr 1 (P_2) and Giza 40 (P_6) can be considered as the most efficient cultivars based on their positive GCA performance, and the five crosses ($P_1 \times P_2$, $P_1 \times P_5$, $P_2 \times P_4$, $P_3 \times P_5$ and $P_5 \times P_6$) had high positive SCA values for some important yield traits

(number of pods, seeds and seed yield per plant). These findings indicate that SCA for seed yield per plant may be influenced by SCA for number of pods and seeds per plant.

Biplot graph to predict best GCA and SCA effects

In this study, the application of biplot techniques for diallel experimental data is sufficient to explain the whole performance variation of the parents and the hybrid combinations (Yan and Hunt 2002). Biplot approach based on diallel data are used to plot the general combining ability (GCA) and specific combining ability (SCA) effects among different genotypes (Yan and Hunt, 2002). Biplot graph was used to compare genotypes on the basis of seed yield and its significant related traits (plant height, number of branches per plant, number of pods per plant, number of seeds per plant and 100-seed weight) and to identify good genotypes to select the best gca and sca effects in the studied faba bean F_1 's, are shown in (Figure 3).

Among Figure (3) of GGE-biplot based on GT (genotype and traits) for comparison of the genotypes with the ideal one and showing GCA and SCA effects in F_1 's faba bean, results revealed the relationship among the studied faba bean genotypes (crosses and its parents) using the seed yield and its related traits. The GT biplot of the mean performance of these traits explained 93.79 % of the total variation of the standardized data. Principal component 1 and principal component 2 (PC1 and PC2) explained 75.21% and 18.57%, 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 2002 and Yan and Kang 2003). Similar results were found in most cases by Girma *et al* 2011) in field pea, Gurmu *et al* 2012 and Sharifi (2018) in faba bean.

This graph of GT biplot in Figure (3) showed that a vector is drawn from the biplot origin to each marker of the traits to visualize the relationships among the studied related traits (Yan and Tinker 2005); describing the interaction between the genotype and the traits. The thick line that passes through the origin and the average traits, considered as the Average-Tester Axis (ATA), a small circle indicating the position of the

average trait, and an arrow pointing to the average trait from the origin in the seed yield direction. Ranking based on the genotype-focused scaling assumed that discriminate for high mean yield were depend on the gain of multiple traits (Yan 2002). The best candidate genotypes were expected to have high mean seed yield with stable performance across all test traits. In practice, such genotypes are very rarely to be found. Therefore, high yielding and relatively genotypes performance for other traits can be considered as references for genotype evaluation (Yan and Tinker 2006).

The GT biplot graph revealed that cross (C24) fell in the central circle indicating its high seed yield and relative performance stability for other traits compared to the rest of studied genotypes (Figs. 2). It is obvious that genotype cross (C24) recorded high values of plant height, number of branches, number of pods, number of seeds, 100-seed weight and thus seed yield. In addition, crosses (C56), (C13), (C14), (C15), (C12) and (C35) were potted close to the ideal genotype or around the center of concentric circle, suggesting their potential for specific adaptability with better seed yield performances. Parents (P₁, P₂ and P₃) located in the middle and were the nearest parent for the central circle, being the best ones.

It is worth mentioning that, the studied genotypes, crosses (C24), (C56), (C13), (C14), (C15), (C12) and (C35) were the top performing and best yield advantages. Hence, they are recommended for further verification and possible release. Meanwhile, all crosses assumed the nearest points to the centric circle best than parents, indicating to their relatively poor performance toward these traits and superiority of these crosses. These crosses were identified as having the best SCA based on showing similarity among these methods.

In the present study, seed yield per plant (SY) was the most discriminating trait followed by number of seeds per plant (seeds) and number of pods per plant (pods) (Figure 3). Meanwhile, plant height (PH), number of branches per plant (Bra) and 100-seed weight (Hs) were non-discriminating and less representative traits (Figure 3). Similarly, Gurmu *et al* (2012) and Sharifi (2018) reported that some genotypes were stable, representative and discriminating among traits for the performance of evaluated faba bean genotypes.

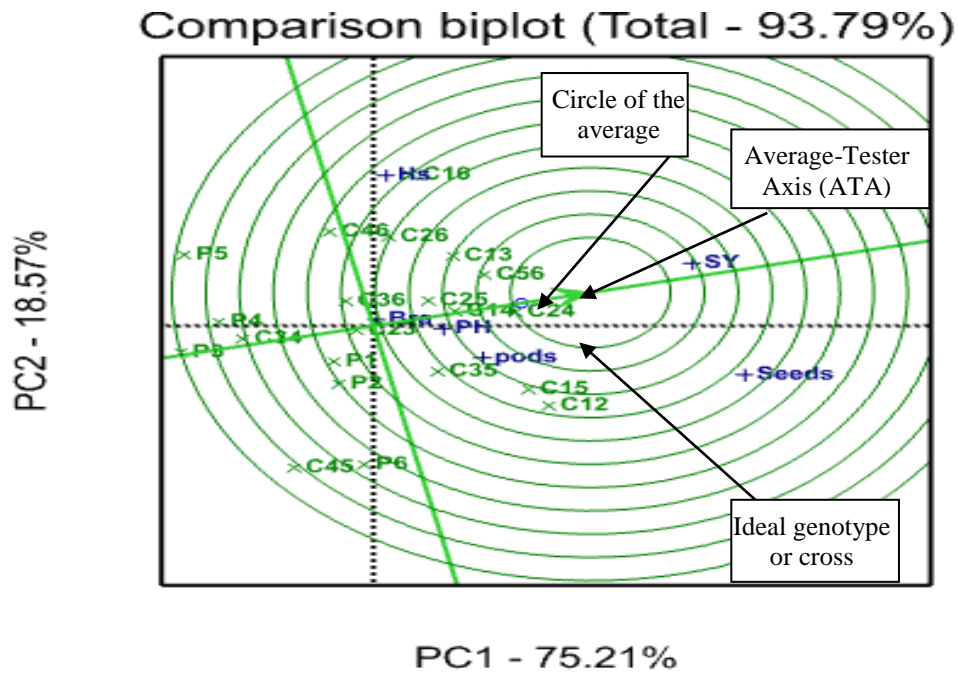


Fig. 3. GGE-biplot based on GT (genotype and traits) for comparison of the genotypes with the ideal one and showing GCA and SCA effects in F₁'s faba bean.

Finally, the GT biplot graph is considered as a successful and effective technique beside or instead of diallel analysis. Undoubtedly, GT biplot graph is preferred because it is easy to interpret and is 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 faba bean.

CONCLUSION

The GCA variance contains highly significant additive effect for all traits except for hundred seed weight. Meanwhile, SCA variance was highly significant for all traits, suggesting that each of additive and non-additive nature of gene actions were involved in controlling these traits through all faba bean genotypes. These results were confirmed by Baker's ratio and heritability estimates, where recorded values ranged from 97.31% for seed yield per plant to 77.52 % for number of branches per plant. High

heritability values coupled with phenotypic (PCV %) and genotypic (GCV %) coefficient of variability, and high genetic advance (GA %) were observed for seed yield per plant, number of seed per plant and number of pods per plant traits. Correlation coefficients indicated that selection for number of pods and seeds per plant in faba bean would be accompanied by high yielding ability. Based on their positive gca and sca effects and (GT) biplot graph, Giza 843 (P1), Misr 1 (P2) and Giza 40 (P6) can be considered as the most efficient cultivars, and the five crosses (P1×P2, P1×P5, P2×P4, P3×P5 and P5×P6) had high sca values for some important yield traits (number of pods, seeds and seed yield per plant), whereas, crosses recorded sca effects higher than parent gca ones. The GT biplot graph is considered a successful and effective technique beside or instead of diallel analysis, suggesting gene action and the best crosses for simultaneous improvement over all studied traits and comparing genotypes based on multiple traits. 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, discriminating among all studied traits in faba bean. In conclusion, the present results revealed that several of the obtained faba bean crosses are highly promising to be used in breeding programs which possess genetic factors for high yield potentiality.

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استخدام التحليل ثنائى الاتجاه لبيانات الجيل الاول للفول البلدى للتنبؤ بالقدرة على الائتلاف

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١. قسم بحوث المحاصيل البقولية - معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية- الجيزة - مصر .
٢. المعمل المركزى لبحوث التصميم و التحليل الاحصائى- مركز البحوث الزراعية- الجيزة - مصر .

أجريت هذه الدراسة خلال الموسمين 2017/18 - 2018/19 داخل الصوبة السلكية بمحطة البحوث الزراعية - مركز البحوث الزراعية بالجيزة- مصر، وذلك بهدف دراسة العلاقة بين طريقة تحليل ثنائى الاتجاه البيانية وطريقة جريفنج لتحليل بيانات الهجن التبادلية فى امكانية التنبؤ بالقدرة على الائتلاف والتعرف على التركيب الوراثية المباشرة. تم تقييم ستة أباء من الفول البلدى و هجن الجيل الأول (١٥) الناتجة فى اتجاه واحد بدون الهجن العكسية باستخدام تصميم القطاعات الكاملة العشوائية فى ثلاث مكررات. وقد أوضحت النتائج وجود اختلافات معنوية لكلا من القدرة العامة والخاصة على الائتلاف لمعظم الصفات. إلا أن نسبة معامل بيكر أبرزت قوة دور الفعل الجينى المضيف فى التحكم فى معظم الصفات المدروسة. اشارت نتائج معامل الارتباط لامكانية رفع محصول بذرة النبات فى الفول البلدى من خلال انتخاب للقيم الاعلى لكل من صفتى عدد القرون والبذور على النبات ؛ حيث سجلتا كلتاهما اعلى قيم كفاءة توريث بنوعيهما (الواسع والضيق) مقترنة بقيم معدل التحسين الوراثى المتوقع العالية. اظهرتا طريقتى تحليل ثنائى الاتجاه البيانية (المقترحة) وطريقة جريفنج (التقليدية) لتحليل بيانات الهجن التبادلية نتائج مترادفة لكل من تأثيرالقدرة العامة والخاصة على الائتلاف والمعنية بتحديد التركيب الوراثية جيزة ٨٤٣ ، ومصر ١ ، و جيزة ٤٠ كأفضل آباء ؛ بينما اعتبرت الهجن الخمسة (جيزة ٨٤٣ × مصر ١ ، جيزة ٨٤٣ × نوبارية ١ ، مصر ١ × جيزة ٣ ، جيزة ٧١٦ × نوبارية ١ ، نوبارية ١ × جيزة ٤٠) كتركيب وراثية مباشرة. لذا تعتبر طريقة تحليل ثنائى الاتجاه افضل طريقة بديلة لاعطاء صورة كاملة عن العلاقات المتداخلة بين التركيب الوراثية والصفات (لمقارنة التركيب الوراثية بناء على صفات متعددة). وعليه، يتم أخذ صفتى عدد القرون والبذور على النبات فى الاعتبار، بالإضافة الى امكانية استخدام الهجن الخمسة المباشرة والتي تحمل العوامل الوراثية عالية المحصول كهجن مباشرة (واعدة) عند تنفيذ برامج التربية لتحسين انتاجية الفول البلدى.

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