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Study of combining ability and heterosis for yield and its components in seven pea genotypes (*Pisum sativum* L.) and progeny by using Line X Tester analysis)

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ABSTRACT

The present investigation was conducted to study the combining ability and heterosis of F1 crosses and their parents for yield and its components in seven pea genotypes Via Line X Tester analysis during two growing seasons. Three varieties of pea as lines (Javor, NS minima, and Oregon sugar pod) and four varieties as testers (Giant sugar pod, Green sage, Lancet, and Provence) have been crossed to produce 12 F1 crosses during the first growing season at Qliasan Research Station. Emasculation and crossing were done by hand, and sufficient seeds for crosses were produced. During the growing season of 2015-2016, the F1 seeds with their parents were implemented in the field experiment using RCBD with three replicates in the Girdjan Research Station, to determine parental combinations through studying the general and specific combining abilities and their variances to improve pea crosses. The results showed that line parent 3 recorded a maximum pod length, and pod yield plant^{-1}, while tester parent 4 produced the maximum values for seed weight pod^{-1}, 100 seeds weight, number of pods plant-1, and seeds yield plant-1. The results indicated that the cross 2×5 produced the maximum values for a number of pods plant^{-1}, pod yield plant^{-1}, and seeds yield plant^{-1}. Parent line 3 showed a maximum negative GCA effect value of -8.92, while tester 7 exhibited a maximum positive GCA effect value of 7.447. Hybrid 2 × 7 had the highest positive heterosis values for two traits number of pods plant^{-1}, and seed yield plant^{-1}.

Keywords: : (Pisum sativum L.); Line × Tester analysis; general combining ability; specific combining ability; heterosis.

INTRODUCTION

Pea is one of the world's earliest cultivated crops, and their seeds are a source of protein for both people and livestock [1]. Legumes like the pea are good for crop rotation because they disrupt insect and disease cycles, increase soil aggregation and microbial diversity, and conserve soil water. Legumes are significant crops that provide almost one-third of the protein humans consume. They also have a significant impact on sources of animal feed and forage, as well as edible and industrial oils [2]. For these reasons, grain legumes are regarded as the least expensive and richest source of plant proteins known as pulses [3].

The pea is a Fabaceae family annual grain legume that originated in Southwest Asia. Afghanistan, Iran, and Ethiopia are still home to wild field peas. Along with soybeans, groundnuts, and beans, it is one of the four most significant agricultural legumes [4]. Peas have a wide range of agricultural and horticulture uses. Green seeds are utilized to make fresh, frozen, or canned vegetables, whereas mature dried seeds serve a variety of functions. It is a high-protein crop (27%) for human consumption [5]. It is now well-accepted that substances used as protein sources are critical to human nutrition [6]. *Pisum sativum* L., often known as field peas, garden peas, and green peas, are cool-season crops produced for their edible seed or seed pods. Green or garden peas are picked before the seed is fully developed for the fresh pack market [7].

A premium vegetable farmed for its freshly shelled, green seeds that are high in protein (7.2%), vitamins, and minerals are the garden pea *Pisum sativum* L. var. *hortense* [8]. Field peas are crucial for increasing the amount of protein in the diet because their protein content can reach up to 40% on a dry weight basis [9]. It was discovered that the pea is one of the six primary pulse crops among legumes that are farmed globally and that it is the world's second highest-yielding legume after the common bean [10]. Peas are regarded as an important forage and vegetable crop, however, even though their total harvested area has greatly risen, their yield and productivity have remained static or constant over time [11]. A systematic method for identifying eligible parents and crosses is offered by Line X Tester analysis. It was applied to improve self and cross-pollinated plants [12]. One of the mating designs that efficiently evaluates genotype combining ability is the (Line X

Tester) analysis. The ideal tester delivers the most information on a line's performance in cross combinations. In contrast, testers with a broad genetic base include heterogeneous cultivars or hybrids and provide information on GCA only in an earlier generation [13].

Breeders can identify suitable parents and promising recombinants/hybrids using mating designs, one of the biometric breeding methods. Although diallel analysis has been utilized widely for these objectives, (Line X Tester) analysis is still a superior mating design to diallel in that it uses more varied sets of parents as males and females with a relatively small number of crosses [14]. The GCA refers to the average performance of line strains in a set of cross combinations. In contrast, the SCA refers to examples that perform better or worse in some cross combinations than anticipated based on the average performance of the parental lines involved in crop combinations [15].

This study attempts to employ the genetic potential for yield and yield component traits in peas. This mating design has been used to determine the inheritance of important traits among a number of genotypes to identify superior parents for the development of a hybrid cultivar.

The aims of this study were:

1- To estimate GCA for (3) genotypes used as female parents and (4) testers used as male parents, and SCA of hybrids for yield and yield component traits.
2- To estimate the heterosis of hybrids for yield and yield component traits in pea genotypes.
3- Evaluation of the field performance of different varieties of peas.

Materials and Methods

Table 1 shows seven pea cultivars selected based on preliminary field observations of their performance, their broad genetic background, and great variations in some field characters, with superiority in the cultivar.

Table 1: Name and sources of pea genotypes used in the mating design in the study

No.	Varieties	In mating design	Source
1	Javor	Line	Australia
2	NS minima	Line	Australia
3	Oregon sugar pod	Line	USA
4	Giant sugar pod	Tester	UK
5	Green sage	Tester	USA
6	Lancet	Tester	Germany
7	Provence	Tester	Italy

In the first growing season, a field study was carried out at Qliasan Research Station, College of Agricultural Sciences, University of Sulaimani, (Lat. 35º 34' 307"; N, Long 45º 21' 992"; E, 765 m above sea level) 2 km north-west of Sulaimani city, during (2014-2015). Three lines cultivated of a pea, **Javor**, **NS minima**, **Oregon sugar pod** (female parents), and four pea genotypes, **Giant sugar pod, Green sage, Lancet,** and **Provence** as testers (male parents), have been crossed to produce 12 F1 crosses according to the (Line X Tester) mating design developed by [12], as shown in Table 2. Necessary precautions have been taken to avoid the contamination of genetic material during crossing. The emasculation of flowers has been done and sufficient hybrid seeds for each cross have been produced by hand pollination. Hybrid seeds of F1 were obtained from all crosses collected, separated, and stored for the next season.

Table 2: The mating design of (Line X Tester) to produce 12 crosses.

Tester ♂ Line ♀	Giant sugar pod (4)	Green sage (5)	Lancet (6)	Provence (7)
	Crosses			
Javor (1)	1×4	1×5	1×6	1×7
NS minima (2)	2×4	2×5	2×6	2×7
Oregon sugar pod (3)	3×4	3×5	3×6	3×7

In the second growing season, the study was carried out at Girdjan Research Station, (Lat. 36º 12' 11"; N, Long. 44º 47' 03"; E, 543 m above sea level) 115 km North West of Sulaimani city, (2015-2016). The soil was Silty Clay with 7.4 pH and contained organic matter 0.3% and available Phosphate 12.794 (mg. Kg^{-1}) soil as shown in (appendix 1). The F1 seeds of twelve crosses (3 X 4) along with their parents were implemented in a field experiment in RCBD with three replications. Each replicate comprises seven parents (Line & tester) and twelve F1 crosses. Each plot consisted of two rows of one material, 3 meters long, 50 cm between rows, 20 cm between plants within a row, 1 meter between plots within a replicate, and 2.5 meters between replicates. The genotypes were assigned at random to experimental units. Recommended cultural practices were done from sowing to maturity to raise a good crop. The meteorological data of the (Girdjan) location

during the present study is represented in (Appendix 2). Five plants from each plot were tagged at random to record the studied traits. The Least Significant Difference LSD Test was used to compare the genotype averages.

Studied traits included

pod length (cm), number of seeds pod^{-1}, seed weight per pod (g), 100 seed weight (g), number of pods plant^{-1}, Pod yield plant^{-1} (g), seed yield plant^{-1} (g), protein content (%), oil content (%) and ash content (%).

Statistical analyses were performed for each trait; all recorded data were examined according to the analysis of variance procedures (ANOVA). Individual analysis and LSD at 5% and 1% significance levels were calculated to evaluate the means [16]. The (Line X Tester) mating design analysis, as described by [12], was used to conduct the general and specific combining ability studies, and was accepted by [17].

General and Specific Combining Abilities

The effect of the general combining ability of line parents and tester parents was calculated using the following equation:

1. Estimation of *GCA* Effects:

a- For Lines:

$\hat{g}_{ii} = \frac{Y_{i..}}{tr} - \frac{Y_{...}}{ltr}$ $\hat{g}_{ii}$: Effect of expected general combining ability for the line "*i*"

l: No. of lines, ***t:*** No. of testers, ***r:*** No. of replications, Check: $\sum \hat{g}_{ii}$ = zero

b- For testers:

$\hat{g}_{jj} = \frac{Y_{.j.}}{lr} - \frac{Y_{...}}{ltr}$ $\hat{g}_{jj}$= Effect of expected general combining ability for tester "*j*"

Check: $\sum \hat{g}_{jj} = zero$

2. Estimation of *SCA*. Effects:

$\hat{S}_{ij} = \frac{Y_{ij.}}{r} - \frac{Y_{i..}}{tr} - \frac{Y_{.j.}}{lr} - \frac{Y_{...}}{ltr}$

$\hat{S}_{ij} =$ Effect of expected specific combining ability for a single cross *ij* when *i* = *j*.

Check: $\sum \hat{S}_{ij} = zero$

The standard error for combining ability effects:

$$S.E_{\ (gca.\,for\,line)} = \sqrt{\frac{MSe}{rt}}$$

$$S.E_{\ (gca.\,for\,tester)} = \sqrt{\frac{MSe}{rl}}$$

$$S.E_{(sca\ Efects)} = \sqrt{\frac{MSe}{r}}$$

$$S.E(\hat{g}_i - \hat{g}_j)\,for\,line = \sqrt{\frac{2MSe}{rt}}$$

$$S.E(\hat{g}_i - \hat{g}_j)\,for\,tester = \sqrt{\frac{2MSe}{rl}}$$

$$S.E(\hat{S}_{ij} - \hat{S}_{ij}) = \sqrt{\frac{2MSe}{r}}$$

Genetic components:

1. Genetic components due to the general combining ability (*GCA*):

The estimation of the general and specific combining abilities variance will be calculated for the average of lines and testers as follows:

$$\sigma^2_{gca}(Line) = \frac{MS_l + MS_{lt}}{rt}$$

$$\sigma^2_{gca}(Tester) = \frac{MS_t + MS_{lt}}{rl}$$

$$\sigma^2_{gca}(Average) = \frac{1}{r(2lt - l - t)}[\frac{(l-1)(MS_l) + (t-1)(MS_t)}{l + t - 2} - MS_{lt}]$$

$$\sigma^2_{sca} = \sigma^2_D = \frac{MS_{lt} - MS_e}{r}$$

$$\sigma^2_A = 2\sigma^2_{gca}$$

2. The estimation of heterosis:

Heterosis is the F_1 superior to mid-parental value, in other words superior to average of two parents.

$$Heterosis(H\%) = \frac{\overline{F}_1 - \overline{M}.P}{\overline{M}.P} \times 100$$

Where: $F_1 =$ Mean of cross

$\overline{M}.P =$ Mid-parental value.

$\overline{M}.P = \frac{P_1 + P_2}{2}$ $P_1 =$ Parent 1, $P_2 =$ Parent 2

Results and discussion

Table 3 confirms the presence of mean square values for the studied traits of pea genotypes derived from (line X tester) analysis. The data represented in the table indicated significant or highly significant differences for genotypes, parents, and crosses for all traits except the number of pods per plant for parents. Regarding the same table mean square values for Lines, Testers, and (Line X Tester) were significant or highly significant for all studied traits except the number of seeds per pod and ash content (%) for Lines, pod length, 100 seed weight and ash content (%) for Tester, pod length, seed weight per pod and 100 seed weight for (Line X Tester).

Table 3. Mean square values for the studied traits of pea genotypes *via* (line X tester) analysis

S. O. V.	Repl.	Geno-types	Parents	Crosses	Par. X Cro.	Lines	Testers	L X T	Mse
d.f	2	18	6	11	1	2	3	6	36
Traits									
PoL (cm)	0.17	1.46^{**}	1.66^{**}	1.10^{**}	4.14^{**}	4.92^{**}	0.43^{ns}	0.17^{ns}	0.16
NSPPo	0.11	1.12^{**}	1.19^{**}	1.05^{**}	1.55^{**}	0.26^{ns}	2.70^{**}	0.48^{**}	0.11
SWPPo (g)	0.011	0.200^{**}	0.319^{**}	0.146^{**}	0.081^{*}	0.397^{**}	0.226^{**}	0.022^{ns}	0.012
100-SW g)	0.75	32.87^{**}	32.17^{**}	28.07^{**}	89.85^{**}	132.8^{**}	7.93^{ns}	3.23^{ns}	3.07
NPoPP	82.17	453.7^{**}	20.55^{ns}	335.4^{**}	4354.5^{**}	771.3^{**}	396.1^{**}	159.8^{**}	17.63
PoYPP (g)	111.9	479.4^{**}	117.90^{*}	230.7^{**}	5384.7^{**}	184.4^{*}	184.0^{**}	269.5^{**}	36.97
SYPP (g)	62.61	326.4^{**}	68.33^{*}	168.9^{**}	3607.1^{**}	143.5^{**}	100.92^{*}	211.4^{**}	26.13
PrCo(%)	0.012	17.12^{**}	34.18^{**}	9.218^{**}	1.658^{ns}	5.49^{*}	11.68^{**}	9.227^{**}	1.266
OilCo(%)	0.293	0.634^{**}	0.762^{**}	0.612^{**}	0.104^{ns}	0.623^{**}	0.846^{**}	0.492^{**}	0.072
AsCo(%)	0.073	0.121^{**}	0.131^{*}	0.108^{*}	0.198^{ns}	0.069^{ns}	0.113^{ns}	0.118^{*}	0.048

* . Significant at 5% probability level **. Significant at 1% probability level ^{ns}. Non-significant

PoL=Pod length, NSPPo=No. of seeds pod^{-1}, SWPPo=Seed weight per pod, 100-SW=100 seed weight

NPoPP=No. of pods plant^{-1}, PoYPP=Pod yield plant^{-1}, SYPP=Seed yield plant^{-1}, PrCo%=Protein content (%)

OilCo%=Oil content (%), AsCo(%)=Ash content (%), * significant at level of 5%, ** significant at level of 1%

1-The average values of the studied traits:

Table 4 shows the average performance of studied traits of pea genotypes for parents (lines and testers) and their crosses F1. The results show that among the parents, line 3 recorded a maximum pod length of 6.10 cm, followed by testers 6 and 4 with 5.71 and 5.59 cm, respectively, while line 2 recorded the lowest pod length of 4.08 cm.

These differences between parental values are reflected significantly on their crosses. As shown in the same table the cross 3×7 with 6.62 cm, recorded the highest value of pod length, followed by the cross 3×4 and 3×6 with 6.39 and 6.33 cm respectively, while the lowest value of pod length exhibited by the cross 1×5 with 4.91 cm. As shown in the table crosses means exceeded parental means by 9.88%. Other researchers reported previously that the pod length of pea genotypes was restricted between 7.6–10.1 cm [18], 6.55–11.31 cm [19], and 3.42–6.31 cm [20]. Data in the same table indicated that among the parents, tester 6 gave a maximum number of seeds pod^{-1} with 4.83 seeds, followed by line 3 with 4.69 seeds, while line 1 recorded the lowest number of seeds pod^{-1} with 3.13 seeds. The differences between parental values significantly affected their crosses. Regarding the cross values, the cross 1×4 exhibited the maximum number of seeds pod^{-1} with 5.26 seeds, followed by the cross 2×4 with 5.16 seeds pod^{-1}, while the cross 1×5 exhibited the lowest number of seeds pod^{-1} with 3.29 seeds. It was found from the same table that the crosses mean predominated parents mean by 7.76%. Previous studies reported that the number of seed pod^{-1} for pea genotypes was restricted between 5.1-7.4 [21], 2.75-4.54 [22], 3.5-5.6 [23], and 4.0-7.6 [24].

Among the parental values, tester parent 4 produced the maximum value of seed weight pod^{-1} with 1.380 g, followed by line 3 and tester 7 with 1.311 and 1.001 g respectively, while line 2 gave the lowest weight of seed pod^{-1} with 0.469 g. These differences between parental values significantly reflected on their crosses. Regarding the same table, cross 3×7 with 1.410 showed the maximum value for seed weight pod-1, followed by the crosses 3×4, 3×6, and 1×4 with 1.378,1.212 and 1.015 g, respectively, while the cross 1×5 with 0.690 g recorded the lowest weight for this trait. It was shown in the same table that the cross means increased by 7.75% compared to the parent's mean. Different seed weight pod^{-1} for pea genotypes were obtained previously by researchers between 1.06–2.57 [25] and 1.87–5.1[26]. Data in Table 4 revealed that tester 4 recorded a maximum value of 100 seed weight at 21.60 g, followed by line 1 and tester 7 with 21.11 and 20.69 g, respectively, while line 2 recorded the lowest value of 100 seed weight, which was 12.56 g. These differences between parental values significantly reflected on their crosses.

Data in the same table showed that cross 3×4, with 26.08, showed the maximum average value of 100 seed weight, while cross 2×6, with 16.74, recorded the lowest value of 100 seed weight.

It was clarified that the cross means increased by 12.18% over the parental means. Other researchers reported previously that 100 seed weight for pea genotypes was restricted between 11.4–19.4 g [27], 20–26 g [28], 3.2–23.27 g [29], and 18.10 to 28.5 g [30]. The mean values for parents and their crosses for a number of pods plant^{-1} were shown in Table 4. Tester parent 4 exhibited the maximum number of pods plant^{-1} with 15.60 pods, followed by lines 1 and 3 with 14.80 and 12.87 pods respectively, while tester 7 recorded the lowest number of pods plant^{-1} with 8.47 pods. These differences between parental values significantly reflected on their crosses. As shown in the same table, the cross 2×5 with 48.57 pods recorded the maximum number of pods plant^{-1}, followed by the crosses 2×7 and 1×7 with 44.03 and 43.53 pods respectively, while the cross 3×4 with 17.00 pods recorded the lowest number of pods plant^{-1}. The results in the same table explained that cross means exceeded parental means by 60.16%. Previous studies recorded that the number of pods per plant^{-1} for pea genotypes lies between 21.78–29.48 pods [31], 9.83–20.17 pods [32], and 8.3–53.6 pods [33].

As shown in the table, line parent 3 revealed the maximum weight of pod yield plant-1 at 21.75 g, followed by tester 4 and line 1 with 21.34 and 12.21g, respectively. Line 2 exhibited the lowest weight of pod yield plant-1 with 6.36 g. These differences between parental values were reflected significantly in their crosses. The cross 2×5 with 46.60 g showed the maximum average value of pod yield plant^{-1}, while the cross 3×5 with 22.06 g recorded the lowest value of pod yield.

It was evident from the same table that the crosses mean increased by 61.25% over the parental means. Previous researchers showed that the pod yield plant^{-1} for pea genotypes was between 17–143 g [34], 37.45–86.12 g [26] and 60.00–143.33 g [35]. It was also found in Table 4, that tester parent 4 exhibited maximum weight for **seed yield plant^{-1}** with 17.29 g, followed by line parent 3 with 15.91 g, while line parent 2 recorded the minimum weight for seed yield plant^{-1} with 5.11g. These differences between parental values significantly reflected on their crosses.

Table 4. Average values of studied traits of pea genotypes for parents (lines & testers) and their crosses

Genotypes	PoL (cm)	NS PPo	SWPPo (g)	100-SW(g)	NPo PP	PoYPP (g)	SYPP (g)	PrCo (%)	OilCo (%)	AsCo (%)
Parents										
Line 1	4.88	3.13	0.841	21.11	14.80	12.21	9.42	19.15	4.82	3.43
Line 2	4.08	3.91	0.469	12.56	11.67	6.36	5.11	18.99	3.92	3.33
Line 3	6.10	4.69	1.311	19.84	12.87	21.75	15.91	23.59	4.31	3.24
Tester - 4	5.59	4.22	1.380	21.60	15.60	21.34	17.29	26.20	4.08	3.12
Tester - 5	4.31	3.36	0.744	19.34	11.07	9.88	8.24	25.62	4.85	3.24
Tester - 6	5.71	4.83	0.756	16.10	9.53	9.58	7.31	20.05	3.43	3.63
Tester - 7	5.11	4.12	1.001	20.69	8.47	8.11	6.25	26.39	4.05	2.99
Parents mean	5.11	4.04	0.929	18.75	12.00	12.75	9.93	22.86	4.21	3.28
Crosses										
1 X 4	6.03	5.26	1.015	23.66	20.97	26.40	20.49	22.10	4.30	3.14
2 X 4	5.33	5.16	0.947	17.57	27.60	30.90	24.76	25.65	4.22	3.58
3 X 4	6.39	4.61	1.378	26.08	17.00	31.22	25.28	26.27	3.91	3.19
1 X 5	4.91	3.29	0.690	22.77	27.60	25.92	20.73	23.25	4.13	2.85
2 X 5	5.01	4.01	0.799	19.04	48.57	46.60	37.99	21.81	3.88	3.10
3 X 5	6.23	3.80	0.867	23.16	21.40	22.06	17.07	21.65	3.82	3.17
1 X 6	5.48	4.22	0.891	22.83	37.63	41.67	36.08	22.38	3.82	3.24
2 X 6	5.16	4.30	0.896	16.74	26.70	22.11	17.57	22.86	3.84	3.25
3 X 6	6.33	5.13	1.212	23.78	21.27	29.22	23.36	21.89	3.89	3.03
1 X 7	5.32	4.10	0.990	20.63	43.53	43.72	34.42	22.89	4.25	3.08
2 X 7	5.20	4.54	0.985	17.09	44.03	43.67	35.16	21.73	5.44	2.96
3 X 7	6.62	4.13	1.410	22.88	25.13	31.27	24.16	26.05	3.94	3.34
Crosses mean	5.67	4.38	1.007	21.35	30.12	32.90	26.42	23.21	4.12	3.16
LSD ($p \leq _{0.05}$)	0.664	0.547	0.181	2.900	6.953	10.068	8.465	1.863	0.445	0.365

LSD ($p \leq _{0.01}$)	0.890	0.734	0.243	3.888	9.324	13.501	11.35	2.498	0.597	0.489

PoL=Pod length, NSPPo=No. of seeds pod^{-1}, SWPPo=Seed weight per pod, 100-SW=100 seed weight NPoPP=No. of pods plant^{-1}, PoYPP=Pod yield plant^{-1}, SYPP=Seed yield plant^{-1}, PrCo%=Protein content (%) OilCo%=Oil content (%), AsCo(%)=Ash content (%),

Concerning the cross values, the cross 2×5 with 37.99 g was found to be the maximum weight for seed yield plant^{-1}, followed by the cross 1×6 with 36.08 g, while the cross 3×5 with 17.07 g recorded the lowest weight for seed yield plant^{-1}. It was found from the table that the means of crosses predominated the parents' mean by 62.42%. Previous researchers illustrated that seed yield plant^{-1} for pea genotypes lies between 9.80–40.63 g [17], 30–43 g [28], and for parents, 3.83–15.42 g and crosses, 4.95–19.50 g [36]. As it was detected from the same table, tester 7 produced the highest percentage value of protein content with 26.39%, followed by testers 4, 5, and line 3 with 26.20, 25.62 and 23.59% respectively. However, line 2, with 18.99%, recorded the lowest percentage value of protein content. These differences between parental values significantly affected their crosses. Regarding the cross values, cross 3×4 exhibited a maximum percentage value of 26.27%, followed by cross 3×7 with 26.05%, and cross 3×5 produced a minimum percentage value of 21.65%.

It was noticed from the same table that the cross mean predominated the parents' mean by 1.51%. Other researchers showed previously that the protein content of pea genotypes ranged between 20.30–24.23% [34], 24.3–26.2% [37], 14.0–22.44% [38], 21.13–27.05% [39], and 20.91–21.66% [40]. Data in the table showed that tester 5 gave the highest percentage value of oil content with 4.85%, followed by lines 1, 3, tester 4, and 7 with 4.82, 4.31, 4.08, and 4.05% respectively. In comparison, tester 6 recorded the lowest percentage value with 3.43%.

The differences between parental values significantly affected on their crosses. Regarding the cross values, cross 2×7 exhibited the maximum percentage value of oil content at 5.44%, while crosses 3×5 and 1×6 recorded the minimum percentage value of oil content at 3.82%. It was found in the same table that the cross mean decreased by 2.14% compared to the parent's mean. Other researchers reported previously that the percentage oil content for pea genotypes was between 15.9–19.3 g kg^{-1} [37] and between 5.0–0.9% [41]. It was found from the same table that tester 6 showed the maximum percentage of **ash content** value of 3.63%. In comparison, tester 7 recorded a minimum percentage value of 2.99%; these differences between parental values significantly affected their crosses. The cross 2×4 with 3.58 % recorded the maximum percentage value, followed by the crosses 3×7 and 2×6 with 3.34% and 3.25% respectively, whereas the cross 1×5 with 2.85% exhibited the minimum percentage value. A previous study by [42] showed that ash content percentage for pea genotypes lies between 24–41 g kg^{-1} DM, in other studies between 3.368–3.704% [43] and 2.12–3.98% [44].

1. The estimation of the heterosis for the F1 crosses:

Table 4 showed significant positive and negative heterosis as a percentage mean deviation of the F1's cross from mid-parental values of all the traits. The differences between parental values and their crosses resulted in heterosis with different values. As it was shown from the table all crosses showed positive heterosis for the trait pod length. The data showed that the cross 3×5 revealed the maximum heterosis value at 19.77%, followed by the crosses 2×5 and 3x7 with 19.62 and 18.10% respectively, while the cross 1×6 recorded the lowest heterosis value at 3.55%. The high positive values for heterosis indicated the over-dominance gene effect for the parent with a higher value. Significant positive and negative heterosis were recorded previously by [45] which showed that heterosis for pod length of pea genotypes varied from 7.4 to -2.5% and [46] recorded significant positive heterosis for pea genotypes. For the trait number of seeds pod^{-1} as shown in the table, it was found that the crosses 3×7, 3×5 and 2×6 produced negative values of heterosis with -6.25%, -5.57%, and -1.52% respectively, these negative values indicated the partial dominance gene effect of the parent with lower value, while the positive heterosis range between 1.409% to 43.02% for the crosses 1×5 and 1×4 respectively. Significant positive and negative heterosis for the number of seed pod^{-1} for pea genotypes were recorded previously by [47] with 42.09% and [48] showed the standard range of heterosis with -51.85–18.52 for the number of seed pod^{-1}. The same table showed the estimation of the heterosis for the trait seed weight pod^{-1}.

The maximum positive heterosis value exhibited by the cross 2×6 with 46.235%, followed by the cross 2×7 and 2×5 with 34.018% and 31.802% respectively, indicating the over-dominance gene effect for the parent with higher value. The maximum negative heterosis value was -15.58% showed by the cross 3×5, followed by the cross 1×5 with -12.89%, indicating the partial dominance gene effect for the parent with a lower value. Significant positive and negative heterosis for seed weight pod^{-1} of pea genotypes were released previously by [25]. The results in the same table indicated the presence of significant heterosis for the trait 100 seed weight. As shown in the table all crosses revealed positive heterosis values except for the cross 1×7 recorded negative heterosis value with -1.268%. As it was found in the same table the maximum positive heterosis value was 32.362% recorded by the cross 3×6, followed by the cross 3×4 with 25.853%. In comparison, the minimum positive heterosis value was 2.787% produced by the cross 2×7. The positive heterosis value indicates the over-dominance gene effect for the parent with a higher value. Significant positive and negative heterosis were recorded previously by different workers on pea genotypes by [49] who found that heterosis for hundred seed weight was mostly positive and large, and found by [45]. For the trait number of pods plant^{-1}, as it was shown in the table all crosses recorded positive heterosis values. The cross 2×7 showed a maximum positive heterosis value of 337.42%, followed by the crosses 2×5 and 1×7 with 327.27 and 274.21% respectively. The cross 3×4 gave the lowest heterosis value with 19.438%. The high positive values for heterosis confirm the over-dominance gene effect for the parent with a higher value. Significant positive and negative heterosis previously reported by other researchers for the number of pods plant^{-1} for pea genotypes, [50] showed positive heterosis for the number of pods plant^{-1} with 119.22%, [51] exhibited the highest significant positive heterosis with 125.78 for this trait and [48] recorded standard heterosis with -63.54 to 27.08 for number of pods plant^{-1}. The results in the same table for the trait pod yield plant^{1} found that all crosses showed positive heterosis value, and the results showed that the maximum positive heterosis value was 503.48% recorded by the cross 2×7 followed by the crosses 2×5 and 1×7 with 473.83 and 330.36% respectively. While the minimum positive heterosis value produced by the cross 3×5 with 39.464%, confirms the over-dominance gene effect for the parent with a higher value. Significant heterosis values for pod yield plant^{-1} for pea genotypes were recorded previously by [52]

Table 5. Heterosis values of all the traits as a percentage mean deviation of the F$_1$'s cross from mid-parental values

Geno-types	PoL (cm)	NS PPo	SW PPo (g)	100-SW (g)	NPoPP	PoYPP (g)	SYPP (g)	PrCo (%)	OilCo (%)	AsCo (%)
1 X 4	15.14	43.02	- 8.54	10.769	37.939	57.365	53.489	- 2.568	- 3.486	- 4.108
2 X 4	10.33	26.84	2.486	2.839	102.45	123.03	121.14	13.496	5.396	11.029
3 X 4	9.36	3.560	2.421	25.853	19.438	44.886	52.285	5.512	- 6.815	0.330
1 X 5	6.91	1.409	- 12.89	12.558	113.40	134.67	134.71	3.836	- 14.54	- 14.67
2 X 5	19.62	10.29	31.802	19.361	327.27	473.83	469.03	- 2.237	- 11.46	- 5.658
3 X 5	19.77	- 5.57	- 15.58	18.207	78.830	39.464	41.351	- 12.01	- 16.56	- 2.069
1 X 6	3.55	6.01	11.584	22.691	209.32	282.54	331.53	14.191	- 7.256	- 8.257
2 X 6	5.39	- 1.52	46.235	16.841	151.89	177.37	183.07	17.118	4.453	- 6.662
3 X 6	7.31	7.79	17.231	32.362	89.881	86.547	101.30	0.351	0.534	- 11.82
1 X 7	6.57	13.07	7.476	- 1.268	274.21	330.36	339.40	0.522	- 4.235	- 4.134
2 X 7	13.31	13.05	34.018	2.787	337.42	503.48	519.14	- 4.235	36.457	- 6.353
3 X 7	18.10	- 6.25	22.021	12.923	135.63	109.45	118.07	4.231	- 5.796	7.331
S. E.	1.66	4.047	5.626	2.886	31.029	47.091	48.170	2.450	4.001	2.104

Table 5 also showed significant heterosis values for the trait seed yield plant^{-1}. It was noticed that all crosses revealed positive heterosis. The results show cross 2×7 gave a maximum heterosis value of 519.14%, followed by cross 2×5 of 469.03%, while cross 3×5 recorded the lowest heterosis value of 41.351%.

The high positive values for heterosis indicated the over-dominance gene effect for the parent with a higher value. Significant heterosis values of seed yield plant^{-1} for pea genotypes were found previously by [47], which found that the highest real heterosis for seed yield plant^{-1} was 432.43%, [48] recorded standard heterosis with -72.61–39.24, and [53] with 104.79%. Data for protein content percentage in Table 5, indicated that most crosses showed positive heterosis values, with the highest positive heterosis value recorded by the cross 2×6 with 17.118, while the cross 3×6 recorded the lowest positive heterosis value with 0.351%, the high positive values for heterosis confirm the over dominance gene effect for the parent with higher value. Four crosses 2×5, 1×4, 2×7, and 3×5 produced negative heterosis values with -2.237, -2.568, -4.235, and -12.01% respectively, the heterosis with the negative values indicating the partial dominance gene effect for the parent with a lower value. High heterotic effects were observed previously by [54] for protein content with the range of heterosis from –5.77 to 11.23%, and different positive and negative heterosis of protein content for pea genotypes were reported previously by [15] and [55].

The same table showed significant positive and negative heterosis for oil content percentage. It was found in the table that the highest positive heterosis produced by the cross 2×7 with 36.457%, while the minimum positive heterosis produced by the cross 3×6 with 0.534%, indicating the over-dominance gene effect for the parent with the higher value, whereas the negative heterosis value range between -16.56% to -3.486% for the crosses 3×5 and 1×4 respectively, these negative values indicated the partial dominance gene effect for the parent with a lower value.

The same table also confirmed significant positive and negative heterosis in the ash content percentage. It appeared from the table that most crosses showed negative heterosis values, the cross 1×5 produced the maximum negative heterosis value of -14.67%, followed by the cross 3×6 with -11.82%, and the cross 3×5 gave the lowest negative heterosis value with -2.069%, negative heterosis values indicated the partial dominance gene effect for the parent with a lower value. But the crosses 2×4, 3×7, and 3×4 showed positive heterosis values with 11.029, 7.331, and 0.330% respectively. The high positive values for heterosis confirm the over-dominance gene effect for the parent with a higher value. The previous researcher revealed that the range of negative heterosis for the percentage ash content of peas was between -2.058 to -14.705% [56].

A quick check of Table 5, indicates that the degrees of heterosis among the different hybrids vary significantly. Only four traits exhibit positive heterosis: pod length, number of pods per plant, pod yield per plant, and seed yield per plant.

According to the findings in the same table, hybrid 2 X 7 had the highest positive heterosis values for the traits number of pods per plant, pod yield per plant, seed yield per plant, and oil content percentage, with 337.42, 503.48, 519.14, and 36.457% respectively, while the same hybrid has the lowest positive heterosis only for the trait 100 seeds weight with 2.787%. Hybrid 3 X 5 had the highest positive heterosis value only for the trait pod length with 19.77%, and the same hybrid had the highest negative heterosis values for three traits, seed weight per pod, percentage protein content, and percentage oil content with -15.58, -12.01, and -16.56% respectively.

The same hybrid 3 X 5 has the lowest positive heterosis values for two traits, pod yield per plant and seed yield per plant with 39.464 and 41.351%.

2. The estimation of the effects of general and specific combining ability:

Table 6 confirms the estimation of the effects of general and specific combining ability for all studied traits. The result of the *GCA* value of pod length trait in the table described that line 3 and both testers 4 and 7 showed positive *GCA* effect values with 0.724, 0.248, and 0.047 respectively, while line 2 recorded the maximum negative value of *GCA* with -0.491. Tester 6 showed the minimum negative value of *GCA* with -0.011, indicating the reduction of pod length in their crosses. Concerning the *SCA* effect values for the crosses, the cross 3×4 showed the maximum negative *SCA* effect value of -0.251, while the cross 2×6 showed a minimum negative *SCA* effect value of -0.010. The cross 1×4 showed a maximum positive *SCA* effect value of 0.343, while the cross 1×6 showed a minimum positive *SCA* effect value of 0.057.

Similar results were reported previously by [51] for *GCA* and *SCA* effects for the pod length of pea. It was clarified from the *GCA* effect values of the number of seeds pod^{-1} for parents, that tester 4 gave the maximum positive *GCA* effect value of 0.629. At the same time, line 3 showed the lowest value of positive *GCA* of 0.039, tester 5 gave the highest negative *GCA* effect value of -0.68, while tester 7 recorded the lowest value of negative *GCA* of -0.12. Concerning the *SCA* effect values for the crosses, the maximum positive *SCA* effect was 0.540 recorded by cross 3×6, followed by the cross 1×4 of 0.410. In contrast, cross 3×4 recorded a maximum negative *SCA* effect value of -0.44, followed by cross 2×6 of -0.37. Similar results were reported previously by [51], [52], and [57].

The same table showed the estimation of the effects of general and specific combining ability of the trait seed weight pod^{-1}. It was found in the table that tester 5 obtained a maximum negative GCA effect value of -0.221, followed by lines 1 and 2 of -0.110 and -0.100, respectively. Line 3 produced a maximum positive *GCA* effect value of 0.210, followed by the testers 7 and 4 of 0.122 and 0.107 respectively. Concerning the *SCA* effect values for the crosses, it was found that the cross 2×5 showed a maximum *SCA* positive effect value of 0.113, while the cross 3×5 showed a maximum negative *SCA* effect value of -0.128. Significant *GCA* and *SCA* effects for seed weight pod^{-1} of peas were recorded previously by [25]. The data in Table 6 also explains the estimation of the effects of general and specific combining abilities for the trait 100 seed weight.

As it was noticed from the values of *GCA* effect due to parental value, it was shown that line 3 produced a maximum positive value of *GCA* with 2.623, while tester 5 recorded the minimum positive *GCA* with 0.303. Line 2 exhibited the maximum negative *GCA* values of -3.74, while tester 6 showed the minimum negative *GCA* of -0.23, indicating the reduction in 100 seed weight in their crosses. Concerning the *SCA* effect values for the crosses, cross 2×5 showed a maximum positive *SCA* effect value of 1.128, while cross 3×6 produced a minimum positive *SCA* effect value of 0.043. It was noticed from the same table that cross 2×4 showed the maximum negative *SCA* value of -1.12, followed by cross 3×5 of -1.121, while cross 1×5 recorded a minimum negative *SCA* effect value of -0.007.

For the trait number of pods plant^{-1}, it was found from the *GCA* effect values for the parents, that line 3 showed a maximum negative *GCA* effect value of -8.92 followed by tester 4 with -8.27, while tester 6 produced a minimum negative *GCA* effect value with -1.59. Whereas tester 7 exhibited the maximum positive *GCA* effect value was 7.447, followed by line 2 with 6.606, and line 1 recorded a minimum positive *GCA* effect value of 2.314. Concerning the *SCA* effect values for the crosses, the maximum negative *SCA* value was -8.44 exhibited by the cross 2×6, while the minimum negative value of *SCA* was -0.14 showed by the cross 2×7. The cross 2×5 showed a maximum positive effect value of 9.439, followed by the crosses 1×6 and 3×4, with 6.786 and 4.064 respectively. Similar results were reported previously by other researchers, [46] obtained significant positive *GCA* effects for pods plant^{-1}, [58] observed significant combining ability variances of the *F1's* for the number of pods plant^{-1}. The data in Table 6 showed the estimation of the general and specific combining ability effects for the trait pod yield plant^{-1}.

As it was indicated from the *GCA* effect values for parents, the tester parent 7 exhibited the maximum positive value of *GCA* effects with 6.659, while line 1 recorded the minimum positive value of *GCA* effect with 1.531, whereas the maximum negative *GCA* value was -4.46 recorded by the line 3, and the minimum negative *GCA* effect value was -1.37 showed by the tester 5. Concerning the *SCA* effect values for the crosses, it was found that the cross 2×5 showed maximum positive *SCA* effect value with 12.15, while the cross 2×7 showed minimum positive *SCA* effect value with 1.193.

The data in the same table revealed that the cross 2×6 showed a maximum negative *SCA* effect value of -11.8, while the cross 2×4 recorded a minimum negative *SCA* effect value of -1.53. A different result was reported previously by [59].

Table 6. Estimation of the effects of general combining ability & specific combining ability for all the traits

Genotypes	PoL (cm)	NS PPo	SW PPo(g)	100 SW(g)	NPo PP	PoY PP(g	SY PP(g)	PrCo (%)	OilCo (%)	AsCo (%)
GCA for Lines & GCA for Testers										
Line 1	-0.232	-0.16	-0.110	1.119	2.314	1.531	1.507	-0.56	0.004	-0.084
Line 2	-0.491	0.124	-0.100	-3.74	6.606	2.923	2.449	-0.20	0.226	0.062
Line 3	0.724	0.039	0.210	2.623	-8.92	-4.46	-3.956	0.753	-0.23	0.022
S. E. Line	0.116	0.095	0.032	0.506	1.212	1.755	1.476	0.325	0.078	0.064
Tester - 4	0.248	0.629	0.107	1.082	-8.27	-3.39	-2.912	1.459	0.022	0.146
Tester - 5	-0.248	-0.68	-0.221	0.303	2.403	-1.37	-1.159	-0.98	-0.18	-0.122
Tester - 6	-0.011	0.170	-0.007	-0.23	-1.59	-1.90	-0.751	-0.83	-0.27	0.011
Tester - 7	0.047	-0.12	0.122	-1.15	7.447	6.659	4.822	0.348	0.422	-0.035
S. E. Tester	0.134	0.110	0.036	0.548	1.400	2.027	1.704	0.375	0.090	0.073
SCA for Crosses										
1 X 4	0.343	0.410	0.012	0.104	-3.20	-4.64	-4.524	-2.02	0.149	-0.079
2 X 4	-0.092	0.024	-0.066	-1.12	-0.86	-1.53	-1.196	1.175	-0.15	0.216
3 X 4	-0.251	-0.44	0.054	1.021	4.064	6.168	5.720	0.843	-0.001	-0.137
1 X 5	-0.242	-0.25	0.015	-0.007	-7.24	-7.14	-6.043	1.568	0.181	-0109
2 X 5	0.121	0.186	0.113	1.128	9.439	12.15	10.281	-0.23	-0.29	-0.002
3 X 5	0.121	0.061	-0.128	-1.121	-2.20	-5.02	-4.238	-1.34	0.106	0.110
1 X 6	0.057	-0.17	0.002	0.589	6.786	9.140	8.902	0.559	-0.03	0.151
2 X 6	-0.010	-0.37	-0.004	-0.632	-8.44	-11.8	-10.550	0.680	-0.24	0.015
3 X 6	-0.048	0.540	0.002	0.043	1.653	2.676	1.648	-1.24	0.269	-0.166
1 X 7	-0.159	0.006	-0.029	-0.686	3.653	2.636	1.665	-0.11	-0.30	0.036
2 X 7	-0.019	0.160	-0.043	0629	-0.14	1.193	1.465	-1.63	0.673	-0.229
3 X 7	0.178	-0.17	0.072	0.057	-3.51	-3.83	-3.131	1.736	-0.37	0.193
S. E. crosses	0.231	0.191	0.063	1.011	2.424	3.510	2.951	0.650	0.155	0.127

The data in the table showed that the maximum negative *GCA* value for the trait seed yield plant^{-1} was recorded by line parent 3 with -3.956, followed by tester parents 4 and 5 with -2.912 and -1.159, respectively, indicating the reduction in seed yield plant^{-1} in their crosses. Tester parent 7 produced a maximum positive *GCA* value of 4.822, followed by line parent 2 with 2.449, confirming the high contribution of these parents in increasing seed yield plant^{-1} in their crosses. Concerning the *SCA* effect values for crosses, it was found that the cross 2×6 with -10.550 gave a maximum negative *SCA* effect value, and the cross 2×5 with 10.281 gave a maximum positive *SCA* value, followed by the cross 1×6 with 8.902. Similar results on seed weight plant^{-1} for pea genotypes were reported previously by [52].

Table 6 also shows the estimation of the effects of general and specific combining abilities for the trait protein content percentage, as it was noticed in the same table, tester 5 exhibited a maximum positive *GCA* effect value of 1.459. In contrast, the tester 7 showed a minimum positive GCA effect value of 0.348, and the tester 5 showed a maximum negative GCA effect value of -0.98. In contrast, line 2 recorded a minimum value of negative *GCA* of -0.20, indicating the reduction in trait protein content in their crosses. Concerning the *SCA* effect values for the crosses, half of the crosses showed positive *SCA* affect values, and the cross 3×7 showed a maximum positive *SCA* effect value of 1.736, followed by the crosses 1×5 and 2×4 of 1.568 and 1.175 respectively. The cross 1×6 showed a minimum positive *SCA* effect value of 0.559, and the cross 1×4 showed a maximum negative *SCA* effect value of -2.02, while the cross 1×7 showed a minimum negative *SCA* effect value of -0.11. Different results on the protein content percentage of pea genotypes were reported previously by [15] and [56].

The results in Table 6 also show the estimation of the effects of general and specific combining abilities for the trait oil content percentage. The data in the table revealed that tester 7 produced the maximum positive *GCA* effect value of 0.422, while line 1 produced the minimum positive *GCA* effect value of 0.004, confirming the high contribution of these parents in increasing oil content in their crosses. Maximum negative *GCA* effects value recorded by tester 6 with -0.27, followed by line 3 with -0.23.

The results in the same table showed that the minimum negative *GCA* effect value was -0.18 recorded by tester 5, indicating the reduction of oil content in their crosses. Concerning the *SCA* effect values for crosses, cross 3×7 with -0.37 gave the maximum negative *SCA* effect value, while the minimum negative *SCA* effect value produced by the cross 3×4 with -0.001 and the cross 2×7 with 0.673 gave maximum positive *SCA* value, and the minimum positive *SCA* effect value produced by the cross 3×5 with 0.106. The results in Table 6 also showed the estimation of the effects of general and specific combining ability for ash content percentage. As it was shown from the parental *GCA* effects, tester 4 recorded maximum positive *GCA* effects with 0.146, while tester 6 showed the minimum positive *GCA* effects with 0.011.

But line 1, testers 5, and 7 showed negative *GCA* effect values with -0.084, -0.122, and -0.035 respectively, negative *GCA* effect values indicating the reduction of ash content percentage in their crosses. Concerning the *SCA* effect values for the crosses, half of the crosses showed positive *SCA* effect values, it was shown from the same table that the cross 2×4 produced a maximum positive *SCA* effect value of 0.216, and the cross 2×6 recorded a minimum positive *SCA* effect value with 0.015. The cross 2×7 showed a maximum negative *SCA* effect value of -0.229, while the cross 2×5 showed a minimum negative *SCA* effect value of -0.002.

Conclusions

From the results of statistical and genetic analysis, the following conclusions can be drawn:

- The parent line NS minima as a good combiner recorded the minimum values in traits pod length, seed weight pod^{-1}, 100 seeds weight, pod yield plant^{-1}, seeds yield plant^{-1}, and percentage of protein content. This line also shows the best possibility of utilization in
- breeding programs to develop good varieties of a pea.
- The parent Oregon sugar pod as a line gave superiority and recorded good combiner in traits pod length and pod yield plant^{-1}.
- The parent Giant sugar pod as a tester recorded superiority and revealed good combiner in four different traits seed yield plant^{-1}, seed weight pod^{-1}, number of pods plant^{-1}, and 100 seeds weight. The parent Lancet as a tester possessed good combiner and superiority in the number of seeds pod^{-1}, and ash content percentage. In contrast, Provence as a tester possessed good combiner and superior protein content percentage. These three testers show the best possible utilization in breeding programs to develop varieties of peas with high yielding and good quality.
- Significant heterosis values as a percentage mean deviation from mid-parental values were detected for all traits due to the effects of the over-dominant genes and the partial dominance genes.
- Hybrid *NS minima* × *Provence* had the highest positive heterosis values for four traits the number of pods plant^{-1}, pod yield plant^{-1}, seed yield plant^{-1}, and oil content percentage.
- Hybrid *Oregon sugar pod* × *Green sage* had the highest positive heterosis value only for the trait pod length.

Recommendations

According to the present study, the following recommendations can be made:

- During this study, most growth traits showed a non-additive genetic variance which can be exploited by adopting the heterosis breeding program.
- We recommend further testing of those hybrids in different environments to determine and ensure their genetic stability.
- As the non-additive gene effect has played an important role in the inheritance of most of the traits, hybridization followed by selection method among segregates and recombined may be recommended utilizing both additive and non-additive gene effects using (line × tester) mating design

Appendices

Appendix 1. Physical & Chemical properties of soil in the Girdjan

Soil Properties of Girdjan location	
Textural class	Silty Clay
Sand (gm.Kg^{-1})	66.5
Silt (gm.Kg^{-1})	429.6
Clay (gm.Kg^{-1})	503.9
E.C (dS.m^{-1})	0.19
Ph	7.413
O.M. (%)	0.3
Total N (%)	0.155
Available Phospha (mg.Kg^{-1})	12.794
$CaCO_3$ (%)	0
Ca^{++} (meq / L)	1.67
K^{+} (mmL)	369.131
Na^{+} (Exch)	254.757
CO_3^{-2} (%)	1.491
HCO_3^{-2} (meq / L)	26.4
Cl^{-} (meq / L)	2.12

Appendix 2. The meteorological data of the Raniah region (*Girdjan*) during the present study

Months	*Girdjan (2015-2016)*

	Air temperature °C			*Precipitation (Rainfall)*
	avg.	*Max.*	*min.*	*Depth (mm)*
November	14.0	22.0	6.0	83.3
December	7.0	13.0	1.0	202.1
January	3.25	10.5	- 4.0	156.6
February	4.3	11.6	- 3.0	69.7
March	9.9	19.8	0.0	225.8
April	17.3	27.0	7.6	89.7
May	22.65	33.0	12.3	-
June	28.5	41.6	15.4	-

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دراسة قدرة الأئتلاف وقوة الهجين للمحصول ومكوناته لسبعة تراكيب وراثية في البازلاء (*Pisum sativum* L.) ونسلها باستخدام تحليل (السلالة × الفاحص)

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لخلاصة

أجري هذا البحث على هجن الجيل الأول وأبائها لسبعة تراكيب وراثية من البازلاء (*Pisum sativum* L.) لدراسة قدرة الائتلاف وقوة الهجين للمحصول ومكوناته عبر تحليل (السلالة × الفاحص) خلال موسمين زراعيين. تم تضريب ثلاثة أصناف من البازلاء (Javor, NS minima, Oregon sugar pod) كسلالة وأربعة أصناف (Giant sugar pod, Green sage, Lancet, and Provence) أخرى كفاحص لإنتاج 12 هجيناً من F1 خلال موسم النمو الأول بمحطة أبحاث قلياسان. تم إجراء عملية الخصي والتضريب يدويًا وتم الحصول على كمية كافية من بذور الهجن المختلفة. خلال موسم النمو 2015−2016 تم تنفيذ تجربة حقلية من بذور F1 مع آبائهما باستخدام تصميم RCBD وبثلاث مكررات في محطة أبحاث كردجان لتحديد التوليفات الأبوية من خلال دراسة قابلية الائتلاف العامة والخاصة وتبايناتها لدراسة تهجينات البازلاء. أظهرت النتائج أن الاب 3 سجل أعلى قيمة لطول القرنة وحاصل القرنة لكل النبات، بينما أنتج الاب الفاحص 4 أقصى قيمة لوزن البذور لكل القرنة، وزن 100 بذرة، عدد القرون لكل النبات، وحاصل البذور لكل النبات. أشارت النتائج إلى أن هجين 2×5 أنتج أعلى القيم لعدد القرون لكل النبات، حاصل القرون لكل النبات، وحاصل البذور لكل النبات. تم توضيح أن الاب 3 أظهر الحد الأقصى لقيمة تأثير GCA السلبية البالغة 8.92−، بينما أظهر الا ب الفاحص 7 الحد الأقصى لقيمة تأثير GCA الإيجابية البالغة 7.447.

. <u>الكلمات المفتاحية</u> : البازلاء; تحليل السلالة × الفاحص; القدرة على الجمع العام; القدرة على الجمع الخاص; التغاير .