

Combining ability and heterosis for yield and quality traits in pea (*Pisum sativum* L.)

Zyada H.G. and Samar A. Bardisi

Hort. Dept., Fac. Agric., Zagazig Univ., Egypt

*Corresponding author: Email: samarbardisi30@gmail.com – hgzyada@yahoo.com

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ABSTRACT

Increase pea yield and quality traits are essential goals in any breeding program. This study was carried out during three winter growing seasons of 2018/ 2019, 2019/ 2020, and 2020/ 2021 on pea using diallel mating design (4×4) without reciprocals at Fac. Agric., Zagazig Univ., Egypt. Analysis of variance showed significant and highly significant mean squares for all the studied traits of genotypes, except the TSS trait, which had insignificant. Parent Master B (P₂) showed positive and significant general combining ability (GCA) effects for pod number/ plant, 100-seed weight, and yield/ plant and parent Entsar 2 (P₄) for plant height, plant dry weight, pod length, pod diameter, and seed number/pod. The pea cross Little Marvel (P₃) × Entsar 2 (P₄) had the highest values of mean and desirable effects of specific combining ability (SCA) for yield/ plant and pod number/ plant. Additive gene action was controlled plant height, plant dry weight, pod length, pod diameter, seed number/pod, pod number/plant, TSS, and protein content, while non-additive controlled the rest characters. Cross Cambados (P₁) × Little Marvel (P₃) exhibited positive and significant SCA effects for branch number, plant dry weight, pod length, seed number/pod, and TSS. Positive and significant heterosis values were recorded in crosses P₃ × P₄ and P₂ × P₃ for yield/ plant and pod number/ plant. Therefore, these genotypes could be used in the future program to improve pea yield.

KEYWORDS: Pea (*Pisum sativum* L.), Diallel cross, GCA, SCA, Heterosis, Yield traits.

1. INTRODUCTION

Pea (*Pisum sativum* L.) is the second most important food legume crop after common bean (Kumari *et al.* 2013). Pea is one of the edible legumes or pulse crops, and one of the most popular vegetable crops all over the world and in Egypt. The world's production of pea is fourth after soybean, peanuts, and dry beans (Smykal *et al.*, 2012). The major goal for pea breeding is to develop high-yielding varieties with stable yields (Abo-Hamda 2019).

Hybridization has been still the main important used method in improving the yield and quality of many vegetable crops. In this connection, pea seems to have received little attention and consequently, genetic information in all characteristics of pea is needed for wide inter varietal crosses to design accurate plans and efficient breeding programs. A diallel method of crossing based on the data of F₁ hybrids is an accurate method for its determination (Suman *et al.*, 2017 and Manjunath *et al.*, 2020).

Diallel technique analysis of Hayman (1954 a, b) has been effectively used in self and cross-pollinated crops to provide a picture of the genetic behavior of the parents and the extent of the nature of heterosis, additive and non-additive effects,

contributing to the phenotypic variance for a particular trait.

Combining ability analysis helps the breeder in identifying potential parents either to be used for heterosis breeding or for hybridization to select desirable pure line varieties through pedigree, bulk, and back cross methods (Nassef and El-Rawy, 2013). In self-pollinated crops like pea, these studies are useful in assessing the combining ability of the parents which, when crossed, would give more desirable segregates. Suman *et al.*, (2017) and Manjunath *et al.*, (2020) observed that both general and specific combining abilities were important for hundred seed weight and the number of seeds per pod. Also, Al-Hamdany (2014) and Askander *et al.*, (2018) reported that general combining ability was significant for the traits plant height, 100 seeds weight, and pod weight but non-significant for seeds pod, while SCA for most characters was significant in pea.

Heterosis breeding depends upon the basic genetic information of varied genotypes, which could be helpful if the heterosis organized in a specific cross of a considerable magnitude. Such heterosis could be exploited in establishing a hybrid variety, or when subjected to self-pollination to get the proceeding segregation generations to isolate pure lines better than its better parent or better than its F₁-hybrids. Positive heterosis over the better

parent for plant length was ranged from 6.44% to 104.21% (Hamed *et al.*, 2015). El-Dakkak (2016) found negative heterosis (-16.82%) based on the tallest parent for this trait. Furthermore, significant and positive heterosis for grain yield/ plant was observed in seven hybrids (Askander *et al.* 2018).

Genetically studies; *i.e.*, estimates of general and specific combining ability (GCA and SCA) are valuable for plant breeders, when planning a breeding program. In addition, heterosis breeding, depending on the basic genetic information of varied genotypes, would be helpful, if the heterosis is organized in a specific cross of a considerable magnitude (Hassan, 2012; Manjunath *et al.*, 2020 and Gharib, 2021).

Therefore, the present study on pea aimed to get information about the inheritance, genetic parameters, and magnitude of heterosis and combining ability for some important traits in pea using the diallel cross system.

2. MATERIALS AND METHODS

The present study was carried out during three winter growing seasons of 2019, 2020 and 2021 on pea, at Fac. Agric., Zagazig Univ., Egypt. This was initiated to study the heterosis of some pea genotypes, using diallel mating design (4×4) without reciprocals. The four cultivars used were Cambados (P₁), Master B (P₂), Little Marvel (P₃), and Entsar 2 (P₄).

2.1. Experimental Procedure

In the 2018/ 2019 season (26 December), the used cultivars were selfed for one season, to get selfed seeds. In the 2019/ 2020 season (14 October), the four cultivars were raised in the field and cross-hand pollination at the flowering stage was done, according to diallel mating design to produce six F₁ hybrid seeds. In the 2020/ 2021 season, the six F₁ hybrids with the four parents were sown on 14th October 2020 and tested in a completely randomized block design with three replicates. Each experimental unit contained one ridge. Each ridge was 3m long. The entries in each experimental unit consisted of 30 plants, planted at a spacing of 10×60 cm. Cultural practices; *i.e.*, irrigation, fertilization, and pests, and weed control were practiced in suitable time as recommended for pea.

2.2. Data Recorded

Observations on morphological traits; *i.e.*, plant height (cm) it was measured at the end of seasons, branch number per plant (it was counted at the end of seasons), plant dry weight (g), pod length (cm), pod diameter (cm), seed number per pod and 100-seed weight (g), yield traits; *i.e.*, pod number per plant, pod weight and total yield per plant (ended by

6 Feb. 2021), and quality traits; *i.e.*, TSS (Brix°) and protein (%), were recorded.

2.3. Statistical Analysis

All the obtained data were subjected to the analysis of variance according to the method described for completely randomized block design by Snedecor and Cochran (1967). Mean squares were further partitioned to parents (with 3d.f.), crosses (with 5d.f.), and residual (parents vs. crosses, with 1 d.f.). General and specific combining ability were calculated according to Method II Model II proposed by Griffing (1956). Also, additive and dominance portions were calculated from the expected mean squares.

$$\sigma^2_A = 2 \sigma^2_g \text{ and } \sigma^2_D = \sigma^2_s$$

Where:

- σ^2_A : Additive component of variation.
- σ^2_D : Dominance component of variation.
- σ^2_g : Variance due to general combining ability.
- σ^2_s : Variance due to specific combining ability.

Heterosis was calculated over mid-parent (MP) and over better parent (BP), according to Rai (1979) as follows:

- a. Mid-parent heterosis (MP) = [(F₁-MP)/MP] × 100
- b. Better parent heterosis (BP) = [(F₁-BP)/BP] × 100

The LSD values were calculated to test the significance of this component of heterotic effect, according to the following formula:

$$\text{LSD for MP heterosis} = t_{p\%} \times \sqrt{2} \text{ MSe}/r$$

Where:

- t_{p%}**: Is a tabulated t value at the stated level of probability for experimental error degree of freedom.
- MSe**: Is the mean squares of the experimental error for the analysis of variance.
- r**: Is the number of replications.
- F₁**: The first filial generation.

3. RESULTS

The results of analysis of variance for 4×4 diallel cross system were conducted for some growth traits (plant height, number of branches/ plant and dry weight/ plant), yield and its components (pod length, pod diameter, number of seed/ pod, 100-seed weight, number of pods/ plant, average pod weight and yield/ plant) and quality traits (TSS and proteins), to study mean performance of genotypes resulted from the diallel cross system, GCA, SCA, and heterosis presented in these traits of pea.

3.1. Mean performance

Analysis of variance as shown in Table 1 showed significant and highly significant mean squares for all the studied traits of genotypes, except the TSS trait which had insignificant.

Table 1. Mean squares of general (GCA), specific (SCA) combining ability and ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ resulted from 4×4 diallel cross system for growth, yield and quality traits of pea in the winter season of 2020/ 2021

S.O.V	d.f.	Growth traits					Yield and its components traits					Quality traits	
		Plant height (cm)	Branch No.	Plant dry wt. (gm)	Pod length (cm)	Pod diameter (cm)	Seed No./pod	100-Seed wt.(gm)	Pod No./plant	Pod wt. (gm)	Yield/plant (g)	TSS (Brix ^o)	Protein (%)
Reps	2	291.33**	1.63 ^{NS}	0.01 ^{NS}	0.17 ^{NS}	0.00 ^{NS}	0.23 ^{NS}	25.60**	8.23 ^{NS}	0.11 ^{NS}	28.90 ^{NS}	9.26 ^{NS}	0.01 ^{NS}
Genotypes	9	485.06**	4.08**	193.06**	3.01**	0.04**	4.48**	79.58**	79.63**	0.54*	3648.71**	24.08 ^{NS}	14.66**
Parents (P)	3	1037.88**	4.44**	243.67**	5.37**	0.05**	5.00**	38.81**	10.44 ^{NS}	0.49 ^{NS}	679.57 ^{NS}	30.05 ^{NS}	7.42**
Crosses (C)	5	162.36**	3.92**	152.82**	1.95**	0.02*	4.99**	37.57**	113.39**	0.31 ^{NS}	5938.22**	16.40 ^{NS}	19.36**
P vs. C	1	440.08**	3.76*	242.44**	1.20*	0.12**	0.36 ^{NS}	411.93**	118.42**	1.85**	1108.56 ^{NS}	44.54 ^{NS}	12.90**
GCA	3	658.96**	0.35 ^{NS}	382.57**	6.65**	0.04**	11.20**	31.85**	80.98**	0.43 ^{NS}	3047.46**	29.90 ^{NS}	15.80**
SCA	6	398.11**	5.94**	98.30**	1.19**	0.04**	1.11**	103.44**	78.96**	0.60*	3949.33**	21.17 ^{NS}	14.09**
Error	18	22.19	0.52	5.13	0.16	0.00	0.12	3.25	4.34	0.18	287.45	15.56	0.03
$\sigma^2_{GCA}/\sigma^2_{SCA}$		1.66	0.06	3.89	5.61	1.23	10.05	0.31	1.03	0.72	0.77	1.41	1.12

NS, *, and ** are insignificant, significant, and highly significant at 5% and 1% levels of probability, respectively.

As for parents, mean squares for parents showed highly significant for all the studied traits, except the number of pods/ plant, average pod weight, and TSS which had insignificant. Crosses reflected significant and highly significant for all the studied traits, except average pod weight and TSS which were insignificant. Concerning mean squares of parents vs. crosses, mean squares of P vs C showed significant and highly significant for all the traits, except seed number/ pod, yield/ plant, and TSS which were insignificant.

As for the analysis of variance for GCA and SCA, data in Table 1 showed that mean squares of GCA and SCA were significant and highly significant for all the studied traits, except the number of branches/ plant, average pod weight, and TSS for GCA and TSS for SCA which were insignificant. For genetic components (σ^2_A and σ^2_D) resulting from analysis of variance for GCA and SCA, data in Table 1 showed that values of σ^2_{GCA} (additive component) and σ^2_{SCA} (dominance component) were positive in all the cases. The values of σ^2_{GCA} were larger than σ^2_{SCA} for plant height, plant dry weight, pod length, pod diameter, seed number/ pod, pod number/ plant, TSS and protein content, while the values of σ^2_{SCA} was larger than σ^2_{GCA} for the number of branches/ plant, 100-seed weight, average pod weight and yield/ plant as shown from the ratio of variance GCA/ variance SCA (Table 1).

3.2. Mean values of parents and F1 hybrids

Since the parents had high variability, the parents (Table 2) scored high and low values, respectively; *i.e.*, P₄ and P₂ for both plant height and plant dry weight; P₄ and P₁ for the number of branches/ plant; P₄ and P₃ for pod length; P₄ and P₂ for pod diameter; P₁ and P₂ for seed number/ pod; P₄ and P₁ for 100-seed weight; P₂ and P₁ for average pod number/ plant; P₃ and P₂ for both average pod weight and yield/ plant; P₄ and P₃ for TSS and P₂ and P₄ for protein content.

For crosses (Table 2), the high and low values respectively were produced from P₃ × P₄ and P₁ × P₄ for plant height; from P₁ × P₃ and P₁ × P₄ for both the number of branches/ plant and plant dry weight; from P₁ × P₃ and P₁ × P₂ for pod length; from P₂ × P₄ and P₂ × P₃ for pod diameter; from P₁ × P₄ and P₂ × P₃ for seed number/ pod; from P₂ × P₃ and P₁ × P₄ for 100-seed weight; from P₃ × P₄ and P₁ × P₄ for pod number/ plant; from P₁ × P₄ and P₂ × P₃ for average pod weight; from P₃ × P₄ and P₁ × P₃ for yield/ plant; from P₁ × P₃ and P₃ × P₄ for TSS, and from P₂ × P₃ and P₁ × P₃ for protein content.

3.3. General combining ability (GCA) effects

According to GCA value (Table 3), the best combiners were P₃ and P₄ for plant height, P₁ and P₄ for plant dry weight, P₁ and P₄ for pod length, P₄ for

pod diameter, P₁ and P₄ for seed number/ pod, P₁ and P₂ for 100-seed weight, P₃ and P₂ for pod number/ plant and P₂ for yield/ plant and protein content.

3.4. Heterosis

3.4.1. Growth traits

For heterosis in plant height (Table 5), data show that mid-parent (MP) heterosis was negative for all the crosses obtained from 4 × 4 diallel mating design, except the crosses P₁ × P₂ and P₂ × P₃ which were positive heterosis. Heterosis in plant height reached (25.72%) in the cross P₁ × P₂ followed by P₂ × P₃ (4.99%) over mid-parent. For branch number/ plant, positive heterosis was present in most of the crosses when calculated from MP, reached 62.50% in the cross P₂ × P₃ followed by 27.78% (P₁ × P₂), 21.05% (P₁ × P₄), and 5.28% (P₂ × P₃ over the mid parent. For plant dry weight, data show that MP heterosis was negative for all the cases, except the cross P₁ × P₃ had positive heterosis.

3.4.2. Yield and its components

Data in Table 5 show that heterosis for pod length, pod diameter, number of seed/ pod, and 100-seed weight was negative for all the cases, except the crosses P₁ × P₂ and P₁ × P₃ were positive for pod length, and P₁ × P₂ and P₁ × P₄ for seed number/ pod.

As for heterosis in average pod number/ plant, data in Table 5 show that MP heterosis was positive for all the crosses, except the cross P₁ × P₄ had negative heterosis. Heterosis for average pod number/ plant reached 46.51% in the cross P₃ × P₄ followed by 21.29% (P₂ × P₄), 13.67% (P₂ × P₃), 9.52% (P₁ × P₂), and 2.99% (P₁ × P₃) over the mid parent.

Heterosis in average pod weight, data show that MB heterosis was negative, except one cross (P₁ × P₄) which had positive heterosis.

Respecting for yield/ plant, MP heterosis reached 70.63% in the cross P₃ × P₄ followed by 17.01% (P₂ × P₃) and 7.04% (P₂ × P₄) over the mid parent. In contrast, the crosses P₁ × P₂, P₁ × P₃, and P₁ × P₄ showed negative heterosis for this trait.

3.4.3. Pod quality traits

For heterosis in TSS data in Table 5 show that MP heterosis was positive for all the crosses, except the cross P₁ × P₄ had negative heterosis. The best heterosis over MP was observed with crosses, P₁ × P₃ (37.85%), P₂ × P₃ (22.71%), P₂ × P₄ (10.40%), P₁ × P₂ (9.72%), and P₂ × P₄ (1.80%).

For heterosis in protein content, data in Table 5 show that MP heterosis was negative for all the crosses, except the crosses P₁ × P₄ and P₂ × P₄ which had positive heterosis (4.71% and 0.27%, respectively).

Table 2. Mean performance of parental genotypes and F₁-hybrids resulted from 4×4 diallel cross system for growth, yield and quality traits of pea in the winter season of 2020/ 2021

Genotypes	Growth traits			Yield and its components traits						Quality traits		
	Plant height (cm)	Branch No.	Plant dry wt. (gm)	Pod length (cm)	Pod diameter (cm)	Seed No./pod	100-Seed wt.(gm)	Pod No./plant	Pod wt. (gm)	Yield/plant (g)	TSS (Brix ^o)	Protein (%)
P ₁	53.54	5.00	30.10	9.97	1.30	10.00	47.00	26.00	5.13	135.67	21.87	18.40
P ₂	43.25	7.00	15.27	8.07	1.20	7.00	52.00	30.00	5.51	165.50	17.14	21.33
P ₃	74.63	5.67	22.30	7.80	1.20	8.00	52.00	29.67	4.64	134.60	15.57	19.94
P ₄	83.63	7.67	35.90	10.47	1.47	9.00	55.77	27.67	4.71	136.00	21.57	17.85
P ₁ x P ₂	60.84	7.67	17.30	9.27	1.20	7.67	48.00	30.67	4.45	135.20	21.40	17.31
P ₁ x P ₃	53.50	8.67	28.17	9.17	1.17	9.67	41.00	28.67	4.00	111.90	25.80	13.35
P ₁ x P ₄	43.23	7.67	22.90	8.80	1.17	10.00	41.00	24.00	4.97	117.20	21.60	18.98
P ₂ x P ₃	61.88	6.67	13.27	7.10	1.10	6.67	48.50	34.00	4.34	175.57	20.07	20.52
P ₂ x P ₄	53.96	5.67	11.50	9.07	1.27	8.00	41.27	35.00	4.60	161.37	21.37	19.65
P ₃ x P ₄	62.25	6.00	27.40	8.60	1.07	7.67	45.00	42.00	4.58	230.87	18.90	18.44
Mean	59.07	6.77	22.41	8.83	1.21	8.37	47.15	32.80	4.69	150.39	20.53	18.58
LSD at 5%	8.08	1.24	3.89	0.68	0.12	0.60	3.09	3.58	0.73	29.08	6.77	0.30
CV %	7.97	10.68	10.11	4.51	5.78	4.18	3.82	20.49	9.01	11.27	19.22	0.95

P₁, P₂, P₃, and P₄ are Cambados, Master B, Little Marvel, and Entsar 2, respectively.

Table 3. General combining ability (GCA) effects resulted from 4×4 diallel cross system for growth, yield and quality traits of pea in the winter season of 2020/ 2021

Parents	Growth traits			Yield and its components traits						Quality traits		
	Plant height (cm)	Branch No.	Plant dry wt. (gm)	Pod length (cm)	Pod diameter (cm)	Seed No./pod	100-Seed wt.(gm)	Pod No./plant	Pod wt. (gm)	Yield/plant (g)	TSS (Brix ^o)	Protein (%)
P ₁	-5.12 ^{**}	0.03 ^{NS}	2.75 ^{**}	0.50 ^{**}	0.01 ^{NS}	0.92 ^{**}	-1.96 ^{**}	-3.08 ^{**}	0.04 ^{NS}	-19.38 ^{**}	1.65 ^{NS}	-1.07 ^{**}
P ₂	-5.36 ^{**}	0.03 ^{NS}	-6.58 ^{**}	-0.43 ^{**}	-0.02 ^{NS}	-0.92 ^{**}	1.00 [*]	0.97 [*]	0.16 ^{NS}	8.53 [*]	-0.92 ^{NS}	1.21 ^{**}
P ₃	5.26 ^{**}	-0.19 ^{NS}	0.23 ^{NS}	-0.61 ^{**}	-0.06 ^{**}	-0.31 ^{**}	0.46 ^{NS}	1.69 ^{**}	-0.21 [*]	5.93 ^{NS}	-1.12 ^{NS}	-0.12 ^{**}
P ₄	5.22 ^{**}	0.14 ^{NS}	3.59 ^{**}	0.54 ^{**}	0.06 ^{**}	0.31 ^{**}	0.51 ^{NS}	0.42 ^{NS}	0.02 ^{NS}	4.92 ^{NS}	0.39 ^{NS}	-0.02 ^{NS}
LSD at 5% (g _i -g _i)	3.30	0.51	1.59	0.28	0.05	0.24	1.26	1.46	0.30	11.87	2.76	0.12

P₁, P₂, P₃, and P₄ are Cambados, Master B, Little Marvel, and Entsar 2, respectively.

Table 4. Specific combining ability (SCA) effects resulted from 4×4 diallel cross system for growth, yield and quality traits of pea in the winter season of 2020/ 2021

Crosses	Growth traits		Yield and its components traits							Quality traits		
	Plant height (cm)	Branch No.	Plant dry wt. (gm)	Pod length (cm)	Pod diameter (cm)	Seed No./pod	100-Seed wt.(gm)	Pod No/plant.	Pod wt. (gm)	Yield/plant (g)	TSS (Brix°)	Protein (%)
P ₁ x P ₂	12.25**	0.84*	-1.29 ^{NS}	0.36 ^{NS}	-0.01 ^{NS}	-0.70**	1.81 ^{NS}	2.01 ^{NS}	-0.44 ^{NS}	-4.34 ^{NS}	0.14 ^{NS}	-1.40**
P ₁ x P ₃	-5.71**	2.07**	2.77*	0.45*	0.00 ^{NS}	0.69**	-4.65**	-0.71 ^{NS}	-0.52*	-25.04**	4.75*	-4.03**
P ₁ x P ₄	-15.95**	0.73 ^{NS}	-5.85**	-1.07**	-0.12**	0.41*	-4.70**	-4.10**	0.22 ^{NS}	-18.72*	-0.97 ^{NS}	1.50**
P ₂ x P ₃	2.91**	0.07 ^{NS}	-2.80*	-0.6**	-0.04 ^{NS}	-0.48*	-0.11 ^{NS}	0.57 ^{NS}	-0.30 ^{NS}	10.71 ^{NS}	1.58 ^{NS}	0.85 ^{NS}
P ₂ x P ₄	-4.97**	-1.27**	-7.93**	0.13 ^{NS}	0.01 ^{NS}	0.24 ^{NS}	-7.39**	2.84*	-0.27 ^{NS}	-2.47 ^{NS}	1.37 ^{NS}	-0.12 ^{NS}
P ₃ x P ₄	-7.30**	-0.71 ^{NS}	1.17 ^{NS}	-0.16 ^{NS}	-0.15**	-0.70**	-3.11**	9.12**	0.08 ^{NS}	69.63**	-0.90 ^{NS}	-0.01 ^{NS}
LSD 5% (Sii-Sjj)	4.66	0.72	2.24	0.39	0.07	0.35	1.79	2.06	0.42	16.79	3.91	0.17
LSD 5% (Sij-Sik)	7.38	1.13	3.55	0.62	0.11	0.55	2.82	3.26	0.66	26.55	6.18	0.28

NS, *, and ** are insignificant, significant, and highly significant at 5% and 1% levels of probability, respectively.

Table 5. Heterosis percentage over mid parent (MP) for growth, yield and quality traits of pea F₁ hybrids

Crosses	Growth traits			Yield and its components traits						Quality traits		
	Plant height (cm)	Branch No.	Plant dry wt. (gm)	Pod length (cm)	Pod diameter (cm)	Seed No./pod	100-Seed wt.(gm)	Pod No/plant.	Pod wt. (gm)	Yield/plant (g)	TSS (Brix°)	Protein (%)
P ₁ x P ₂	25.72**	27.78**	-23.73**	2.77 ^{NS}	-4.00 ^{NS}	-9.80**	-3.03 ^{NS}	9.52*	-16.33**	-10.22 ^{NS}	9.72 ^{NS}	-12.85**
P ₁ x P ₃	-16.51**	62.50**	7.51 ^{NS}	3.19 ^{NS}	-6.67 ^{NS}	7.41**	-17.17**	2.99 ^{NS}	-18.16**	-17.19*	37.85**	-30.33**
P ₁ x P ₄	-36.97**	21.05**	-30.61**	-13.87**	-15.66**	5.26*	-20.21**	-10.56*	1.02 ^{NS}	-13.72 ^{NS}	-0.54 ^{NS}	4.71**
P ₂ x P ₃	4.99 ^{NS}	5.26 ^{NS}	-29.37**	-10.50**	-8.33*	-11.11**	-6.73**	13.67**	-14.48**	17.01*	22.71 ^{NS}	-0.56 ^{NS}
P ₂ x P ₄	-14.94**	-22.73**	-55.05**	-2.16 ^{NS}	-5.00 ^{NS}	0.00 ^{NS}	-23.41**	21.39**	-9.95*	7.04 ^{NS}	10.40 ^{NS}	0.27 ^{NS}
P ₃ x P ₄	-21.33**	-10.00 ^{NS}	-5.84 ^{NS}	-5.84*	-20.00**	-9.80**	-16.49**	46.51**	-2.07 ^{NS}	70.63**	1.80 ^{NS}	-2.43**
LSD at 5%	8.08	1.24	3.89	0.68	0.12	0.60	3.09	3.58	0.73	29.08	6.77	0.30

NS, * and ** are insignificant, significant, and highly significant at 5% and 1% levels of probability, respectively.

4. DISCUSSION

Analysis of variance of 4×4 of the diallel cross system in pea reflect highly significant mean squares for genotypes and also parents and crosses among them, except pod number/ plant, average pod weight, yield/ plant, and TSS for parents, average pod weight, and TSS for crosses, and TSS for genotypes (Table 1). Moreover, GCA and SCA mean squares were highly significant for all the studied traits, except branch number, average pod weight, and TSS for GCA, and TSS for SCA were appeared insignificant. Significant GCA and SCA mean squares for all the studied traits in pea were also revealed by Joshi *et al.* (2016), Suman *et al.* (2017), Hama-amin (2020), and Towfiq *et al.* (2020).

In this respect, general and specific combining ability estimates (GCA and SCA) help in the identification of the best combiner and promising parents and desirable crosses for the improvement of plant traits through selection and breeding. The variance of GCA and SCA identify the relative importance of additive and non-additive causes of variation (Amin and Haridy, 2019).

Therefore, the four parents crossed in this work; *i.e.*, Cambados (P₁), Master B (P₂), Little Marvel (P₃), and Entsar 2 (P₄) had sufficient diversity. Similar results were also reported by Askander *et al.* (2018) and Gharib (2021).

4.1. General combining ability

The best combiners for growth traits (Table 3), which exhibited high GCA effect were P₃ (Little Marvel) for plant height and P₄ (Entsar 2) for dry weight/ plant.

Respecting yield and its component traits, the cultivars which showed high GCA effect were P₄ (Entsar 2) for pod length and pod diameter, P₁ (Cambados) for seed number/ pod, P₂ (Master B) for 100-seed weight, P₃ (Little Marvel) for pod number/ plant and P₂ (Master B) for yield/ plant. Concerning pod quality traits, P₂ (Master B) for protein content in seeds.

These results reflect the existence of favorable genes for all studied traits in the tested parental genotypes, which could be utilized in the breeding programs to improve pea. This finding is coherent with that of Kalia and Sood (2009).

Therefore, the performance of each trait was mainly cultivar-dependent. So that the choice of parents for a particular character should be based on its performance. Obtained results are in accordance with Askander *et al.* (2018) and Parveen *et al.*, (2019).

4.2. Specific combining ability

For growth traits (Table 4), the crosses that showed high SCA effect were P₁× P₂

(Capados×Master B) for plant height and P₁× P₃ (Cambados×Little Marvel) for branch number and dry weight/ plant. According for yield and its components, the crosses that showed high SCA effect were P₁× P₃ (Cambados×Little Marvel) for seed number/ pod and P₃× P₄ (Little Marvel×Entsar 2) for average pod number/ plant and yield/ plant.

Concerning pod quality traits, the cross that showed high SCA effect was P₁× P₄ (Cambados×Entsar 2) for protein content.

Similar results also showed that some crosses were observed superior for the SCA effects, indicating the presence of non-allelic interaction. These observed can be further utilized to develop and enhance the yield potential of pea cultivars and breeding programs (Suman *et al.*, 2017).

4.3. Heterosis

In this respect, MP heterosis is mostly used in biometrical studies. The crosses which showed high MP values (Table 5) were P₁ × P₂ for plant height and P₂ × P₃ for branch number/ plant. For yield traits, the crosses having high MP values were P₁ × P₂ for pod length, P₁ × P₂ for seed number/ pod, P₃ × P₄ for average pod number/ plant, and P₁ × P₄ for average pod weight. Moreover, the crosses which showed high MP values in plant yield was P₃ × P₄. The best heterosis over MP in TSS was observed in the cross P₁ × P₃ which was reached 37.85%. These results are in line with the finding of Hasan *et al.*, (2010), Braret *et al.*, (2012) and Galal *et al.*, (2019) who found positive heterosis in some studied crosses for horticultural traits of pea. These results indicated that heterosis did not reflect the GCA of the cross parents, but this is due to parent per se performance. Moreover, heterosis (MP) in plant yield reached to 70.63% (P₃ × P₄) and 17.01% (P₂ × P₃). So that transgressive segregants would be expected in the progeny of these crosses. And selection in advanced generation for high performed lines would be better than the better parent and /also than hybrid itself.

These results are in agreement with those by Brar *et al.* (2012), Galal *et al.* (2019), and Gharib (2021) which indicated that all studied traits showed significant mid-parent heterosis in the desired direction in some crosses. Also, all studied traits exhibited different types of potency ratios.

5. CONCLUSION

The obtained results indicated considerable genetic variations among the evaluated commercial pea cultivars as well as among the obtained F₁ hybrids for all the studied traits. Accordingly, crossing followed by selection in segregating generations can be applied to develop new high-yielding breeding lines.

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الملخص العربي

القدرة علي التآلف وقوة الهجين لصفات المحصول والجودة في البسلة

هاني جمال زيادة، سمر عبد الله برديسي

قسم البساتين - كلية الزراعة - جامعة الزقازيق

زيادة محصول البسلة وصفات الجودة هي الأهداف الأساسية لأي برنامج تربية، أجريت هذه الدراسة خلال ثلاثة مواسم نمو شتوية لأعوام ٢٠١٨ / ٢٠١٩، ٢٠١٩ / ٢٠٢٠ و ٢٠٢٠ / ٢٠٢١ علي البسلة باستخدام تصميم الداى أليل "التهجين الدوري" (٤ × ٤) بدون هجن عكسية بكلية الزراعة، جامعة الزقازيق، مصر.

أظهر تحليل التباين إختلافات معنوية جداً بين التراكيب الوراثية لجميع الصفات تحت الدراسة، ماعدا صفة TSS كانت غير معنوية، وأظهر الأب ماستر بي (P₂) معنوية موجبة لتأثيرات القدرة العامة علي التآلف لصفات عدد القرون لكل نبات، وزن ١٠٠-بذرة، ولصفة المحصول/ نبات، والأب انتصار ٢ (P₄) لصفات ارتفاع النبات، الوزن الجاف للنبات، طول القرن، قطر القرن، وعدد البذور لكل قرن. أعطى هجين البسلة (P₄) 2 Entsar × (P₃) Little Marvel أعلى قيم متوسطات وتأثيرات مرغوبة للقدرة الخاصة علي التآلف لصفتي المحصول وعدد القرون لكل نبات.

تحكم الفعل الجيني المضيف في وراثه صفات ارتفاع النبات، الوزن الجاف للنبات، طول القرن، قطر القرن، عدد البذور لكل قرن، عدد القرون لكل نبات، TSS، ومحتوي البروتين، بينما كان الفعل الجيني غير المضيف المتحكم في باقي الصفات، أظهر الهجين (P₃) Little Marvel × (P₁) Cambados إيجابية ومعنوية لتأثيرات القدرة الخاصة علي التآلف لصفات عدد الأفرع/ نبات، الوزن الجاف للنبات، طول القرن، عدد البذور لكل قرن، و TSS، وسجلت الهجن P₃ × P₄ و P₂ × P₃ قيم موجبة ومعنوية لصفتي المحصول وعدد القرون لكل نبات، ولذلك يمكن التوصية باستخدام هذه التراكيب الوراثية في برامج التربية لتحسين محصول البسلة.