

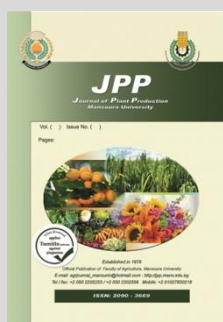
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### Estimation of Gene Action and Heterosis in F<sub>1</sub> And F<sub>2</sub> Diallel Crosses among Seven Genotypes of Field Bean

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#### ABSTRACT

Heterosis, gene action, combining ability (GCA and SCA) effects and variances were studied in 21 F<sub>1</sub> and F<sub>2</sub> crosses derived from 7x7 half diallel scheme of field bean. To detect prospective and efficient material for immediate use in breeding programs to enhance field bean productivity. F<sub>1</sub> and F<sub>2</sub> with parents were arranged in RCBD with 3 replicates to evaluate seed yield and its components traits in 2018/2019 season. Mean squares (MS) for genotype and its partitioning (parent, crosses and parent vs crosses) were significant for all studied traits in both generations. P<sub>1</sub>xP<sub>5</sub> and P<sub>3</sub>xP<sub>6</sub> exhibited significant heterotic effect for seed yield plant<sup>-1</sup> in F<sub>1</sub> and F<sub>2</sub> generations. Significant GCA and SCA MS were found for all studied traits, where proportion of additive was great for most traits in both generations, revealing predominance of additive gene effects. P<sub>2</sub> (Sakha 2), P<sub>5</sub> (M-13), P<sub>7</sub> (M-1017) in F<sub>1</sub> and P<sub>6</sub> (M-148) in F<sub>2</sub> were good combiners for seed yield and at least one of its components. More than 25 % of studied crosses showed positive and significant SCA effects for seed yield in F<sub>1</sub> and F<sub>2</sub> generations. The cross P<sub>1</sub>xP<sub>5</sub> showed desirable SCA effects in both generation for seed yield and resistance to chocolate spot disease%. Significant and larger values of dominance component (H<sub>1</sub>) than additive were obtained for all studied traits resulting in more values of (H<sub>1</sub>/D)<sup>0.5</sup> which were exceeded unity in both generations. Low narrow-sense heritability was exhibited in both generations for all traits, indicating that presence of non-additive genetic effects.

**Keywords:** Combining ability, Field bean, Gene action and Heterosis.

#### INTRODUCTION

Field bean (*Vicia faba* L.) is the most principle winter leguminous crop in Egypt. It use as a source of food protein in human diets. The annual production supplies below about one-half of the total consumption in Egypt (FAO, 2018). To satisfy the national requirement of that legume either the area or yield per unit area should be increased. Thus, increasing yield of this crop is the ultimate goal of the plant breeder (El-Abssi *et al.* 2019a).

Several methods are available to study the inheritance of quantitative traits. The diallel is of common usage in this respect for its power and versatility. Different approaches to the diallel analysis for estimating certain genetic parameters in terms of gene models have been developed. The knowledge of combining ability would be of great value to plant breeder, as it provides information about possibilities and methods of improvement for different traits. More and more information on the nature and magnitude of gene effects and genetic variances would certainly be useful for the proper utilization of variability in improvement of this crop. Also, Hayman's diallel analysis (1954) is one which has been extensively used by plant breeders to derive quite information about the materials at their disposal.

In an often-cross pollinated crop like field bean hybridization is difficult and number of hybrid seeds obtained is often too few to evaluate diallel crosses. Thus, labor required to obtain sufficient F<sub>1</sub> hybrid seeds might be disproportionate to the information to be gained.

Consequently, dense planting is restricted too. In fact in many hermaphrodite plants like field bean, it's easier to raise large F<sub>2</sub>'s than to produce F<sub>1</sub> seed in large quantity (Ashri *et al.* 2014). F<sub>2</sub> analysis might be used for such species. Better information could be obtained when both F<sub>1</sub> and F<sub>2</sub> generations are compared at the same year. The choice of a suitable breeding procedure for genetic amelioration depends largely upon the relative magnitude of different components for genetic variation (Bishnoi *et al.* 2018, El-Abassi *et al.* 2019 a & b).

This study was conducted to compare the results of heterosis, performance, genetic parameters obtained from F<sub>2</sub> crosses with those F<sub>1</sub>. Also, the possibility F<sub>2</sub> diallel cross was used in situation the F<sub>1</sub> diallel for certain quantitative characters in 7x7 diallel set of field bean.

#### MATERIALS AND METHODS

The field experiments were carried out during three successive seasons of 2016-2017, 2017-2018 and 2018-2019 in the Agricultural Research and Experimental Center, Faculty of Agriculture, Moshtohor, Benha Univ. Seven field bean genotypes representing a wide range of variability namely; Variety (Var.) Misr 1 (P<sub>1</sub>), Var. Sakha 2 (P<sub>2</sub>) and Var. Giza 843 (P<sub>3</sub>) obtained from Agriculture Research Center, Egypt and lines (L) M-104 (P<sub>4</sub>), L M-13 (P<sub>5</sub>), L M-148 (P<sub>6</sub>) and L M-1017(P<sub>7</sub>) in F<sub>7</sub> developed from crosses between imported genotype Equadols (France) x Giza 843 , 29 (Netherlands) x Sakha 2, NEB 319 (ICARDA) x Giza 40 and Asbany (Spain) x L M-127,

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respectively. The aforementioned genotypes were used in all diallel fashion without reciprocals giving a total of 21 F<sub>1</sub> crosses during 2016-2017 growing season. In the second season 2017-2018, hybrid seeds were sown to obtain F<sub>2</sub> seeds and evaluated. In the same time, parents were crossed again to obtain adequate F<sub>1</sub> hybrid seeds. In the third season 2018-19, two adjacent experiments were conducted, the first trial contained parents and F<sub>1</sub> hybrids, and the second experiment involved the parents and F<sub>2</sub> crosses. Each experiment was grown in a randomized complete block design (RCBD) with three replications. Each F<sub>1</sub> and parent was represented by single ridge of 6 meter long containing 30 plants in each replication, where, 4 ridges (6 m) for F<sub>2</sub> were planted to get 120 plants. Ridge-to-ridge and plant-to-plant spacing were kept at 60 and 20 cm, respectively. Dry method of planting was used in this concern and the rest of cultural practices were followed as recommended for ordinary field bean in the area. Also, the experiment was bordered by susceptible line M 808 to chocolate spot as spreader. Observation were recorded on 10, 10 and 40 randomly plants from each plot of parents, F<sub>1</sub> and F<sub>2</sub>, respectively. Data were scored on; number of branches plant<sup>-1</sup>, number of pods plant<sup>-1</sup>, 100-seed weight (g), seed yield plant<sup>-1</sup> (g) and chocolate spot (*Botrytis fabae*) degree estimating the percentages given are proportions of the leaf area covered by the fungal symptoms according to Leach and Moore (1966) and El-Hosary *et al.* (1984). Disease assessment was detected on 15<sup>th</sup> March 2019.

The analysis of variance for combining ability and estimation of genetic effects were computed according to methods suggested by Griffing (1956) for method 2 model 1. The genetic parameters were estimated using the

procedure described by Hayman (1954). Heritability in broad and narrow-sense were estimated according to Mather and Jinks (1971) for F<sub>1</sub>'s data, and Verhalen and Murray (1969) for the F<sub>2</sub>'s data. Heterosis in F<sub>1</sub> and remain heterosis in F<sub>2</sub> expressed as the percentage deviation of F<sub>1</sub> or F<sub>2</sub>, respectively mean performance from mid and better parent. The data obtained of chocolate spot (*Botrytis fabae*) degree were transformed to scale of square roots before analysis.

## RESULTS AND DISCUSSION

Ordinary analysis of variance and diallel analysis as constructed by Griffing (1965) method 2 model 1 of both F<sub>1</sub> and F<sub>2</sub> generations for all studied traits have been presented in Table 1. ANOVA revealed significant mean squares for all sources of variations (Genotypes, parents, crosses, parent *vs* crosses (heterosis) and both types of combining ability for all traits in both F<sub>1</sub> and F<sub>2</sub> generations, except, heterosis for chocolate spot %. The results indicate that, the differential in the material and sufficient amount of genetic variability adequate for further biometrical assessment. Large magnitude of parents *vs* crosses mean squares were found in F<sub>1</sub> analysis compared with F<sub>2</sub> ones for all studied characters. These results are logic consequence inbreeding depression present in the F<sub>2</sub> which would decrease the heterosis effects. Significant differences among faba bean genotypes for yield and its components traits in different sets of material were reported by Darwish *et al.* (2005), Alghamdi (2009), El-Bramawy and Osman (2012), Hazem, *et al.* (2013), Abdalla *et al.* (2015), Abdalla *et al.* (2017) and Bishnoi *et al.* (2018).

**Table 1. Ordinary analysis of variance (ANOVA) and combining ability analysis in F<sub>1</sub> and F<sub>2</sub> generations for all studied characters.**

SOV	Df	Mean squares					
		Number of branches plant <sup>-1</sup>	Number of pods plant <sup>-1</sup>	No. of seeds pod <sup>-1</sup>	100-seed weight (g)	seed yield plant <sup>-1</sup> (g)	chocolate spot %
F <sub>1</sub> diallel cross							
Blocks	2	0.08	0.17	0.001	9.46	0.21	0.66
Genotypes	27	0.80**	53.93**	0.54**	340.27**	190.98**	4.04*
Parent (P)	6	1.02**	38.26**	0.42**	767.79**	63.46**	6.30**
F <sub>1</sub> crosses	20	0.71**	59.73**	0.27**	221.74**	161.27**	3.57**
P <i>vs</i> F <sub>1</sub> (heterosis)	1	1.24**	31.86**	6.56**	145.81**	1550.37**	0.002
Error	54	0.13	1.49	0.02	9.15	4.32	1.01
GCA	6	0.29**	20.39**	0.16**	283.79**	32.99**	1.20**
SCA	21	0.26**	17.29**	0.19**	64.75**	72.42**	1.39**
Error	54	0.04	0.50	0.01	3.05	1.44	0.34
GCA/SCA		1.13	1.18	0.84	4.38	0.46	0.86
F <sub>2</sub> diallel generation.							
Blocks	2	0.11	14.92	0.28	24.02	21.01	2.15
Genotypes	27	0.79**	42.40**	0.34*	274.77**	139.11**	7.44**
Parent (P)	6	1.08**	44.69**	0.53**	585.27**	77.00**	10.44**
F <sub>2</sub>	20	0.72**	33.10**	0.26*	188.11**	160.23**	6.91**
P <i>vs</i> F <sub>2</sub>	1	0.51*	21.53**	0.59**	145.10**	89.40**	0.0002
Error	54	0.24	6.77	0.11	22.03	11.18	1.21
GCA	6	0.37**	14.15**	0.13**	195.11**	16.96**	2.00**
SCA	21	0.23**	14.13**	0.11**	62.02**	54.77**	2.62**
Error	54	0.08	2.26	0.04	7.34	3.73	0.40
GCA/SCA		1.57	1.002	1.19	3.15	0.31	0.76

\* and \*\* refer to significant if p < 0.05 and p < 0.01, respectively.

Both types of combining ability mean squares were highly significant for all studied traits in F<sub>1</sub> and F<sub>2</sub> generations. For development of an efficient hybridization

program and select the suitable way of selection, must determine the relative importance of additive and non-additive gene action. To determine the genetic effects of

greatest importance, GCA/SCA ratio were computed. Values exceeding largely the unity were detected for all studied traits except, No. of seeds pod<sup>-1</sup> in F<sub>1</sub> as well as seed yield plant<sup>-1</sup> and chocolate spot % in both generations, indicating that largest part of the total genetic variability was due to additive and additive x additive gene effects. For the exceptional cases, however, non-additive types of gene action seemed to be more prevalent. The GCA/ SCA ratios were higher in magnitude in F<sub>2</sub> than F<sub>1</sub> generation for number of branches plant<sup>-1</sup> and number of seeds pod<sup>-1</sup>, revealing that the additive and additive x additive gene effects were increased and non-additive gene effects were also reduced in the F<sub>2</sub> generation. Vice versa, for the other remains traits the non-additive gene effects were increase comparing with the additive one.

The genetic variance was previously reported to be mostly due to additive for yield traits by El-Bramawy and Osman (2012). On the other hand, the non-additive genetic variance was previously reported to be the most prevalent for seed yield plant<sup>-1</sup> by El-Harty *et al.*, (2007), Obiadalla-Ali *et al.*, (2013) and El-Abssi *et al.* (2019a) ; No. of branches plant<sup>-1</sup> by Sattar *et al.*, (2012); and Ashrei *et al.*, (2014); For 100-seed weight by Abd-Elrahman *et al.*, (2012) and Farag and Afiah (2012).

**Performance of parents and their hybrids in F<sub>1</sub> and F<sub>2</sub> generations**

Mean values of all studied faba bean genotypes were significant and obtainable in Table 2 and 3. The high number of branches plant<sup>-1</sup> was significantly differed from one genotype to another over all faba bean genotypes (parents and their hybrids). The branches number of faba

bean parents ranged from 2.90 (P<sub>6</sub> M-148) to 4.58 (P<sub>7</sub>, M-1017), while, the minimum average of branches for hybrids (3.03 in F<sub>1</sub>, 2.53 in F<sub>2</sub>) was detected by the cross P<sub>1</sub>x P<sub>2</sub>. But, maximum value (4.63 in F<sub>1</sub>, 4.28 in F<sub>2</sub>) was scored by the cross P<sub>1</sub> x P<sub>7</sub>. Therefore, it can note that the crosses P<sub>1</sub>xP<sub>5</sub>, P<sub>1</sub>xP<sub>7</sub>, P<sub>2</sub>xP<sub>3</sub>, P<sub>2</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>6</sub>, P<sub>2</sub>xP<sub>7</sub>, P<sub>3</sub>xP<sub>4</sub>, P<sub>3</sub>xP<sub>5</sub>, P<sub>3</sub>xP<sub>6</sub>, P<sub>4</sub>xP<sub>6</sub>, P<sub>5</sub>xP<sub>7</sub> and P<sub>6</sub>xP<sub>7</sub> had the highest No of branches in F<sub>1</sub> plants. Meanwhile, The F<sub>2</sub> crosses P<sub>1</sub>xP<sub>3</sub>, P<sub>1</sub>xP<sub>5</sub>, P<sub>1</sub>xP<sub>7</sub>, P<sub>3</sub>xP<sub>4</sub>, P<sub>3</sub>xP<sub>5</sub> and P<sub>3</sub>xP<sub>7</sub> exhibited the highest values for the mention trait. The parent P<sub>1</sub> (Misr 1) gave the highest values for number of pods plant<sup>-1</sup> (33.00). Moreover, P<sub>5</sub> (M-13) showed the lowest values. On the other side, the F<sub>1</sub> hybrids, P<sub>3</sub>xP<sub>4</sub> and P<sub>4</sub>xP<sub>5</sub> recorded the highest values for number of pods plant<sup>-1</sup>. Meanwhile, the F<sub>2</sub> crosses P<sub>3</sub>xP<sub>6</sub> and P<sub>5</sub>xP<sub>6</sub> recorded the highest values for this character.

The parent P<sub>6</sub> (M-148) gave the highest value for number of seeds pod<sup>-1</sup>. Moreover, P<sub>1</sub> (Misr 1) showed the lowest value. Nine F<sub>1</sub> hybrids (P<sub>1</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>3</sub>, P<sub>2</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>6</sub>, P<sub>2</sub>xP<sub>7</sub>, P<sub>4</sub>xP<sub>5</sub>, P<sub>4</sub>xP<sub>7</sub> and P<sub>5</sub>xP<sub>7</sub>) had the highest number of seeds pod<sup>-1</sup>. However, sixteen F<sub>2</sub> hybrids (P<sub>1</sub>xP<sub>2</sub>, P<sub>1</sub>xP<sub>3</sub>, P<sub>1</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>3</sub>, P<sub>2</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>6</sub>, P<sub>2</sub>xP<sub>7</sub>, P<sub>3</sub>xP<sub>4</sub>, P<sub>3</sub>xP<sub>6</sub>, P<sub>3</sub>xP<sub>7</sub>, P<sub>4</sub>xP<sub>5</sub>, P<sub>4</sub>xP<sub>7</sub>, P<sub>5</sub>xP<sub>6</sub>, P<sub>5</sub>xP<sub>7</sub> and P<sub>6</sub>xP<sub>7</sub>) exhibited highest value for the mention trait.

The parent P<sub>2</sub> (Sakha 2) possessed the highest values for 100-seed weight. Moreover, the parent P<sub>4</sub> (M-104) gave the lowest values for the same traits. The F<sub>1</sub> hybrid P<sub>3</sub>xP<sub>4</sub> revealed the highest values for 100-seed weight, while, the F<sub>2</sub> crosses P<sub>1</sub>xP<sub>3</sub>, P<sub>1</sub>xP<sub>4</sub>, P<sub>1</sub>xP<sub>6</sub>, P<sub>2</sub>xP<sub>3</sub>, P<sub>2</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>6</sub>, P<sub>2</sub>xP<sub>7</sub>, P<sub>3</sub>xP<sub>4</sub>, P<sub>3</sub>xP<sub>5</sub>, P<sub>3</sub>xP<sub>7</sub>, P<sub>4</sub>xP<sub>6</sub> and P<sub>4</sub>xP<sub>7</sub> revealed the highest values of this trait.

**Table 2. Characteristics of all studied genotypes for yield components traits and chocolate spot disease %.**

genotype	Number of branches plant <sup>-1</sup>		Number of pods plant <sup>-1</sup>		No. of seeds pod <sup>-1</sup>		100-seed weight (g)		*chocolate spot %	
	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> )	3.70 DJ	3.59 BH	27.13 C	28.41 A	2.60 HI	2.82 EG	65.12 HJ	63.12 BG	0.50 f	0.50 e
Sakha 2 (P <sub>2</sub> )	4.48 AB	4.45 AB	18.67 LM	17.16 FI	2.83 H	3.26 BG	88.14 A	84.31 A	14.50 ab	18.83 ac
Giza 843 (P <sub>3</sub> )	3.57 FK	3.47 CI	22.24 GI	22.86 BE	3.22 G	3.57 AD	57.48 LM	55.57 GI	3.50 df	8.17 ce
M-104 (P <sub>4</sub> )	3.40 HK	3.33 CI	27.20 C	25.62 AC	2.96 HI	3.78 AC	54.67 M	52.77 HI	0.50 f	0.50 e
M-13 (P <sub>5</sub> )	3.38 HK	3.33 CI	20.65 HL	19.35 DI	2.96 HI	3.50 AD	55.43 M	57.76 FI	12.83 ac	16.17 bd
M-148 (P <sub>6</sub> )	2.90 K	3.00 GI	19.77 JM	21.14 CG	3.61 AD	3.65 AD	63.11 IK	62.96 BG	0.50 f	24.50 ab
M-1017(P <sub>7</sub> )	4.48 AB	4.58 A	25.55 CE	24.68 AC	2.96 HI	2.68 G	71.92 CG	68.12 BE	11.17 ad	24.50 ab
P <sub>1</sub> xP <sub>2</sub>	3.03 JK	2.53 I	26.57 CD	17.90 EI	3.56 BD	3.59 AD	69.95 DH	56.73 FI	6.50 bf	11.17 bd
P <sub>1</sub> xP <sub>3</sub>	3.76 CI	3.65 AH	23.48 EG	20.65 CH	3.06 G	3.32 AF	66.13 GJ	63.63 BG	21.17 a	41.17 a
P <sub>1</sub> xP <sub>4</sub>	3.74 CI	3.24 DI	22.68 FH	21.14 CG	3.16 FG	3.34 AF	69.49 DH	65.40 BF	3.17 cf	9.83 ce
P <sub>1</sub> xP <sub>5</sub>	4.44 AC	4.17 AE	29.87 B	22.08 BF	3.68 AC	3.82 AC	62.17 JL	60.83 DH	0.50 f	0.50 e
P <sub>1</sub> xP <sub>6</sub>	3.67 EJ	3.19 FI	26.70 CD	19.53 DI	3.52 BD	3.34 AF	68.33 EI	63.80BG	3.17 cf	8.17 ce
P <sub>1</sub> xP <sub>7</sub>	4.63 A	3.83 AG	19.29 KM	16.27 GI	3.24 EG	2.71 FG	69.08 EH	50.74 I	3.17 cf	8.17 ce
P <sub>2</sub> xP <sub>3</sub>	4.40 AD	3.20 EI	24.57 DF	18.20 EI	3.58 AD	3.42 AE	75.03 CD	67.28 BE	19.50 a	24.50 ab
P <sub>2</sub> xP <sub>4</sub>	3.94 AH	3.75 AG	19.41 KM	18.18 EI	3.58 AD	3.70 AD	72.60 CF	69.83 BD	6.17 bf	8.17 ce
P <sub>2</sub> xP <sub>5</sub>	3.78 BI	3.69 AH	19.01 KM	18.33 EI	3.66 AD	3.59 AD	75.88 C	71.48 B	1.83 ef	16.50 bd
P <sub>2</sub> xP <sub>6</sub>	4.24 AF	4.21 AD	17.68 M	15.53 HI	3.68 AC	3.32 AF	75.97 C	70.23 BC	0.50 f	0.50 e
P <sub>2</sub> xP <sub>7</sub>	4.34 AE	4.28 AC	21.69 GJ	17.16 FI	3.71 AB	3.75 AD	73.00 CE	67.75 BE	1.83 ef	9.83 ce
P <sub>3</sub> xP <sub>4</sub>	4.41 AC	3.78 AG	32.30 A	10.94 J	2.46 I	3.32 AF	82.86 B	69.59 BD	3.17 cf	7.83 ce
P <sub>3</sub> xP <sub>5</sub>	4.12 AG	4.08 AF	22.40 FH	20.69 CG	3.56 BD	3.09 DG	69.07 EH	63.25 BG	1.83 ef	9.83 ce
P <sub>3</sub> xP <sub>6</sub>	4.00 AH	3.29 DI	27.64 C	26.63 AB	3.42 CE	3.71 AD	69.77 DH	60.97 CH	0.50 f	0.50 e
P <sub>3</sub> xP <sub>7</sub>	3.80 BI	3.66 AH	20.11 IL	17.93 EI	3.55 BD	3.78 AC	75.88 C	64.93 BF	16.83 ae	26.17 ab
P <sub>4</sub> xP <sub>5</sub>	3.23 IK	2.73 HI	32.80 A	19.57 DI	3.85 A	3.89 AB	54.82 M	52.06 HI	6.50 bf	12.83 bd
P <sub>4</sub> xP <sub>6</sub>	4.56 A	3.20 EI	22.53 FH	21.32 CG	3.47 BE	3.20 CG	64.68 HK	62.54 BG	6.50 bf	16.17 bd
P <sub>4</sub> xP <sub>7</sub>	3.50 GK	3.48 CI	21.13 HK	15.22 I	3.63 AD	3.63 AD	74.99 CD	67.23 BE	9.50 ae	24.50 ab
P <sub>5</sub> xP <sub>6</sub>	3.10 IK	2.89 GI	29.65 B	23.88 AD	3.40 DF	3.50 AD	59.50 KM	54.68 GI	7.83 ae	7.83 ce
P <sub>5</sub> xP <sub>7</sub>	4.58 A	3.02 GI	27.65 C	17.69 FI	3.69 AC	3.98 A	67.16 FJ	56.42 FI	6.17 bf	24.50 ab
P <sub>6</sub> xP <sub>7</sub>	4.32 AE	3.56 BH	26.34 CD	21.27 CG	3.48 BE	3.67 AD	64.09 HK	60.27 EH	1.83 ef	8.50 de

Means followed by the same letter for each tested parameter are not significantly different by Duncan's test (P < 0.05)

\* Small letter of Duncan's test (P < 0.05) in chocolate spot % transferred from the statistical analysis of the transformed data after performing the square-root

**Table 3. Mean performance of all studied genotypes for seed yield plant<sup>-1</sup> and heterosis% for crosses relative to mid and better parent in F<sub>1</sub> and F<sub>2</sub> generations**

genotype	Seed yield plant <sup>-1</sup> (g)		Estimation of heterosis in F <sub>1</sub> For seed yield plant <sup>-1</sup> (g)		Estimation of remain heterosis in F <sub>2</sub> For seed yield plant <sup>-1</sup> (g)	
	F <sub>1</sub>	F <sub>2</sub>	relative to M.P	relative to B.P	relative to M.P	relative to B.P
Misr 1 (P <sub>1</sub> )	40.70 IK	40.72CG				
Sakha 2 (P <sub>2</sub> )	44.31 GI	43.74 CE				
Giza 843 (P <sub>3</sub> )	34.79 M	35.22 GI				
M-104 (P <sub>4</sub> )	40.70 IK	39.92 DG				
M-13 (P <sub>5</sub> )	36.82 LM	37.32 EI				
M-148 (P <sub>6</sub> )	43.13 GJ	42.78 CE				
M-1017(P <sub>7</sub> )	48.46 EF	50.85 AB				
P <sub>1</sub> xP <sub>2</sub>	60.34 AB	32.46 IJ	41.97**	36.18**	-23.13**	-25.78**
P <sub>1</sub> xP <sub>3</sub>	40.10 JL	39.75 DG	6.26	-1.46	4.67	-2.40
P <sub>1</sub> xP <sub>4</sub>	44.15 GI	41.50 CG	8.47*	8.47	2.93	1.91
P <sub>1</sub> xP <sub>5</sub>	62.20 AB	46.78 BC	60.48**	52.83**	19.88**	14.87*
P <sub>1</sub> xP <sub>6</sub>	54.63 C	40.03 DG	30.33**	26.66**	-4.13	-6.43
P <sub>1</sub> xP <sub>7</sub>	38.82 KL	18.43 K	-12.93**	-19.90**	-59.76**	-63.76**
P <sub>2</sub> xP <sub>3</sub>	54.37 CD	42.17 CF	37.47**	22.69**	6.80	-3.59
P <sub>2</sub> xP <sub>4</sub>	46.53 FH	43.42 CE	9.48**	5.01	3.80	-0.73
P <sub>2</sub> xP <sub>5</sub>	49.05 EF	44.54 CD	20.92**	10.70**	9.90	1.84
P <sub>2</sub> xP <sub>6</sub>	46.08 FH	32.99 HJ	5.39	3.98	-23.74**	-24.58**
P <sub>2</sub> xP <sub>7</sub>	54.30 CD	41.03 CG	17.06**	12.06**	-13.24*	-19.31**
P <sub>3</sub> xP <sub>4</sub>	45.49 FH	27.49 J	20.54**	11.78**	-26.83**	-31.13**
P <sub>3</sub> xP <sub>5</sub>	46.70 FG	38.53 DI	30.44**	26.84**	6.22	3.23
P <sub>3</sub> xP <sub>6</sub>	60.03 B	54.78 A	54.10**	39.20**	40.46**	28.05**
P <sub>3</sub> xP <sub>7</sub>	50.67 DE	41.53 CG	21.73**	4.56	-3.49	-18.32**
P <sub>4</sub> xP <sub>5</sub>	60.20 AB	35.60 FI	55.33**	47.92**	-7.81	-10.81
P <sub>4</sub> xP <sub>6</sub>	42.64 HJ	38.00 DI	1.75	-1.12	-8.10	-11.17
P <sub>4</sub> xP <sub>7</sub>	48.60 EF	39.22 DH	9.02**	0.29	-13.57*	-22.86**
P <sub>5</sub> xP <sub>6</sub>	52.90 CD	41.36 CG	32.33**	22.65**	3.27	-3.32
P <sub>5</sub> xP <sub>7</sub>	63.87 A	37.89 DI	49.79**	31.80**	-14.05*	-25.48**
P <sub>6</sub> xP <sub>7</sub>	53.39 CD	44.11 CD	16.58**	10.17**	-5.77	-13.25*

Means followed by the same letter for each tested parameter are not significantly different by Duncan's test (P < 0.05).

\* and \*\* refer to significant if p < 0.05 and p < 0.01, respectively.

For chocolate spot %; the more resistance parents for this disease were P<sub>1</sub> (Misr 1) and P<sub>4</sub> (M-104). While, the parents P<sub>2</sub> (Sakha 2) and P<sub>7</sub> (M-1017) were the more sensitive to chocolate spot. Three crosses (P<sub>1</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>6</sub> and P<sub>3</sub>xP<sub>6</sub>) in F<sub>1</sub> and F<sub>2</sub> generation exhibited high resistance hybrids to chocolate spot disease. On the other hand, the crosses P<sub>1</sub>xP<sub>3</sub>, P<sub>2</sub>xP<sub>3</sub>, P<sub>3</sub>xP<sub>7</sub> and P<sub>4</sub>xP<sub>7</sub> were the most susceptible crosses for the aforementioned disease.

For seed yield plant<sup>-1</sup> (Table 3); the parent no 7 (M-1017), four F<sub>1</sub> hybrids (P<sub>1</sub>xP<sub>2</sub>, P<sub>1</sub>xP<sub>5</sub>, P<sub>4</sub>xP<sub>5</sub> and P<sub>5</sub>xP<sub>7</sub>) and one F<sub>2</sub> hybrid (P<sub>3</sub>xP<sub>6</sub>) showed the highest values for this trait. The high seed yield plant<sup>-1</sup> of the mention parent of crosses could be attributed to its high one or more yield components. Subsequently, these hybrids could be promising for prospective faba bean breeding programs aiming at improving seed yield.

Concerning heterosis for seed yield plant<sup>-1</sup> (Table 3), all F<sub>1</sub> crosses excluding the crosses P<sub>1</sub>xP<sub>3</sub>, P<sub>1</sub>xP<sub>7</sub>, P<sub>2</sub>xP<sub>6</sub> and P<sub>4</sub>xP<sub>6</sub> showed significant and desirable heterosis relative to mid-parent. While, the most significant and desirable heterosis relative to better parent was exhibited by the crosses P<sub>1</sub>xP<sub>2</sub>, P<sub>1</sub>xP<sub>5</sub>, P<sub>1</sub>xP<sub>6</sub>, P<sub>2</sub>xP<sub>3</sub>, P<sub>2</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>7</sub>, P<sub>3</sub>xP<sub>4</sub>, P<sub>3</sub>xP<sub>5</sub>, P<sub>3</sub>xP<sub>6</sub>, P<sub>4</sub>xP<sub>5</sub>, P<sub>5</sub>xP<sub>6</sub>, P<sub>5</sub>xP<sub>7</sub>, P<sub>6</sub>xP<sub>7</sub> and the values of heterosis reached 36.18, 52.83, 26.66, 22.69, 10.70, 12.06, 11.78, 26.84, 39.20, 47.92, 22.65, 31.80 and 10.17%, respectively.

As for F<sub>2</sub>, the two crosses (P<sub>1</sub>xP<sub>5</sub> and P<sub>3</sub>xP<sub>6</sub>) showed significant positive remain heterotic effects relative to mid-parent and better parent. The two F<sub>2</sub> crosses (P<sub>1</sub>xP<sub>5</sub> and (P<sub>3</sub>xP<sub>6</sub>) exceed the mid-parent reached 19.88 and

40.46 %. Also, the heterosis relative to better parent recorded 14.87 and 28.05%, respectively. Significant positive heterotic effects relative to higher yielding parent were obtained by Alghamdi (2009), Zeinab and Helal (2014) and Bishnoi *et al.* (2018)

Regarding to heterosis, the mean performance of the parents and their hybrids, it could be concluded that these hybrids had highly promising characters for breeding faba bean genotypes. Thus, it should possess the genetic factors for high yield potential. These results could be confirmed the possibility of selection for these characters through the crosses. Moreover it allowed the greed light in the front of plant breeders to build future breeding program for high potential yield in faba bean crop. These findings were in agreement with who's reported by Abdalla *et al.* (2017b), Abou-Zaid *et al.* (2017) and Bishnoi *et al.* (2018) they found superiority in their evaluated faba bean hybrids.

**Combining ability effects**

The GCA and SCA effects ( $\hat{g}_i$  and  $\hat{S}_{ij}$ ) of individual parent and cross for each trait from both F<sub>1</sub> and F<sub>2</sub> generations for all studied traits have been presented in Tables 4 and 5, respectively.

**Number of branches plant<sup>-1</sup>**

Among the parents, Sakha 2 (P<sub>2</sub>) and M-1017(P<sub>7</sub>) were good general combiners (as judged by their GCA effects analysis in both F<sub>1</sub> and F<sub>2</sub> generations). Five crosses (P<sub>1</sub>xP<sub>5</sub>, P<sub>1</sub>xP<sub>7</sub>, P<sub>3</sub>xP<sub>4</sub>, P<sub>4</sub>xP<sub>6</sub> and P<sub>5</sub>xP<sub>7</sub>) out of 21 F<sub>1</sub>'s showed desirable SCA effects while rest of the crosses were either poor or showed inconsistent estimates of SCA effects. The crosses P<sub>1</sub>xP<sub>7</sub> and P<sub>5</sub>xP<sub>7</sub> included parent No

7 which good general combining ability, while, the other crosses involved parents with poor GCA effects. As for F<sub>2</sub> hybrids, three crosses (P<sub>1</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>6</sub> and P<sub>3</sub>xP<sub>5</sub>) showed significant positive SCA effects estimates. Parents involved in the cross P<sub>2</sub>xP<sub>6</sub> were one good and other poor general combiner.

**Table 4. Estimates of parental GCA effects ( $\hat{g}_i$ ) for all studied traits in F<sub>1</sub> and F<sub>2</sub> generations.**

Parent	Number of branches plant <sup>-1</sup>	Number of pods plant <sup>-1</sup>	Number of seeds pod <sup>-1</sup>	100-seed weight (g)	Seed yield plant <sup>-1</sup> (g)	chocolate spot %
F <sub>1</sub>						
Misir 1 (P <sub>1</sub> )	-0.07	1.12**	-0.12**	-1.95**	-0.90*	-0.26
Sakha 2 (P <sub>2</sub> )	0.16*	-2.95**	0.08**	10.29**	1.07**	0.39*
Giza 843 (P <sub>3</sub> )	0.04	0.25	-0.09**	0.67	-2.53**	0.23
M-104 (P <sub>4</sub> )	-0.12	1.39**	-0.14**	-3.20**	-2.30**	-0.17
M-13 (P <sub>5</sub> )	-0.14*	1.10**	0.07**	-6.75**	2.09**	0.14
M-148 (P <sub>6</sub> )	-0.18**	-0.30	-0.02	-2.91**	0.69	-0.62**
M-1017(P <sub>7</sub> )	0.32**	-0.61**	0.22**	3.85**	1.87**	0.30
LSD $\hat{g}_i$ 5%	0.13	0.44	0.05	1.08	0.74	0.36
LSD $\hat{g}_i$ 1%	0.17	0.58	0.06	1.44	0.99	0.48
LSD $\hat{g}_i$ - $\hat{g}_j$ 5%	0.20	0.67	0.07	1.65	1.13	0.55
LSD $\hat{g}_i$ - $\hat{g}_j$ 1%	0.26	0.89	0.10	2.20	1.51	0.73
F <sub>2</sub>						
Misir 1 (P <sub>1</sub> )	-0.06	1.62**	-0.22**	-2.93**	-1.93**	-0.63**
Sakha 2 (P <sub>2</sub> )	0.25**	-2.24**	0.03	9.96**	0.70	0.12
Giza 843 (P <sub>3</sub> )	0.03	0.11	0.02	-0.88	-0.34	0.27
M-104 (P <sub>4</sub> )	-0.17	-0.24	0.10	-2.00*	-1.41*	-0.37
M-13 (P <sub>5</sub> )	-0.12	0.13	0.13*	-3.98**	0.18	0.11
M-148 (P <sub>6</sub> )	-0.22*	1.18*	0.04	-0.98	2.12**	-0.29
M-1017(P <sub>7</sub> )	0.29**	-0.55	-0.09	0.81	0.68	0.78**
LSD $\hat{g}_i$ 5%	0.17	0.93	0.12	1.68	1.19	0.39
LSD $\hat{g}_i$ 1%	0.23	1.24	0.16	2.23	1.59	0.52
LSD $\hat{g}_i$ - $\hat{g}_j$ 5%	0.27	1.42	0.18	2.56	1.82	0.60
LSD $\hat{g}_i$ - $\hat{g}_j$ 1%	0.36	1.89	0.24	3.41	2.43	0.80

\* and \*\* refer to significant if  $p < 0.05$  and  $p < 0.01$ , respectively.

**Number of pods plant<sup>-1</sup>**

On basis of GCA effect analysis for studied parents genotypes, P<sub>1</sub> (Misir 1), P<sub>4</sub> (M-104) and P<sub>5</sub> (M-13) in F<sub>1</sub> as well as P<sub>1</sub> (Misir 1) and P<sub>6</sub> (M-148) in F<sub>2</sub> were exhibited good general combiners. However, the other parents showed undesirable  $\hat{g}_i$  effects for this trait. Positive and significant SCA effects for this trait were revealed by ten F<sub>1</sub> crosses (P<sub>1</sub>xP<sub>2</sub>, P<sub>1</sub>xP<sub>5</sub>, P<sub>1</sub>xP<sub>6</sub>, P<sub>2</sub>xP<sub>3</sub>, P<sub>3</sub>xP<sub>4</sub>, P<sub>3</sub>xP<sub>6</sub>, P<sub>4</sub>xP<sub>5</sub>, P<sub>5</sub>xP<sub>6</sub>, P<sub>5</sub>xP<sub>7</sub> and P<sub>6</sub>xP<sub>7</sub>), while, the desirable SCA effects  $\hat{S}_{ij}$  in F<sub>2</sub> generation, as exhibited by the cross P<sub>3</sub>xP<sub>6</sub>. The aforementioned crosses contain one or more good combiner parents or involving poor x poor general combiners.

**Number of seeds pod<sup>-1</sup>**

The parental genotype P<sub>2</sub> (Sakha 2), P<sub>5</sub> (M-13) and P<sub>7</sub> (M-1017) in F<sub>1</sub> and P<sub>5</sub> (M-13) in F<sub>2</sub> had significant and highly significant positive  $\hat{g}_i$  effects for number of seeds pod<sup>-1</sup>. Eleven crosses out of 21 F<sub>1</sub>'s showed significant positive SCA effects while rest of the crosses were showed undesirable estimates of SCA effects. Likewise, the four crosses P<sub>1</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>7</sub>, P<sub>3</sub>xP<sub>7</sub> and P<sub>5</sub>xP<sub>7</sub> had SCA effects with more positive significant.

**100-seed weight**

The parental genotypes P<sub>2</sub> (Sakha 2) and P<sub>7</sub> (M-1017) in F<sub>1</sub> and P<sub>2</sub> (Sakha 2) in F<sub>2</sub> had significant and highly significant positive  $\hat{g}_i$  effects for 100-seed weight. Seven F<sub>1</sub>'s crosses (P<sub>1</sub>xP<sub>6</sub>, P<sub>2</sub>xP<sub>5</sub>, P<sub>3</sub>xP<sub>4</sub>, P<sub>3</sub>xP<sub>5</sub>, P<sub>3</sub>xP<sub>6</sub>, P<sub>3</sub>xP<sub>7</sub> and P<sub>4</sub>xP<sub>7</sub>) showed significant positive  $\hat{S}_{ij}$  effects while other crosses in F<sub>1</sub> showed negative or insignificant  $\hat{S}_{ij}$  effects. Likewise, the five crosses (P<sub>1</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>5</sub>, P<sub>3</sub>xP<sub>4</sub>,

P<sub>3</sub>xP<sub>5</sub> and P<sub>4</sub>xP<sub>7</sub>) showed positive and significant  $\hat{S}_{ij}$  effects.

**Seed yield plant<sup>-1</sup>**

The parental genotypes P<sub>2</sub> (Sakha 2), P<sub>5</sub> (M-13), P<sub>7</sub> (M-1017) in F<sub>1</sub> trial and P<sub>6</sub> (M-1017) in F<sub>2</sub> trial had exhibited good combiners for Seed yield plant<sup>-1</sup>. The most positive and significant inter and intra-allelic interactions for this trait were represented; by P<sub>1</sub>xP<sub>5</sub>, P<sub>1</sub>xP<sub>6</sub>, P<sub>2</sub>xP<sub>3</sub>, P<sub>2</sub>xP<sub>7</sub>, P<sub>3</sub>xP<sub>6</sub>, P<sub>3</sub>xP<sub>7</sub>, P<sub>4</sub>xP<sub>5</sub> and P<sub>5</sub>xP<sub>7</sub> for F<sub>1</sub> crosses, P<sub>1</sub>xP<sub>4</sub>, P<sub>1</sub>xP<sub>5</sub>, P<sub>2</sub>xP<sub>4</sub>, P<sub>2</sub>xP<sub>5</sub> and P<sub>3</sub>xP<sub>6</sub> for F<sub>2</sub> generation.

**Chocolate spot %**

The parent P<sub>6</sub> (M-148) in F<sub>1</sub> and P<sub>1</sub> (Misir 1) in F<sub>2</sub> trials, showed good combiner for this trait. Furthermore, the crosses P<sub>1</sub>xP<sub>5</sub> and P<sub>2</sub>xP<sub>6</sub> exhibited high negative and significant SCA effects for this trait in both generations.

Depending upon the information on gene action controlling yield and its attributes and the genetic variability a successful breeding program were carried out. In this context, both types of gene action (additive and dominance) were significant for the studied traits i.e., seed yield/ plant and 100 seed weight Attia and Salem (2006). Non-additive gene action was played an important role in governing the genetic system of yield and its attributes Bishnoi *et al.* (2018). Moreover, additive gene action played an important role in the inheritance of resistance to chocolate spot Beyene *et al.* (2016).

In general, such combinations of high SCA specially in F<sub>2</sub> generation in the same time, involved good combiner for both parents, they could be exploited for breeding varieties. Nevertheless, if the parental combination showed desirable high  $\hat{S}_{ij}$  involve only one good combiner, such combinations would throw out desirable transgressive segregates provided that the

additive genetic system in the good combiner (as well as complementary and epistatic effects in the crosses) act in the same direction to reduce undesirable characteristics and maximize the character under consideration.

**Table 5. Estimates of specific combining ability effects of the crosses for all studied traits in F<sub>1</sub> and F<sub>2</sub> generations.**

Cross	Number of branches plant <sup>-1</sup>		Number of pods plant <sup>-1</sup>		No. of seeds pod <sup>-1</sup>		100-seed weight (g)		Seed yield plant <sup>-1</sup>		Chocolate spot %	
	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>	F <sub>1</sub>	F <sub>2</sub>
P <sub>1xP<sub>2</sub></sub>	-0.97**	-1.20**	4.30**	-1.45	0.29**	0.30	-7.14**	-16.82**	11.46**	-6.03**	0.12	0.59
P <sub>1xP<sub>3</sub></sub>	-0.12	0.14	-1.98**	-1.05	-0.04	0.05	-3.12	3.81	-5.18**	2.30	2.59**	3.60**
P <sub>1xP<sub>4</sub></sub>	0.02	-0.07	-3.92**	-0.21	0.11	-0.02	5.65**	6.69**	-1.37	5.12**	0.04	0.61
P <sub>1xP<sub>5</sub></sub>	0.74**	0.81**	3.55**	0.36	0.42**	0.43*	-0.23	2.50	12.29**	8.81**	-1.21*	-1.94**
P <sub>1xP<sub>6</sub></sub>	0.00	-0.07	1.78**	-3.25*	0.35**	0.12	3.56*	3.55	6.12**	0.12	0.50	0.29
P <sub>1xP<sub>7</sub></sub>	0.47*	0.06	-5.32**	-4.78**	-0.18*	-0.46**	-0.86	-14.08**	-10.87**	-20.05**	-0.42	-0.78
P <sub>2xP<sub>3</sub></sub>	0.30	-0.62*	3.17**	0.36	0.27**	-0.10	-4.23**	-4.31	7.12**	2.09	1.76**	1.39*
P <sub>2xP<sub>4</sub></sub>	-0.01	0.13	-3.13**	0.69	0.33**	0.13	-2.86	-0.05	-0.95	4.40*	0.18	-0.39
P <sub>2xP<sub>5</sub></sub>	-0.15	0.02	-3.24**	0.47	0.19**	-0.03	5.49**	5.55*	-2.82*	3.94*	-1.39**	0.14
P <sub>2xP<sub>6</sub></sub>	0.35	0.64*	-3.18**	-3.38*	0.31**	-0.21	1.77	-0.18	-4.39**	-9.55**	-1.10*	-2.29**
P <sub>2xP<sub>7</sub></sub>	-0.04	0.20	1.15	-0.03	0.09	0.39*	-8.96**	-3.96	2.65*	-0.08	-1.55**	-1.29*
P <sub>3xP<sub>4</sub></sub>	0.58**	0.37	6.57**	-8.90**	-0.63**	-0.23	20.60**	9.98**	1.61	-10.48**	-0.45	-0.31
P <sub>3xP<sub>5</sub></sub>	0.31	0.63*	-3.04**	0.48	0.28**	-0.43*	6.27**	5.26*	-1.58	-1.03	-1.23*	-0.77
P <sub>3xP<sub>6</sub></sub>	0.23	-0.06	3.60**	5.37**	0.23*	0.18	3.19*	-2.20	13.16**	13.28**	-0.94	-2.44**
P <sub>3xP<sub>7</sub></sub>	-0.46*	-0.21	-3.62**	-1.60	0.11	0.39*	5.83**	2.62	2.61*	1.47	0.25	0.89
P <sub>4xP<sub>5</sub></sub>	-0.41*	-0.52*	6.22**	-0.29	0.60**	0.18	-9.78**	-9.87**	11.69**	-2.88	0.27	0.66
P <sub>4xP<sub>6</sub></sub>	0.94**	0.05	-2.65**	0.41	0.33**	-0.41*	-0.06	0.34	-4.46**	-2.43	1.04	1.50*
P <sub>4xP<sub>7</sub></sub>	-0.60**	-0.19	-3.75**	-3.96**	0.24**	0.15	8.34**	7.39**	0.31	0.23	0.91	1.37*
P <sub>5xP<sub>6</sub></sub>	-0.49*	-0.31	4.75**	2.60	0.04	-0.15	-2.90	-5.81*	1.40	-0.66	1.20*	-0.22
P <sub>5xP<sub>7</sub></sub>	0.50**	-0.69**	3.06**	-1.87	0.08	0.48**	1.79	-3.87	11.19**	-2.69	-0.04	0.89
P <sub>6xP<sub>7</sub></sub>	0.27	-0.06	3.15**	0.65	-0.04	0.26	-6.38**	-2.48	2.11	1.59	-0.53	-1.53**
LSD Sij 5%	0.37	0.51	1.27	2.70	0.14	0.34	3.14	4.88	2.16	3.47	1.05	1.14
LSD Sij 1%	0.49	0.68	1.69	3.60	0.18	0.46	4.18	6.49	2.88	4.63	1.39	1.52
LSD sij-sik 5%	0.55	0.75	1.89	4.02	0.20	0.51	4.67	7.24	3.21	5.16	1.55	1.69
LSD sij-sik 1%	0.74	1.00	2.51	5.35	0.27	0.68	6.22	9.65	4.27	6.87	2.07	2.26
LSD sij-skl 5%	0.52	0.71	1.76	3.76	0.19	0.48	4.37	6.78	3.00	4.83	1.45	1.58
LSD sij-skl 1%	0.69	0.94	2.35	5.00	0.25	0.63	5.81	9.02	4.00	6.43	1.93	2.11

\* and \*\* refer to significant if p < 0.05 and p < 0.01, respectively.

**Genetic components and heritability**

The half diallel analysis of Hayman method (Hayman 1954) provided six genetic statistical parameters. They are D, H1, H2, h<sup>2</sup>, F and E (Table 6). Several ratios were derived as given by method of Hayman (1954) and Jinks (1954) to provide further genetic information about each trait. For all studied traits additive component (D) reached the significant level of probability (p < 0.01) for all studied traits in both F<sub>1</sub> and F<sub>2</sub> generations. These results indicate that the additive gene effects were involved in the inheritance of these traits in both generations. Significant values for the dominance component (H1) were obtained for all traits in both generations and large of magnitude than D one for most traits, indicating that the dominance type of gene action was the most prevalent genetic component in inheritance of these traits. These results are in agreement with those reported by Farag and Helal (2004), Abdalla *et al.* (2015), Abou-Zaid *et al.* (2017) and El-Abssi *et al.* (2019b).

Highly significant values for dominance components associated with gene distribution (H2) were obtained for all traits in both generations. The H2 values were differ than the H1 values for most traits indicating unequal allele recessive and dominance frequency in the parents. These agree with findings obtained by Hayman (1954 b). The overall dominance effects of heterozygous loci (h<sup>2</sup>) proved significant for all traits in both generations, indicating that the dominance was due to heterozygosity and was unidirectional with appreciable heterotic effect.

The proportions of dominant to recessive gene in parents KD/KR were more than unity for all studied

characters indicating that the dominant alleles given these in both generations. The distributions of the relative frequencies of dominant versus recessive gene (F) were not significant for Number of pods plant<sup>-1</sup>, 100-seed weight (g) in F<sub>1</sub>; Number of branches plant<sup>-1</sup> and chocolate spot % in F<sub>2</sub>. Thus, it could be concluded that an equality of the relative frequencies of dominant and recessive alleles were present in parents for studied traits. For other cases significant F values were obtained indicating a symmetry of gene frequency among the parental population were detected. The same conclusion was obtained for proportion of genes with positive and negative effects by H2/4H1. The weighted measure of average degree of dominance (H1/D)<sup>0.5</sup> exceeded unity for all studied traits in both generations, indicating that presence of over dominance for these traits. Consequently, selection for any of these traits in the early segregating generations will be of little use.

Heritability estimates in both broad and narrow sense for the studied attributes were computed according to Mather and Jinks (1971) In addition, the computed t<sup>2</sup> was low and not significant for most traits as shown in Table 6. Knowledge of size for heritability is vital in predicting the expected selection gain in faba bean. Low values for heritability in broad sense were obtained for all traits except seed weight plant<sup>-1</sup>, revealing that most phenotypic variability in each trait was due to environmental causes. Moderate or high heritability values in broad sense along with medium or low ones in narrow sense were exhibited in both generations, indicating that most genetic variances were due to non-additive genetic effects. These finding support the aforementioned results on genetic components

in which H1 estimates played a greater role in the inheritance of these characters. Therefore, the bulk method program for improving such traits might be promising El-

Galaly et al. (2009), Obiadalla-Ali et al. (2013) and El-Abssi et al. (2019b).

**Table 6. Hayman's analysis for all studied traits in F<sub>1</sub> and F<sub>2</sub> generations.**

component	Number of branches plant <sup>-1</sup>	Number of pods plant <sup>-1</sup>	No. of seeds pod <sup>-1</sup>	100-seed weight (g)	seed yield plant <sup>-1</sup> (g)	Chocolate spot %
F <sub>1</sub>						
D	0.30**	12.27**	0.13**	252.88**	19.76**	1.77**
H1	0.32*	15.07*	0.17*	237.95**	29.36**	2.73**
H2	0.97**	74.84**	0.61**	300.61**	260.16**	5.51**
h <sup>2</sup>	0.86**	61.02**	0.50**	205.81**	231.58**	4.22**
F	0.21**	5.71	1.22**	25.71	288.60**	-0.16
E	0.04	0.48	0.01	3.05	1.39	0.33
(H1/D) <sup>0.5</sup>	1.80	2.47	2.14	1.09	3.63	1.77
H2/4H1	0.22	0.20	0.20	0.17	0.22	0.19
KD/KR	1.84	1.66	1.88	2.52	1.51	2.55
r	0.15	0.26	0.22	0.50	0.14	0.11
r <sup>2</sup>	3.36	12.56	2.11	17.27	20.07	2.16
h <sup>2</sup> (b.s)	4.35	40.59	2.17	64.38	73.74	1.75
h <sup>2</sup> (n.s)	0.44	0.42	0.59	0.27	0.71	0.04
t <sup>2</sup>	0.53	0.06	38.08	0.46	2.25	6.37
B	0.81	0.45	0.10	0.37	0.36	-0.06
F <sub>2</sub>						
D	0.28**	12.54*	0.14**	187.72**	21.82**	3.07**
H1	0.21*	19.83*	0.19**	192.18**	46.96**	5.44**
H2	0.75**	52.94**	0.37**	269.38**	227.04**	11.27**
h <sup>2</sup>	0.72**	39.03**	0.29**	193.17**	192.32**	8.10**
F	0.06	38.88**	0.09**	23.47**	14.80**	-0.20
E	0.08	2.35	0.04	7.37	3.84	0.41
(H1/D) <sup>0.5</sup>	1.64	2.05	1.64	1.20	3.23	1.92
H2/4H1	0.24	0.18	0.19	0.18	0.21	0.18
KD/KR	1.58	2.25	2.39	2.49	2.00	2.72
r	0.17	0.21	0.14	0.39	0.08	0.14
r <sup>2</sup>	3.59	23.88	2.48	-44.28	44.87	5.32
h <sup>2</sup> (b.s)	3.83	20.15	3.03	71.61	34.74	2.65
h <sup>2</sup> (n.s)	0.61	0.84	0.88	0.47	0.46	0.83
t <sup>2</sup>	0.00	4.52	0.03	1.71	1.15	0.24
b	0.21	-0.06	0.95	0.88	-0.06	-0.61

\* p< 0.05; \*\* p< 0.01

Where: E= expected environmental variation, D= additive effect variance, F= relative frequencies of dominant Vs recessive genes in the parents, H1 = dominance effects, H2 = non-additive effects, h<sup>2</sup>= Overall dominance gene effects of the heterozygous loci in all crosses, (H1/D)<sup>0.5</sup> = mean degree of dominance at each locus, H2/4H1 = average frequency of + versus - alleles at loci exhibiting dominance, KD/KR = total number of dominant / receive alleles in the parents, h<sup>2</sup> (b.s) = broad sense heritability and h<sup>2</sup> (ns) = narrow sense heritability.

**Graphical (wr/vr) analysis.**

Graphical presentation (Vr,Wr) of different traits in both generations are given in Figures from 1 to 6. Significant regressions from zero were obtained in all traits in both generations and the slope of regression lines significantly from unity. This result might revealed that complementary type of epistasis was involved. The regression lines were intercept the (Wr) axis below the origin in the F<sub>1</sub> for No of branches plant<sup>-1</sup>, No. of pods plant<sup>-1</sup>, No of seeds pod<sup>-1</sup> and seed yield plant<sup>-1</sup>, F<sub>2</sub> for 100-seed weight and F<sub>1</sub>and F<sub>2</sub> for chocolate spot%, suggesting over dominance. This finding coincide with obtained above by (H1/D)<sup>0.5</sup> (Table 6). Meanwhile, intersects the (Wr) axis above the origin in the remnant cases reflecting partial dominance. Presence of over dominance, however, was the conclusion draw from computing the ratio of (H1) to (D) for these cases in Table 6. This contradiction between both types of analysis might be a logical result of the presence of complementary type of non-allelic interaction which inflated the raiois of (H1) to (D) and

distorted the (Vr,Wr) graphs (Hayman 1954 and Mather and Jinks, 1971).

The array points scattered along the regression line for all cases indicating that wide diversity among the parental genotypes. The parental genotype P<sub>3</sub> appeared to possess the largest number of recessive genes responsible for the expression of the number of branches in both of F<sub>1</sub> and F<sub>2</sub> plants. Also, P<sub>7</sub> and P<sub>4</sub> in this trait have the highest number of dominant genes in F<sub>1</sub> and F<sub>2</sub>, respectively. While, genotypes P<sub>5</sub> and P<sub>6</sub> and P<sub>1</sub> and P<sub>7</sub> seemed to contain most of recessive ones in F<sub>1</sub> and F<sub>2</sub> generations, respectively in this trait (Fig 1).

For number of pods plant<sup>-1</sup>, P<sub>2</sub> and P<sub>7</sub> in F<sub>1</sub> and P<sub>2</sub> in F<sub>2</sub> contained most dominant genes responsible for the expression of this trait. Meanwhile P<sub>5</sub> and P<sub>4</sub> in F<sub>1</sub> and P<sub>4</sub> and P<sub>7</sub> in F<sub>2</sub> seemed to carrying the most recessive genes (Fig 2). For No of seeds pod<sup>-1</sup>, the parental P<sub>3</sub> in F<sub>1</sub> and P<sub>2</sub> and P<sub>7</sub> in F<sub>2</sub> seemed to carry most of the dominant genes responsible for this trait. However, P<sub>4</sub> and P<sub>3</sub> in F<sub>1</sub> and P<sub>4</sub> and P<sub>5</sub> in F<sub>2</sub> possessed more recessive gene (Fig 3).



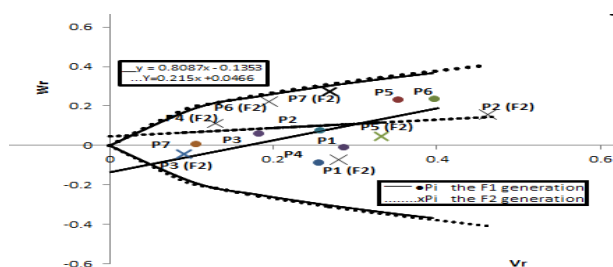


Fig. 1.  $W_r/V_r$  graph for no of branch plant<sup>-1</sup> in F<sub>1</sub> and F<sub>2</sub> generations.

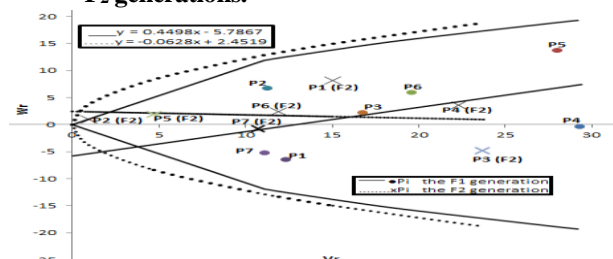


Fig. 2.  $W_r/V_r$  graph for Number of pods plant<sup>-1</sup> in F<sub>1</sub> and F<sub>2</sub> generations.

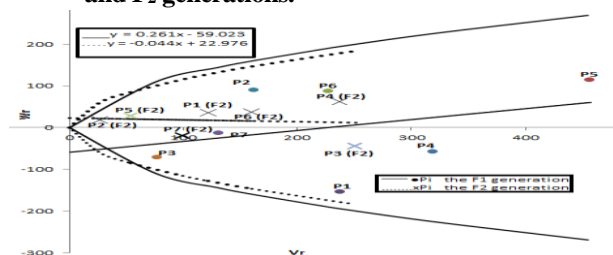


Fig. 3.  $W_r/V_r$  graph for No. of seeds pod<sup>-1</sup> in F<sub>1</sub> and F<sub>2</sub> generations.

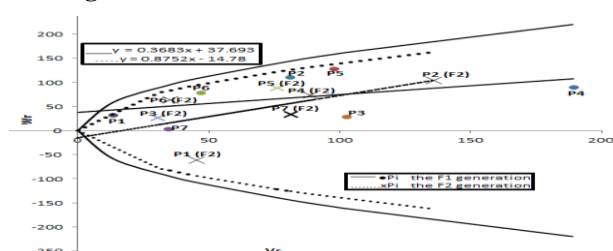


Fig. 4.  $W_r/V_r$  graph for 100-seed weight (g) in F<sub>1</sub> and F<sub>2</sub> generations.

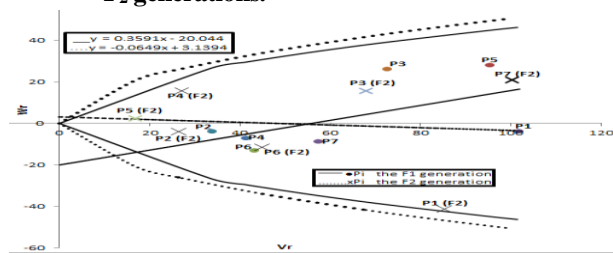


Fig. 5.  $W_r/V_r$  graph for seed yield plant<sup>-1</sup> in F<sub>1</sub> and F<sub>2</sub> generations.

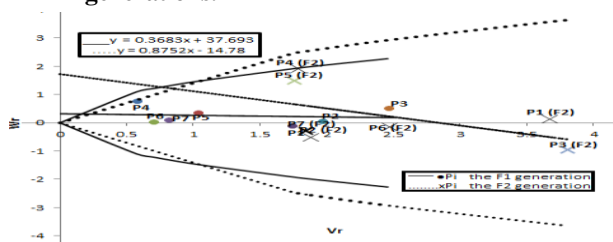


Fig. 6.  $W_r/V_r$  graph for chocolate spot % in F<sub>1</sub> and F<sub>2</sub> generations.

For 100-seed weight, P<sub>1</sub> and P<sub>7</sub> in F<sub>1</sub> and P<sub>1</sub>, P<sub>3</sub> and P<sub>6</sub> in F<sub>2</sub> contained the most dominant gene responsible for the expression of this trait. Meanwhile, P<sub>4</sub>, P<sub>3</sub> and P<sub>5</sub> in F<sub>1</sub> and P<sub>4</sub>, P<sub>2</sub> and P<sub>7</sub> in F<sub>2</sub> contained the most recessive ones.

For seed yield plant<sup>-1</sup>, P<sub>2</sub> and P<sub>4</sub> in F<sub>1</sub> and P<sub>2</sub>, P<sub>4</sub> and P<sub>5</sub> in F<sub>2</sub>, contained most number of dominant genes responsible the expression for this trait. Meanwhile, P<sub>1</sub> and P<sub>5</sub> in F<sub>1</sub> and P<sub>1</sub> and P<sub>7</sub> in F<sub>2</sub> seemed to carry the most for the recessive genes (Fig 5).

For chocolate spot%, the parental P<sub>4</sub>, P<sub>5</sub>, P<sub>6</sub> and P<sub>7</sub> in F<sub>1</sub> and P<sub>2</sub> and P<sub>7</sub> in F<sub>2</sub>, contained most dominant genes responsible for the expression of this trait. Meanwhile, P<sub>3</sub> in F<sub>1</sub> and P<sub>3</sub> and P<sub>1</sub> in F<sub>2</sub> seemed to be carrying the most recessive gene (Fig 6).

For the previous results it could be concluded that most of parental genotypes carry dominant or recessive genes in most traits were the same in F<sub>1</sub> and F<sub>2</sub> generation

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## تقدير الفعل الجيني و قوة الهجين للجيل الأول و الثاني في الهجن التبادلية بين سبعة تراكيب وراثية للفول البلدي

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يهدف البحث الى تقدير قوة الهجين و الفعل الجيني و تباينات و تأثيرات القدرة العامة و الخاصة على التالف للمحصول و مكوناته في هجيني الجيل الاول و الثاني الناتجين من التهجين النصف تبادلي بين سبعة تراكيب وراثية من الفول البلدي و ذلك لأجل تحديد التراكيب المتميزة لأستخدامها مباشرة في برامج التربية لتحسين انتاجية الفول البلدي. تم تقييم كل جيل مع الالاء بأستخدام تصميم قطاعات كاملة العشوائية بثلاثة مكررات و ذلك لصفات محصول البنور/ نبات و مكونات المحصول و الأصابة بمرض التبقع الشيكولاتي في موسم 2018/ 2019. كان التباين الراجع الى التراكيب الوراثية الأباء الهجن قوة الهجين معنوياً في الجيل الاول و الثاني في معظم الصفات. اظهر الهجينين P1xP5 و P3xP6 قوة في الهجين لمحصول البنور/ النبات في كلا الجيلين الاول و الثاني. كان التباين الراجع للقدرة العامة و الخاصة على التالف معنوياً لكل الصفات المدروسة و النسبة بينهم كانت اكبر من الوحدة لجميع الصفات عدا عدد البنور /قرن في الجيل الاول و محصول البنور/ نبات و نسبة الاصابة بالتبقع الشيكولاتي في كلا الجيلين و هذا يدل على أن الفعل الجيني المضيف و المضيف x الذي يتحكم في اظهار تلك الصفات. أظهر الأب الثاني (سحا 2) , الأب الخامس (M-13) و الأب السابع (M-1017) في الجيل الاول و الاب السادس (M-148) في الجيل الثاني قدرة عالية على التالف و مرغوبة لمعظم الصفة محصول البنور/ نبات تحت الدراسة و مكون او اكثر من مكونات المحصول. اظهرت اكثر من 25% من الهجن قدرة خاصة على التالف معنوية موجبة لصفة محصول البنور/ نبات. أظهر الهجين P1xP5 قدرة خاصة على التالف معنوية موجبة في كلا الجيلين الاول و الثاني لمحصول البنور/ نبات و المقاومة للأصابة بالتبقع الشيكولاتي. كان تأثير السيادة (H1) معنوي لكل الصفات المدروسة و كان اكبر من الجزء المضيف و كانت النسبة  $(H1/D)^{0.5}$  اكبر من الوحدة في كل الصفات المدروسة. كانت قيمة كفاءة التوريث بمعناها الواسع عالية بالمقارنة بدرجة التوريث بالمعنى الضيق التي ظهرت منخفضة الى متوسطة و هذا يدل على ان الجزء السيادة هو الذي يتحكم في اظهار الصفات . كانت قيمة الكفاءة الوراثية مرتفعة بالمدى الواسع و متوسطة او منخفضة بالمدى الضيق لمعظم الصفات و هذا بسبب تأثير الفعل الجيني الغير مضيف. و لذلك يمكن الاعتماد على نتائج الجيل الثاني في تقدير الفعل الجيني المسأل عن توريث الصفات