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Heterosis, combining ability, and genetic parameters in pea.

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ABSTRACT

This research was carried out to study the inheritance of some traits of pea through using a (line × tester) mating design, three inbred lines of peas used as (Lines), and four other inbred lines used as (Testers). These inbred lines were crossed to produce 12 F1 crosses. During the autumn of 2014, the parental inbred lines were grown, emasculation and crossing were done by hand, and sufficient seeds for crosses were produced. During the growing season of 2015-2016, the F1 seeds of twelve crosses with their parents were implemented in the field experiment using CRBD with three replicates in Girdjan Research Station, to estimate heterosis, general and specific combining abilities effects for parents and hybrids respectively, and genetic parameters for traits: plant height (cm), the number of branches plant^{-1}, the number of days to 50% flowering, the number of days to harvest, number of seeds pod^{-1}, number of pods plant^{-1}, and seed yield plant-1 (g). The analysis showed that the mean square due to genotypes was highly significant for all traits. The tester parent, Giant sugar pod surpassed other parents for plant height, and number of branches plant^{-1}. The hybrid NS minima × Provence gave the maximum negative heterosis value for the number of days to harvest. The same hybrid NS minima × Provence had the highest positive heterosis values for two traits, the number of pods per plant^{-1}, and seed yield per plant^{-1}.

***Keywords*:** Line × Tester analysis; GCA and SCA; heterosis; degree of dominance; Heritability.

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INTRODUCTION

Southwest Asia is the birthplace of the pea, or *Pisum sativum* L., an annual grain legume belonging to the Fabaceae family. It is among the top four most important legumes grown, ranking alongside beans, groundnuts, and soybeans [1]. Peas were among the first crops to be domesticated worldwide; their seeds served as protein-rich food for humans and livestock [2]. Legumes comprise around one-third of the protein humans consume and are an important source of culinary and industrial oils and animal feed. Legumes are an essential nitrogen source in natural and agricultural environments because of their symbiotic nitrogen fixation ability, one of their most important characteristics [3]. As a legume plant, peas are good for crop rotation because they break the cycles of pests and diseases, increase soil aggregation and microbial diversity, and preserve soil moisture. Legumes are important crops that provide over one-third of the protein humans consume. They also significantly influence the supply of animal feed, fodder, and industrial and consumable oils [4]. For those reasons, grain legumes are considered the cheapest and richest source of plant proteins known as pulses [5]. The pea, a grain legume that is annual and belongs to the Fabaceae family, originates in Southwest Asia. There are still wild field peas in Ethiopia, Afghanistan, and Iran. Together with beans, groundnuts, and soybeans, it is one of the four most important farmed legumes [4]. Additionally, through their anticancer and other health-promoting properties, legumes contain natural compounds or secondary metabolites like isoflavonoids that are thought advantageous to human health [6]. It is a certain fact now that nutrients used as protein sources are very important for human nutrition [7]. Peas have several uses in horticulture and agriculture. Dhal is made from the mature, dried seeds, while the green seeds are utilized to make fresh, frozen, or canned vegetables. For human consumption, it is a crop with a high protein content (27%) [8]. Cool-season crops such as green peas, garden peas, and field peas (*Pisum sativum* L.) are farmed for their edible seeds or pods. Green beans, often known as garden peas, are collected before the seed is ripe enough for the fresh pack market [9]. Grown for its fresh-shelled green seeds, which are high in protein (7.2%), vitamins, and minerals, the garden pea (*Pisum sativum* L. var. *Hortense*) is a desirable vegetable [10]. Field peas, as their protein level reaches up to 40 per cent on a dry weight basis, play an important role in improving protein in the diet [11]. It was noted that peas are the second-highest-yielding legume in the world, after common beans, and are one of the six main pulse crops grown worldwide [12]. Pea is considered an important forage and vegetable crop; its output and productivity have become static or constant over the years, even though its total harvested area has increased extremely [13]. An organized method for identifying suitable parents and crosses is offered by line x tester analysis. Self- and cross-pollinated plants were improved by its application [14]. One mating strategy that effectively assesses the capacity of genotypes to combine is the line × tester analysis. A wide genetic basis tester involves diverse cultivars or hybrids and only offers information on GCA in previous generations. In contrast, the ideal tester maximizes information on a line's performance in cross combinations [15]. Mating designs, which assist breeders in identifying possible parents and promising recombinants/ hybrids, are one of the biometric breeding techniques. Although line × tester analysis is still a better mating design than diallel, it has been widely utilized for these objectives, due to its utilization of more distinct sets of parents as males and females with comparatively fewer crosses [16]. The GCA is the average performance of line strains in a series of cross combinations. However, compared to what would be predicted based on the average performance of the parental lines used in crop combinations, the SCA in those cases performs comparatively better or worse in specific cross combinations [17]. This study aims to use the genetic potential for growth qualities in peas. The mating design has been employed in genetic research to select superior parents for producing hybrid cultivars and to ascertain the inheritance of significant features among various genotypes. The aims of the study were:

1- To estimate GCA and SCA values for some traits among (3) inbred lines used as Line parents and (4) inbred lines used as Tester parents in pea.

2- To obtain information regarding the GCA effects of the parents and SCA effects of the hybrids, and estimating heterosis, the average degree of dominance, heritability and other genetic parameters for some important traits in pea genotypes.

3- Evaluating crosses' trait performance about the genotypes of their parents.

Materials and Methods

Seven pea cultivars were selected based on preliminary field observations of their performance, broad genetic background, and variations in some field characters with superior cultivation. Seven different pea cultivars were used to produce *F1* hybrids, as shown in Table 1.

Table 1: Name, sources, and pedigree 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 experiment was laid out at Qliasan Research Station, College of Agricultural Engineering Sciences, University of Sulaimani, during 2014-2015. As indicated in Table 2, 12 *F1* crosses were produced by crossing three varieties of pea as (Line parents) and four varieties of pea as (Tester parents) in accordance with the (line × tester) mating pattern created by [14]. In order to overcome the variations in blooming times between parents and complete the hybridization process within an appropriate period, the parental genotypes have been grown on three planting dates separated by five days. The necessary safety measures have been implemented to prevent genetic material contamination during crossing. Flowers have been emasculated, and manual pollination has yielded enough hybrid seeds for every cross. Hybrid seeds of *F1* were obtained from all crosses collected, separated, and stored for the next season

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

Tester	*Giant sugar pod*	*Green sage*	*Lancet*	*Provence*
Line	*A*	*B*	*C*	*D*
		Crosses		
Javor (1)	*1×A*	*1×B*	*1×C*	*1×D*
NS minima (2)	*2×A*	*2×B*	*2×C*	*2×D*
Oregon sugar pod (3)	*3×A*	*3×B*	*3×C*	*3×D*

During the second growing season (2015-2016) the experiment was laid out at the Girdjan Research Station, (Lat. 36° 12' 11''; N, Long. 44° 47' 03''; E, 543 MASL) 115 km North West of Sulaimani city. The physical and chemical characteristics of the soil at the Girdjan location are shown in Appendix 1. In 25-26/11/2015, The *F1* seeds of twelve crosses (3×4) along with their parents were implemented in a field experiment using randomized complete block design CRBD with three replications. Each replication consists of seven varieties and twelve *F1* crosses. Each plot consists of two rows, 3 meters long, 50 cm between rows, 20 cm between plants within the row, 1 meter between plots within the replicate, and 2.5 meters between replicates. The experimental units were randomly assigned genotypes. Recommended cultural practices were done from sowing to maturity to produce a quality crop (Appendix 2). Five plants from each plot were tagged at random for recording studied traits. The Least Significant Difference Test was used to compare the genotypes.

Studied traits: The studied traits included plant height (cm), number of branches plant^{-1}, number of days to 50% flowering, number of days to harvest, number of seeds pod^{-1}, number of pods plant^{-1}, and seed yield plant^{-1} (g).

Statistical analyses were performed for each trait; ANOVA, or analysis of variance, was used to assess all recorded data. To assess the means, individual analysis and LSD were computed at a 5% and 1% significant level [18].

General and Specific Combining Abilities:

The following formula was used to determine the effect of the general combining ability of line parents and tester parents:

1. Estimation of *GCA* Effects:

a- For Lines:

$\hat{g}_{ii} = \frac{Y_{i..}}{tr} - \frac{Y_{...}}{ltr}$ $\hat{g}_{ii}$: Effect of general combining ability for 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 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: $\sum \hat{S}_{ij} = zero$

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 general combining ability (*GCA*):

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

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

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

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

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

2. Heterosis estimation:

The deviation of *F1* from mid-parental value, or superior to the average of two parents, is known as heterosis.

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

Where: $F_1 =$ Mean of hybrid

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

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

3. Heritability:

According to [19], the variances of general and specific combining abilities, as well as the variance of experimental error, will be used to evaluate heritability in both the broad and narrow sense. When the narrow sense heritability is greater than 50%, it is deemed high; when it falls between 20% and 50%, it is deemed moderate; and when it falls below 20%, it is deemed low.

In the broad and narrow sense, heritability was estimated as follows:

$$h^2{}_{b.s} = \frac{\sigma_G^2}{\sigma_P^2} = \frac{\sigma_A^2 + \sigma_D^2}{\sigma_A^2 + \sigma_D^2 + \sigma_e^2} = \frac{2\sigma_{gsa}^2 + \sigma_{sca}^2}{2\sigma_{gca}^2 + \sigma_{sca}^2 + \sigma_e^2}$$

$$h^2{}_{n.s} = \frac{\sigma_A^2}{\sigma_P^2} = \frac{\sigma_A^2}{\sigma_A^2 + \sigma_D^2 + \sigma_e^2} = \frac{2\sigma_{gsa}^2}{2\sigma_{gca}^2 + \sigma_{sca}^2 + \sigma_e^2}$$

Where:

$h^2{}_{b.s}$: Broad sense heritability $\quad\quad$ $h^2{}_{n.s}$: Narrow sense heritability

$\sigma_{gsa}^2 =$ Variance of general combining ability, $\quad$ $\sigma_{sca}^2 =$ Variance of specific combining ability

$\sigma_e^2 =$ Variance of experimental error, $\quad$ $\sigma_A^2 =$ Additive genetic variance

$\sigma_D^2 =$ Non-additive (Dominance variance), $\quad$ $\sigma_G^2 =$ Total genetic variance.

$\sigma_P^2 =$ Phenotypic variance (genetic and environmental variance)

4. The average degree of dominance ($\bar{a}$):

The degree of dominance was estimated as: $\bar{a} = \sqrt{\frac{2\sigma_D^2}{\sigma_A^2}} = \sqrt{\frac{2\sigma_{sca}^2}{2\sigma_{gsa}^2}} = \sqrt{\frac{\sigma_{sca}^2}{\sigma_{gsa}^2}}$

Results and Discussion

The data in Table 3 shows analysis of variance results for studied traits according to (line X tester) analysis. It is indicated that mean square of genotypes, and crosses was highly significant for all the traits except the number of branches plant^{-1} for crosses which was significant, for the parents three traits were highly significant, plant height, the number of days to 50% flowering, the number of seeds pod^{-1}**,** and only significant for Seed yield plant^{-1}. In comparison, the other three traits were not significant. In the same table, the mean square values for Lines, Testers, and (Line X Tester) was significant or highly significant for all the studied traits, except for Lines' number of seeds pod^{-1}**,** and Tester's plant height; for (Line X Tester), the mean square was not significant for plant height, and the number of branches plant^{-1}.

Table 3. Mean square studied traits of pea from (line X tester) analysis

S. O.V.	Repl.	Geno-types	Parents	Crosses	Parent vs Crosses	Lines	Testers	L X T	Mse
d.f. Traits	2	18	6	11	1	2	3	6	36
PH	165.7	1237.1**	840.9**	1252.4**	3446.3**	5811.5**	322.9 ^{ns}	197.5 ^{ns}	126.9
NBPP	0.28	3.76**	0.71^{ns}	1.69*	44.81**	4.17**	2.08*	0.67 ^{ns}	0.64
ND50F	8.26	58.52**	47.49**	45.35**	269.53**	56.69**	35.78**	46.36**	4.10
NDH	42.86	38.38**	11.71^{ns}	55.05**	15.00 ^{ns}	125.78**	26.15*	45.93**	6.19
NSPPo	0.11	1.12**	1.19**	1.05**	1.55**	0.26 ^{ns}	2.70**	0.48**	0.11
NPoPP	82.17	453.74**	20.55 ^{ns}	335.41**	4354.5**	771.26**	396.1**	159.8**	17.63
SYPP	62.61	326.40**	68.33*	168.92**	3607.1**	143.50**	100.92*	211.4**	26.13

PH=Plant height (cm), NBPP=Number of branches plant^{-1}, ND50F=Number of days to 50% flowering, NDH=Number of days to harvest, NSPPo=Number of seeds pod^{-1}, NPoPP=Number of pods plant^{-1},
SYPP = Seed yield plant^{-1}(g).

1. **Means of studied traits:**

Table 4, shows the mean performance of parents and their hybrids for studied traits of pea genotypes. The results indicated that tester parent A gave the highest value of plant height at 84.44 cm, followed by line parent 2, and line parent 3 at 77.97, and 62.26 cm respectively. In comparison, the lowest value of plant height was 40.34 cm exhibited by the tester parent D. These differences in plant height between parents affected significantly their crosses' plant height. Regarding the cross values, the maximum plant height was 103.19 cm exhibited by the cross 2×C, while the cross 1×D with 48.63 cm obtained the minimum value of plant height. The results showed that the cross's mean exceeded the parents' mean by 21.42%. Previous researchers showed that plant height for pea genotypes was restricted between 29.7–65.0 cm for parents and 56.7–85.7 cm for crosses [20], 51.60–85.40 for parents but 54.13–98.90 for crosses [21] and 31.83–94.67 [22]. The mean values of the trait number of branches plant^{-1} for parents and their crosses presented in Table 4, indicated that the tester parent A recorded the maximum number of branches plant^{-1} with 3.23, followed by line parent 1, and line parent 3 at 2.83, and 2.57 branches plant^{-1} respectively. In contrast, line parent 2 recorded the minimum number of branches plant^{-1} with 1.77. These differences between parental values in the number of branches plant^{-1} affected significantly their cross branches. Regarding the same table, cross 1×C with 5.63 showed a maximum number of branches plant^{-1}, followed by cross 1×D with 4.87 branches, while cross 2×A with 2.60 recorded the minimum number of branches plant^{-1}. It was evident from the same table that the means of crosses predominated the parent's mean by 42.79%. Previous researchers showed that the number of branches plant^{-1} for pea genotypes was noticed between 2.5-4.1 [23], 2-8 [24] and 2.13-5.2 [25]. The data in Table 4 for the trait number of days to 50% flowering showed that, within the parents, tester parent A was the earliest in reaching 50% flowering with 106.33 days followed by tester parent B with 107.33 days, while line parent 3 was the latest in reaching 50% flowering with 116.00 days among all parents. These differences in the number of days to 50% flowering between parental values affected significantly their crosses. Regarding the cross values, cross 2×A required the maximum number of days to reach 50% flowering at 120.00 days, followed by cross 1×B with 119.00 days, while cross 3×A required the minimum number of days to reach 50% flowering at 106.33 days. It was shown in the same table that the crosses mean delayed parent's mean by 3.90%. Previous studies showed that the number of days to reach 50% flowering for pea genotypes lies between 63.5–101.5 [26], 41.33–53.9 [27], and First year 104.05, Second year 97.74 [28]. Data recorded on the number of days to harvest in Table 4 showed that the maximum days to harvest among parents was 178.67 days exhibited by line parent 2, followed by tester parent D, which required 177.67 days to reach harvest, while tester A recorded the shortest period to reach harvest with 173.33 days. These differences in required days to harvest between parents affected significantly their crosses. Regarding the cross values, cross 2×D required minimum days to reach harvest with 171.00 days, while cross 1×A exhibited maximum days to reach harvest with 184.00 days, followed by cross 1×B which required 183.00 days. The results in the same table detected that the cross mean delayed parent's mean by 0.61%. Previous researchers reported different results on the number of days to harvest for pea genotypes [29], [30], and [31]. Data in the same table indicated that among the parents, tester C gave a maximum number of seeds pod^{-1} of 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 affected significantly their crosses. Regarding the cross values, the cross 1×A exhibited the maximum number of seeds pod^{-1} with 5.26 seeds, followed by the cross 2×A with 5.16 seeds pod^{-1}, while the cross 1×B 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 [32], 2.75-4.54 [33], 3.5-5.6 [30], and 4.0-7.6 [34]. The mean values for parents and their crosses for a number of pods plant^{-1} were shown in Table 4. Tester parent A exhibited the maximum number of pods plant^{-1} with 15.60 pods, followed by parent lines 1 and 3 with 14.80 and 12.87 pods respectively, while tester D 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×B with 48.57 pods recorded the maximum number of pods plant^{-1}, followed by the crosses 2×D and 1×D with 44.03 and 43.53 pods respectively, while the cross 3×A 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 plant^{-1} for pea genotypes lies between 21.78–29.48 pods [35], 9.83–20.17 pods [22], and 8.3–53.6 pods [36]. It was found in Table 4, that the tester parents A exhibited maximum weight for seed yield plant^{-1} of 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. Mean of lines & testers and their hybrids for studied traits

Genotypes	PH(cm)	NBPP	ND50%F	NDH	NSPPo	NPoPP	SYPP(g)
			Parents				
Line 1	48.87	2.83	113.33	174.00	3.13	14.80	9.42
Line 2	77.97	1.77	115.67	178.67	3.91	11.67	5.11
Line 3	62.26	2.57	116.00	176.33	4.69	12.87	15.91
Tester - A	84.44	3.23	106.33	173.33	4.22	15.60	17.29
Tester - B	55.13	2.10	107.33	174.33	3.36	11.07	8.24
Tester - C	44.92	2.23	110.33	175.67	4.83	9.53	7.31
Tester - D	40.34	2.50	108.33	177.67	4.12	8.47	6.25
Parents mean	59.13	2.46	111.05	175.71	4.04	12.00	9.93
			Crosses				
L1 X A	70.23	4.67	118.67	184.00	5.26	20.97	20.49

L2 X A	97.21	2.60	120.00	177.00	5.16	27.60	24.76
L3 X A	84.27	3.67	106.33	176.00	4.61	17.00	25.28
L1 X B	58.42	4.60	119.00	183.00	3.29	27.60	20.73
L2 X B	101.97	4.53	116.67	171.33	4.01	48.57	37.99
L3 X B	54.93	4.23	118.33	172.33	3.80	21.40	17.07
L1 X C	55.73	5.63	115.67	179.67	4.22	37.63	36.08
L2 X C	103.19	4.40	113.33	176.67	4.30	26.70	17.57
L3 X C	64.81	4.33	110.67	175.33	5.13	21.27	23.36
L1 X D	48.63	4.87	115.33	174.67	4.10	43.53	34.42
L2 X D	98.07	3.60	115.67	171.00	4.54	44.03	35.16
L3 X D	65.57	4.47	117.00	180.33	4.13	25.13	24.16
Crosses mean	75.25	4.30	115.56	176.78	4.38	30.12	26.42
LSD ($p \leq _{0.05}$)	18.65	1.32	3.35	4.12	0.55	6.95	8.47
LSD ($p \leq _{0.01}$)	25.01	1.77	4.49	5.53	0.73	9.32	11.35

PH=Plant height, NBPP= Number of branches plant^{-1}, ND50%F= Number of days to 50% flowering, NDH= Number of days to harvest, NSPPo= Number of seeds pod^{-1}, NPoPP= Number of pods plant^{-1}, SYPP=See yield plant^{-1} (g)

Regarding the cross values, the highest weight for seed yield plant^{-1} was found to be cross 2×B at 37.99 g, followed by cross 1×C at 36.08 g, and the lowest weight for seed yield plant^{-1} was found to be cross 3×B at 17.07 g. It was found from the table that the means of crosses predominated the parent's mean by 62.42%. Previous researchers illustrated that seed yield plant^{-1} for pea genotypes lies between 9.80–40.63 g [37], 30–43 g [38], and for parents 3.83–15.42 g and crosses 4.95–19.50 g [21].

2. Estimation of heterosis as deviation of *F1* from mid parents:

Significant positive and negative heterosis was displayed in Table 5 as a percentage mean deviation of the *F1's* cross from the mid-parental values of all the traits. Different values were produced in heterosis due to the variations in parental values and their crosses. Data in the table for the trait plant height showed that, all crosses revealed positive heterosis values except the cross 3×B which recorded a negative value of -6.411%. The maximum positive heterosis value was 67.940% recorded by the cross 2×C followed by the cross 2×D with 65.774%, indicating the over-dominance gene effect for the parent with a higher value. In comparison, the minimum positive heterosis value was 5.371% produced by the cross 1×A. Significant values of positive and negative heterosis were recorded previously by [32], [33] and [30] recorded that the highest positive heterosis for plant height of pea genotype was 31.54%. Table 5, showed significant heterosis values for the trait number of branches plant^{-1}, all crosses revealed positive heterosis values. The cross 2×B gave the highest value of heterosis with 134.483% followed by the crosses 1×C and 2×C with 122.368% and 120.000% respectively, while the cross 2×A recorded the lowest value of heterosis with 4.000%. The high positive values for heterosis indicated the over-dominant gene effect for the parent with a higher value. Significant heterosis values were recorded previously by [27] which detected standard heterosis for the number of primary branches with -36.89 to 46.78. Table 5, showed significant heterosis values for the trait number of days to 50% flowering. All crosses showed positive heterosis values except for 3×A and 3×C, which produced negative heterosis values with -4.348 and -2.209% respectively. The partial dominance gene effect for the parent with a lower value is reflected in the negative values of heterosis. The maximum positive heterosis value was 8.108% exhibited by the cross 2×A followed by the cross 1×A with 8.042%, while the lowest positive heterosis value was 0.295% produced by the cross 2×C. The overdominance gene effect for the parent with a greater value was indicated by the positive values of heterosis. Prior research by [39] found significant values of both positive and negative heterosis for the number of days required for 50% flowering, which showed that ten out of sixteen crosses recorded negative heterosis for days to flowering, and [21] detected that most crosses have significant negative heterosis for days to 50% flowering.

For the number of days to harvest, significant positive and negative heterosis values were estimated (Table 5). The maximum positive heterosis value was 5.950% recorded by the cross 1×A, followed by the cross 1×B with 5.072%, indicating the effect of over dominance gene effect for the parent with a higher value. While the maximum negative heterosis value was -4.022% shown by the cross 2×D, followed by the cross 2×B with -2.927 %, because the parent with the lower value has a partial dominant gene effect, the negative heterosis value validates this effect. Previous research by [33] revealed significant heterosis with positive and negative values for the number of days to harvest, and [40] detected the negative heterosis for this trait ranged between -7.64 to -0.19%. For the trait number of seeds pod^{-1} as shown in the table, it was found that the crosses 3×D, 3×B and 2×C produced negative values of heterosis with -6.25%, -5.57%, and -1.52% respectively, these negative values revealed 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×B and 1×A respectively. Significant positive and negative heterosis for the number of seed pod^{-1} for pea genotypes were recorded previously by [41] with 42.09% and [42] showed the standard range of heterosis with -51.85–18.52 for the number of seed pod^{-1}. For the trait number of pods plant^{-1}, as it was shown in the table all crosses recorded positive heterosis values. The cross 2×D showed a maximum positive heterosis value of 337.42%, followed by the crosses 2×B and 1×D with 327.27 and 274.21% respectively. The cross 3×A 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, [43] showed positive heterosis for the number of pods plant^{-1} with 119.22%, [44] exhibited the highest significant positive heterosis with 125.78 for this trait and [42] recorded standard heterosis with -63.54 to 27.08 for number of pods plant^{-1}.

Table 5. Heterosis as deviation of F_1 from mid-parents for studied traits

Genotypes	PH (cm)	NBPP	ND50%F	NDH	NSPPo	NPoPP	SYPP (g)
L1 X A	5.371	53.846	8.042	5.950	43.02	37.939	53.489
L2 X A	19.711	4.000	8.108	0.568	26.84	102.45	121.14
L3 X A	14.883	26.437	-4.348	0.667	3.560	19.438	52.285
L1 X B	12.346	86.486	7.855	5.072	1.409	113.40	134.71
L2 X B	53.210	134.48	4.634	-2.927	10.29	327.27	469.03
L3 X B	-6.411	81.429	5.970	-1.711	- 5.57	78.830	41.351
L1 X C	18.851	122.37	3.428	2.765	6.01	209.32	331.53
L2 X C	67.940	120.00	0.295	-0.282	- 1.52	151.89	183.07
L3 X C	20.931	80.556	-2.209	-0.379	7.79	89.881	101.30
L1 X D	9.035	82.500	4.060	-0.664	13.07	274.21	339.40
L2 X D	65.774	68.750	3.274	-4.022	13.05	337.42	519.14
L3 X D	27.810	76.316	4.309	1.883	- 6.25	135.63	118.07
S. E.	6.894	10.954	1.147	0.859	4.047	31.029	48.170

PH=Plant height, NBPP= Number of branches plant^{-1}, ND50%F= Number of days to 50% flowering, NDH= Number of days to harvest, NSPPo= Number of seeds pod^{-1}, NPoPP= Number of pods plant^{-1}, SYPP=See yield plant^{-1} (g)

The data for the trait seed yield plant^{-1}, in the same table, shows that all crosses have positive heterosis. The results indicate cross 2×D gave a maximum heterosis value of 519.14%, followed by cross 2×B of 469.03%, while cross 3×B 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 [41], which found that the highest real heterosis for seed yield plant^{-1} was 432.43%, and [42] recorded standard heterosis with -72.61–39.24, and [45] with 104.79%. It was found in Table 5 that the degrees of heterosis among the hybrids vary significantly. Only three traits exhibit positive heterosis, number of branches plant^{-1}, the number of pods plant^{-1}, and seed yield plant^{-1}. Hybrid L2 X D had the highest positive heterosis values for the traits number of pods plant^{-1}, and seed yield plant^{-1}, with 337.42, and 519.14 respectively, which causes an increase in the number of pods plant^{-1} and an increase in the seed yield plant^{-1}, while the same hybrid has the lowest negative heterosis for the trait number of days to harvest with -4.022%.

3. Estimation of general and specific combining ability effects:

Table 6, confirmed the estimation of general and specific combining ability effects for all studied traits. Data on the trait plant height shows that the line parents 1, 3 and testers B, C, and D showed negative values of GCA with -16.998, -7.859, -3.479, -0.675, and -4.497, respectively, showing how these parents' contributions to their crossings' reduction of plant height. Maximum positive *GCA* values were 24.857 recorded by line parent 2 and followed by tester parent A with 8.652, showing how much these parents contributed to the increased plant height in their crosses. Regarding the *SCA* effect values for the crosses, cross 3×A revealed maximum positive *SCA* effect value of 8.222, followed by the crosses 2×B, and 2×C (5.336, and 3.758) respectively. In contrast, the cross 2×A showed maximum negative *SCA* effect value of -11.548 followed by the cross 3×B with -8.981. [46] obtained significant negative *GCA* effects for pea plant height with -5.60 cm, and the same results were obtained by [8], and [47]. Table 6, also showed the effects of general and specific combining ability for the trait number of branches plant^{-1}. Data in the same table confirmed the positive values of *GCA* effects for the testers B, C and D with 0.156, 0.489 and 0.011 respectively, while the line parent 1 showed maximum positive *GCA* effect value with 0.642. The potential of these parents to increase the number of branches plant^{-1} in their crossings was validated by these positive values of *GCA* effects. The maximum negative *GCA* effects value was -0.656 exhibited by the tester parent A, followed by the line parent 2 with -0.517, while the line parent 3 recorded minimum negative value of *GCA* effects with -0.125, indicating the reduction in number of branches plant^{-1} in their crosses. Concerning to the *SCA* effect values for the crosses, cross 2×A recorded the highest negative *SCA* effect value with -0.528, while the cross 1×D gave the lowest negative *SCA* effect value with -0.086. The maximum positive *SCA* effect value was 0.594 recorded by the cross 2×B, while the cross 2×C produced minimum positive *SCA* effect value with 0.128. The same table estimates the effects of general and specific combining ability for the trait number of days to 50% flowering. The tester parent B recorded a maximum positive *GCA* effect value of 2.444, followed by line parent 1 with 1.611, while line parent 3 showed a maximum negative *GCA* value of -2.472. Regarding the *SCA* effect values for the crosses, cross 3×A recorded a maximum negative *SCA* effect value of -6.194, while the maximum positive *SCA* effect value was 4.139 recorded by the cross 2×A, followed by cross 3×D with 3.472. Similar results were reported previously by [48]. The same table shows the effects of *GCA* and *SCA* for the trait number of days to harvest. Data in table showed that line parent 1 exhibited maximum positive *GCA* values with 3.556, followed by the tester parent A with 2.222, while line parent 3, testers B, D, and line 2 produced negative values of *GCA* with -0.778, -1.222, -1.444 and -2.778 respectively, indicating the reduction in number of days to harvest in their crosses. Concerning the *SCA* effect values for crosses, cross 3×D showed a maximum positive *SCA* effect value of 5.778, while the cross 2×A produced a minimum positive *SCA* effect value of 0.778.

Cross 1×D exhibited a maximum negative *SCA* effect value of -4.222, whereas crosses 1×C and 3×C recorded a minimum negative *SCA* effect with the same value of -1.111. It was clarified from the *GCA* effect values of the number of seeds pod^{-1} for parents, that tester A 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 B gave the highest negative *GCA* effect value of -0.68, while tester D 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×C, followed by the cross 1×A of 0.410. In contrast, cross 3×A recorded a maximum negative *SCA* effect value of -0.44, followed by cross 2×C of -0.37. Similar results were reported previously by [44], [46], and [47]. 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 A with -8.27, while tester C produced a minimum negative GCA effect value of -1.59. Tester D exhibited the maximum positive GCA effect value of 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×C, while the minimum negative value of *SCA* was -0.14 showed by the cross 2×D. Cross 2×B showed a maximum positive effect value of 9.439, followed by the crosses 1×C and 3×A, with 6.786 and 4.064 respectively. Similar results were reported previously by [49], which obtained significant positive *GCA* effects for a number of pods plant^{-1}, and [50] observed significant combining ability variances of the *F1's* for the number of pods plant^{-1}. 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 A and B with -2.912 and -1.159, respectively, indicating the reduction in seed yield plant^{-1} in their crosses. Tester parent D produced a maximum positive *GCA* value of 4.822, followed by line parent 2 with 2.449, demonstrating the parents' significant contribution to the seed yield increase in their crosses. Concerning the *SCA* effect values for crosses, it was found that cross 2×C with -10.550 gave a maximum negative *SCA* effect value and the cross 2×B with 10.281 gave a maximum positive *SCA* value, followed by the cross 1×C with 8.902. Similar results on seed yield plant^{-1} for pea genotypes were reported previously by [47].

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

Genotypes	PH(cm)	NBPP	ND50%F	NDH	NSPPo	NPoPP	SYPP(g)
GCA for Lines & GCA for Testers							
Line 1	-16.998	0.642	1.611	3.556	-0.16	2.314	1.507
Line 2	24.857	-0.517	0.861	-2.778	0.124	6.606	2.449
Line 3	-7.859	-0.125	-2.472	-0.778	0.039	-8.92	-3.956
S. E. Line	3.252	0.230	0.584	0.718	0.095	1.212	1.476
Tester - A	8.652	-0.656	-0.556	2.222	0.629	-8.27	-2.912
Tester - B	-3.479	0.156	2.444	-1.222	-0.68	2.403	-1.159
Tester - C	-0.675	0.489	-2.333	0.444	0.170	-1.59	-0.751
Tester - D	-4.497	0.011	0.444	-1.444	-0.12	7.447	4.822
S. E. Tester	3.755	0.266	0.675	0.830	0.110	1.400	1.704
SCA for Crosses							
L1 X A	3.327	0.381	2.056	1.444	0.410	-3.20	-4.524
L2 X A	-11.548	-0.528	4.139	0.778	0.024	-0.86	-1.196
L3 X A	8.222	0.147	-6.194	-2.222	-0.44	4.064	5.720
L1 X B	3.644	-0.497	-0.611	3.889	-0.25	-7.24	-6.043
L2 X B	5.336	0.594	-2.194	-1.444	0.186	9.439	10.281
L3 X B	-8.981	-0.097	2.806	-2.444	0.061	-2.20	-4.238
L1 X C	-1.847	0.203	0.833	-1.111	-0.17	6.786	8.902
L2 X C	3.758	0.128	-0.750	2.222	-0.37	-8.44	-10.550
L3 X C	-1.012	-0.331	-0.083	-1.111	0.540	1.653	1.648
L1 X D	-5.124	-0.086	-2.278	-4.222	0.006	3.653	1.665
L2 X D	2.454	-0.194	-1.194	-1.556	0.160	-0.14	1.465
L3 X D	2.671	0.281	3.472	5.778	-0.17	-3.51	-3.131
S. E. crosses	6.504	0.460	1.169	1.437	0.191	2.424	2.951

PH=Plant height, NBPP= Number of branches plant^{-1}, ND50%F= Number of days to 50% flowering, NDH= Number of days to harvest, NSPPo= Number of seeds pod^{-1}, NPoPP= Number of pods plant^{-1}, SYPP=See yield plant^{-1} (g).

4. **Estimation of some genetic parameters for the studied traits:**

Table7, shows the estimation of the genetic parameters (ratio $\sigma^2_{gca}/\sigma^2_{sca}$, average degree of dominance and broad and narrow sense heritability) for studied traits of the pea. The variation component caused by *GCA* was greater than that caused by *SCA*, according to data on trait plant height, making the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ more than unity 1.598, while the average degree of dominance value was less than unity 0.791, demonstrating more significant of the additive gene effect (partial dominance) and its considerable contribution to regulating the transmission of this trait. Heritability in the broad sense was 70% and in the narrow sense was 53.3%, confirming the importance of the progeny selection method will be more effective in future breeding programs to improve this trait. The same results were obtained by [8], [51], and [52] which were in agreement with this study. Some genetic parameters of the trait number of branches plant^{-1} are also presented in (Table 7). Data in the table indicated that the variance component for *GCA* was larger than of *SCA*, causing the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ to become more than unity 14.191, indicating the importance of additive gene effect (partial dominance) in controlling the inheritance of this trait. These results were confirmed by the average degree of dominance value which was less than unity 0.265. Heritability in the broad sense was 63.2% while in the narrow sense was 61.1%, these results confirmed that the selection method will be more effective in future breeding programs to improve this trait. Similar results were shown previously by [35]. The results in Table 7 for the trait number of days to 50% flowering showed that the variance component due to *GCA* was smaller than *SCA*, making the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ became less than unity 0.197, while the average degree of dominance was more than unity 2.250, indicating the high contribution of non-additive gene effect (over dominance) in controlling the inheritance of this trait. Heritability in the broad sense was 93.5%, while in the narrow sense was 26.5%, this confirmed the importance of heterosis breeding or the hybridization method will be effective in improving this trait. Similar results were reported previously by [48], [53], and [54] which revealed that the minimum value of heritability is estimated for days to flowering. Some genetic parameters for the trait number of days to harvest also represented in Table 7, the variance component due to *GCA* was smaller than *SCA*, making the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ became less than unity 0.246, indicating the importance and high contribution of non-additive gene effect (over dominance) in controlling the inheritance of this trait. These results were confirmed by the average degree of dominance value which was more than unity 2.016. Heritability in (b.s) was 90.5% while in (n.s) was 29.9%, these results confirmed that the hybridization method will be effective in improving this trait. Similar results were observed previously by [35]. The data on the trait number of seeds pod^{-1}, shows that the variance component due to *GCA* was smaller than *SCA*, making the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ become less than unity 0.358 and the average degree of dominance was more than unity 1.672, indicating the high contribution of non-additive gene effect (over dominance) than additive gene effect (partial dominance) in controlling the inheritance of this trait. Heritability in broad sense was 85.5%, while in narrow sense was 35.7%, these results confirmed the importance of heterosis breeding or hybridization method will be effective to improve this trait. Similar results were reported previously by [44], [46], [47] and [55] reported the lowest value of heritability in broad sense for number of seeds pod^{-1} among all the traits. Some genetic parameter on the trait number of pods plant^{-1}, presented in the same table, and it was shown that the variance component due to *GCA* was smaller than *SCA*, making the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ became less than unity 0.220, while the average degree of dominance value was more than unity 2.133, indicating the importance of non-additive gene effect (over dominance) in controlling the inheritance of this trait. Heritability in broad sense was 92.1%, while in narrow sense was 28.1%, confirmed the importance of heterosis breeding or hybridization method will be effective to improve this trait. Similar results were reported previously by [50], and [47] noticed that *SCA* variances were much higher than the *GCA* variances for number of pods plant^{-1}, [49] obtained significant positive *GCA* effects for number of pods plant^{-1}, [56] recorded high heritability for number of pods plant^{-1} and [57] found high heritability in broad sense for number of pods plant^{-1}.

Soil Properties	Girjan
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}) Soil	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

Table 7. Estimation of ratio $\sigma^2_{gca}/\sigma^2_{sca}$, average degree of dominance and broad and narrow sense heritability for studied traits of pea

Traits	$\sigma^2_{gca}/\sigma^2_{sca}$	σ^2_A	$\sigma^2_D = \sigma^2_{sca}$	$\bar{a}$	$h^2 b.s$	$h^2 n.s$
PH(cm)	1.598	75.212	23.538	0.791	0.700	0.533
NBPP	14.191	0.352	0.012	0.265	0.632	0.611
ND50%F	0.197	5.564	14.088	2.250	0.935	0.265
NDH	0.246	6.516	13.244	2.016	0.905	0.299
NSPPo	0.358	0.089	0.125	1.672	0.855	0.357
NPoPP	0.220	20.828	47.377	2.133	0.921	0.281
SYPP(g)	0.234	28.878	61.753	2.068	0.912	0.291

PH=Plant height, NBPP= Number of branches plant^{-1}, ND50%F= Number of days to 50% flowering, NDH= Number of days to harvest, NSPPo= Number of seeds pod^{-1}, NPoPP= Number of pods plant^{-1}, SYPP=See yield plant^{-1} (g)

Some genetic parameters are also revealed in Table 7 about the trait seed yield plant-1, the variance component due to GCA was smaller than SCA, making the ratio of $\sigma gca2\sigma sca2$ became less than unity, 0.234, demonstrating the importance of non-additive gene effect (over dominance) in controlling the inheritance of this trait. These results were confirmed by the average degree of dominance value, which was more than unity, 2.068. Heritability in the broad sense was 91.2%, while in the narrow sense it was 29.1%. These results confirmed the importance of heterosis breeding or the hybridisation method, which will effectively improve this trait. Similar results on seed yield plant^{-1} for pea genotypes were reported previously by [47] which found in their study that the *SCA* variances were much higher than the *GCA* variances for the seed yield plant^{-1}.

Conclusions

From the results of statistical and genetic analysis of seven pea varieties and their crosses, the following conclusions can be laid:

- The presence of high variability between lines, testers and their crosses reflected significantly in the exhibiting large differences among all traits.
- The parent line NS minima as a good combiner, recorded the minimum values in traits number of branches plant^{-1}, pod yield plant^{-1}, and seeds yield plant^{-1}. This line also shows the best possibility of utilization in breeding programs to develop good pea varieties.
- The parent line Oregon sugar pod gave superiority and recorded good combiner in traits number of days to 50% flowering, and pod yield plant^{-1}, which shows the possibility of utilization in breeding programs to develop varieties of pea.
- The parents' Giant sugar pod, as a tester, recorded superiority and revealed good combiner in four different traits: plant height, number of branches plant^{-1}, seed yield plant^{-1}, and number of pods plant^{-1}.
- The parents Lancet and Provence, as testers, possessed good combiners and superiority in the number of seeds pod^{-1}. These two testers show the best possibility of utilization in breeding programs to develop varieties of pea.
- Significant heterosis values as a percentage mean deviation from mid-parental values were detected for all traits due to the influences of the over-dominance genes effect and partial dominance genes effect.
- The variance component due to *GCA* was larger than *SCA* for the traits plant height, number of branches plant^{-1} confirming the high contribution of additive gene effect in controlling the inheritance of these traits.
- The variance component due to *SCA* was larger than *GCA* for the other five traits, confirming the high contribution of non-additive gene effect in controlling the inheritance of those traits.
- The average degree of dominance was less than unity for the traits plant height, number of branches plant^{-1}, indicating the importance and high contribution of additive gene effect (partial dominance) in controlling the inheritance of both traits, while for the other traits were more than unity indicating the high contribution of non-additive gene effect (over dominance) in controlling the inheritance of those traits.
- Heritability was high for all traits in the broad sense, while it was high for the number of branches plant-1 in the narrow sense. This confirmed the importance of the progeny selection method in future breeding programs to improve this trait. For the other traits, which ranged from moderate to low, these results confirmed the importance of the hybridization method in improving those traits.
- Hybrid *NS minima* × *Provence* had the highest positive heterosis values for two traits a number of pods plant^{-1}, and seed yield plant^{-1}.
- Hybrid *Oregon sugar pod* × *Green sage* has the lowest positive heterosis values for two traits, pod yield plant^{-1}, and seed yield per plant^{-1}.

Recommendations

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

- The results of this investigation recommend conducting further works on these crosses with their parents during the future seasons and using those in the future breeding program.
- During this study, most of the studied traits showed non-additive genetic variance, which can be exploited by adopting a hybridization 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 traits, hybridization followed by a selection method among segregates and recombined may be recommended utilizing both additive and non-additive gene effects using a (line × tester) mating design.

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تقديرات قوة الهجين والقدرة على الاتحاد والمعالم الوراثية في البازلاء.

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الخلاصة

أجري هذا البحث لدراسة وراثة بعض صفات البازلاء من خلال استخدام النظام التزاوجي (السلالة x الفاحص)، اذ اعتمدت ثلاث سلالات نقية (Javor, NS minima, Oregon sugar pod) كسلالات ابوية واربعة اخرى كفواحص (Giant sugar pod, Green sage, Lancet, and Provence). زرعت السلالات خلال الموسم الخريفي لعام 2014 واجريت التهجينات بينها للحصول على 12 هجين فردي، وتم إنتاج كمية كافية من بذور الهجن المختلفة. خلال موسم النمو 2015–2016 تم زراعة بذور هجين الجيل الأول مع أبائها في التجربة الحقلية باستخدام تصميم القطاعات العشوائية الكاملة بثلاث مكررات في محطة أبحاث گردجان، بهدف تقديرات قوة الهجين وتاثيرات القدرتين العامة والخاصة على الاتحاد للاباء والهجن على التوالي وتبايناتها لصفات ارتفاع النبات (سم)، عدد الأفرع على النبات، عدد أيام حتى تزهير 50% من النباتات، عدد أيام حتى الحصاد، عدد البذور في القرنة، عدد قرون على النبات، وحاصل البذور للنبات (غ). أظهرت النتائج أن متوسط المربعات العائد للتراكيب الوراثية كان معنوياً عاليا للصفات جميعها. تفوق الأب الفاحص Giant sugar pod على بقية الآباء في ارتفاع النبات وعدد الأفرع على النبات بينما سجلت أقل عدد للأيام اللازمة للتزهير 50% وأقل عدد أيام للحصاد. سجل الهجين Javor × Giant sugar pod أقصى عدد أيام للحصاد. أعطى الهجين NS minima × Provence أعلى قوة هجين سالبة لعدد الأيام اللازمة للحصاد. وكذلك نفس الهجين NS minima × Provence أعطى أعلى قوة هجين موجبة لصفتين عدد القرون على نبات، وحاصل البذور على النبات.

الكلمات المفتاحية : تحليل (السلالة× الفاحص)؛ GCA و SCA؛ التغاير. درجة الهيمنة؛ التوريث.