



Enhancement of Certain Yield Attributes Through Selection in Some Pea Backcross Populations

Hala S. A. Mousa*, Abo-Bakr A.A. El-Dakkak* and Ahmed H. Hussein*

* Horticulture Research Institute, Agriculture Research Center, Giza, Egypt

ABSTRACT

The present study was carried out at Shandaweel Research Station, Agriculture Research Center, Egypt. During the three growing winter seasons of 2019/2020, 2020/2021 and 2021/2022 using two F₃-populations stemmed from backcrosses between three cultivars of pea to improve pod yield using selection by two cycles. The main genetic parameters studied were PCV, GCV, broad sense heritability, genetic advance and response to selection estimated in the F₄ and F₅ generations. High values of GCV and PCV were found for pod yield and its components, indicating a lot of variation and that their expression is less affected by the environment. In addition to, high heritability with high genetic advance was recorded for pod yield and its components indicating that these characteristics can be used for pea improvement by selection. For population II, the highest superior families were 21, 5 and 32 for pod yield by (121.0, 151.4, 200.0 and 231.6 %), (94.23, 121.0, 163.7 and 191.4 %) and (79.2, 103.98, 143.3 and 168.9 %) than the bulk sample, the best parent, check cv. (Sweet 2) and mid parent respectively. On the other hand, families No. 7 and 16 were significantly higher in pod yield for population I. by (43.23, 51.70, 114.1 and 124.2 %) and (34.9, 42.88, 101.61 and 111.13%) than the bulk sample, the best parent, mid parent and check cv. (Sweet 2), respectively, which can be used for further pea breeding programs.

Keywords: Genetic advance- (P.C.V.) - (G.C.V.)- Realized and correlated response to selection and heritability.

INTRODUCTION

The pea (*Pisum sativum* L.), a significant leguminous vegetable crop, is only suitable for cultivation in temperate and subtropical regions. It is planted for a variety of reasons, including its eye-catching foliage, mature, green seeds, and pods. Its high content of antioxidants, vitamins, and minerals, together with its 23–33% protein content, confer numerous health benefits. Poor farming families benefit even more from animal feed made from leftover peas, which is also a wonderful source of nutrition. To keep up with the growing demand for peas, most breeding efforts now prioritize the development of high-yielding cultivars. Breeders must to choose a breeding plan that facilitates the simultaneous improvement of yield and yield component features.

For a successful breeding program, crop improvement depends upon the extent of heritability of the desirable characters and the magnitude of genetic variability (Kumari et al., 2009). The improvement of any crop, the selection of superior genotypes, and the improvement of any trait require genetic variability, heritability, and genetic advance

(Pandey et al., 2023). Yield is a complex trait shaped by various genetic factors interacting with the environment. The success of any breeding program aimed at improving yield depends on the genetic variability present in the base population and the effectiveness of selection. (Kumari et al., 2008). The percentage of phenotypic variance attributable to heritable genes is known as heritability (Kumar et al., 2010). Breeders can use heritability as a guide for selecting traits with high heritability, which often leads to improvements (Kumar et al., 2024). Mousa, (2010) found high broad-sense heritability for pod length, number of seeds per pod, shell out percentage, pod yield per plant, plant height, and pod diameter. Sharma and Sharma (2013) found that the highest GCV and high heritability were observed for days to 50% flowering, green pod yield and plant height along with moderate genetic advance. It indicates that most likely the heritable is due to the preponderance of additive gene effects and the potential of selection for these characters to improve garden pea yield. Pod yield/plant demonstrated a significant and nearly



equivalent selection advance (Mousa et al., 2016). Alternative breeding plans for the enhancement of particular qualities can be determined based on studies on genetic advancement and heritability (Kumar et al., 2010). Since these characteristics were crucial in raising crop production per plant,

MATERIALS AND METHODS

The present study was carried out at the field of Shandaweel Agriculture Research Station, Sohag governorate, Agriculture Research Center, Egypt. During the three growing winter seasons of 2019/2020, 2020/2021, and 2021/2022. The basic materials used in this investigation consisted of two F₃ populations stemmed from backcrosses between two pea cultivars and one stabled line (obtained from the breeding pea program of El-Dakkak et al., 2015). The two F₃-populations from backcrosses, viz. Pop. I (Sweet 1 x Line 14) x Line 14 and Pop. II (Sweet 1 x Super 2) x Super 2 were raised at 10 November 2019, each of both populations was represented by 500 plants (selection intensity 10%). Twenty rows of 25 plants each were used to sow the 500 F₃ plants from each population, with plants placed 20 cm apart within rows that were 70 cm apart. Additionally, each population's parents were cultivated in three rows next to the local check cultivar Sweet 2. Every population was subjected to pedigree selection. All different agricultural practices i.e. irrigation, fertilization and pest management were applied as recommended by Egyptian Ministry of Agriculture.

- Out of 500 plants, the 50 best plants (selection intensity: 10%) were chosen for each population and labeled.
- Selfed seeds (selected F₄ seeds) on each chosen plant were harvested and preserved at the end of the growth season.
- Each chosen plant's selfed seed was regarded as the seeds from the initial pedigree selection cycle (C₁) for pod yield in each population.
- During the winter season of 2020/2021, the 50 F₄ selected families of each population, along with the parents, bulk and the check cultivar (Sweet 2), were

direct selection for these qualities may result in an overall increase in crop yield. Therefore, the goal of this study was to determine how well pedigree selection works to identify genotypes with a high genetic potential for pod yield and its components of peas.

sowed in a randomized complete blocks design with three replications on October 15, 2020. Every family comprised of two rows that measured five meters in length, 0.7 meters in width, and 0.2 meters in between each plant. The 5 best plants were selected in both populations for the next season.

In 2021/2022 season, the five F₅-selected families for each of populations were sown along with the parents and F₅ bulk population and evaluated in separate experiments in a randomized complete block design of three replications (RCBD). Plants were sown in rows 70 cm apart and 10 cm between hills.

Statistical analysis:

Data recorded were analyzed separately for individual plants on a random sample of ten guarded plants from each family in F₄ and F₅ generations. The means of the ten plants were subjected to the statistical and genetic analyses for the following characters: pod length cm (PL), pod width cm (PW), number of seeds/pod (NS/P), shelling percentage % (SP), 100 seed weight g (100-SW), days to 50% flowering (DF), number of branches/plant (NB/P), stem length cm (SL) and pod yield/plant g (PY/P). The genetic parameters were estimated in F₄ and F₅ generations. The collected data were statistically analyzed according to the method described by Snedecor and Cochran (1980). All statistical analyses were performed using analysis of variance technique by means of MSTATC computer software package (Freed et al., 1991).

- The estimates of broad sense heritability (h^2) were based on Allard (1960) and Falconer (1989). According to Stanfield's (1983) theory of heritability, $0 \leq x < 0.2$ = low, $0.2 \leq x \leq 0.5$ = medium, and $x > 0.50$ = high.



- The phenotypic (PCV) and genotypic (GCV) coefficients of variability were computed. Using the formula proposed by Johnson et al. (1955).
- Genetic advance (GA) was computed as follows: $GA = K \times \delta^2g / \sqrt{\delta^2ph}$, where $K = 1.76$, constant (based on selection intensity of 10 %). Genetic advance as a percentage of mean (anticipated genetic advance): $GAM \% = (GA / \bar{X}) \times 100$. According to Hadiati et al. (2003), GAM% falls into three categories: low (0–7%), medium (7.1–14%), and high (> 14.1).
- The realized gain from selection were expressed as deviation percentage of the mean of selected families from the bulk population, mid-parents and the best

parent means for the pedigree selection method (Falconer, 1981).

- Data for the studied traits were subjected to Principal Component (PC) Analysis for the two populations, based on 7 different traits, *i.e.*, two vegetative traits (NB/P and SL) and 5 pod yield traits (PL, PW, NS/P, 100-SW, and PY/P) using Minitab -V.17 statistical software. The PC was used to determine the extent of variation in the new selected lines. Eigenvalues were obtained from PC, which was used to determine the relative discriminative power of the axes and their associated characters (Pradhan et al., 2015). The new lines were categorized in a bi-plot figure and compared with the cluster analysis.

RESULTS AND DISCUSSION

1. Variances and means:

Means of variaces for selected families, parents, check and bulk sample for the F_3 (base), F_4 (C_1) and F_5 (C_2) generations of the two populations are presented in **Table (1)**. The results showed that, highly significant differences between genotypes for PY/P and all other studied characters in the two cycles of selection for the both of pea populations except for 100-SW, which was significant only in F_5 generation (C_2) for Pop. I. The overall PY/P mean of the bulk sample ranged from 147.79 and 94.75 g in the 1st cycle to 186.30 and 161.6 g in the 2nd cycle. Additionally, the selected families for PY/P in the two populations ranged from 191.85 and 166.42 g in the first cycle to 246.99 and 295.9 g in the second cycle for population I and II, respectively.

2. The genetic parameters:

2.1. PCV, GCV:

Means of genotypic (GCV) and phenotypic (PCV) coefficients of variability as well as GCV/ PCV percentage are presented in **Table (2)**. The results indicated that (PCV) were higher than (GCV) for all the traits of pea suggesting a limited impact of the environment and potentiality of selection effective. These

results are in agreement with those obtained by Tasnim et al. (2022). The highest phenotypic as well as genotypic coefficients of variation were observed in case of NB/P for both populations while the lowest values of PCV and GCV were for PY/P in Pop. I and NS/P for Pop. II. Similar results were reported by Pujari et al. (2021), Yadav et al. (2021) and Raj et al. (2023). The selection for PY/P reduced the genotypic coefficient of variability from (26.52 and 22.79%) after the first cycle to (5.39 and 4.34 %) after the 2nd cycle of selection in Pop. I and II, respectively. Falconar (1989) showed that selection reduces genetic variance of the following generation. Data recorded that all studied characters had high GCV/PCV percent. These values varied after the second selection cycle, ranging from 89.38% for NB/P to 99.45% for PY/P in Pop.I and from 84.86% for SL to 97.75% for PY/P in Pop.II. These results indicated that about 84% of phenotypic variances was due to genetic ones. Therefore, these traits might be more genotypically predominant and it would be possible to achieve further improvement in them. These results are in agreement with obtained by El-Dakkak et al. (2014).



Table (1). Average all studied traits of F₃, F₄ and F₅ generations in the two populations of peas.

Generation	F ₃ generation (Base)					F ₄ generation (C ₁)					F ₅ generation (C ₂)						
	Traits	F ₃	P ₁	P ₂	Check	Selected families	MS	P ₁	P ₂	Check	Bulk	Selected families	MS	P ₁	P ₂	Check	Bulk
Population I																	
PL (cm)	9.28	10.4	10.78	10.00	10.57	2.25**	10.52	11.01	10.34	10.28	11.13	2.38**	10.41	11.21	10.00	10.53	
PW (cm)	1.2	1.30	1.20	1.25	1.45	0.09**	1.29	1.16	1.20	1.15	1.37	0.07**	1.30	1.26	1.30	1.45	
NS/P	7.5	7.50	8.33	8.33	7.46	0.97**	7.90	8.50	8.28	7.56	7.94	2.46**	8.10	8.80	8.00	7.58	
SP (%)	42.13	41.02	40.14	45.00	55.14	37.31**	41.61	43.15	47.00	43.11	44.33	55.06**	41.50	44.15	46.00	48.07	
100-SW(g)	33.52	50.01	38.07	44.41	57.30	206.09**	51.27	39.61	45.33	35.22	41.08	16.03*	52.22	40.71	46.67	42.97	
DF	54	39.67	53.00	60.00	55.80	51.37**	41.17	55.00	58.00	53.00	60.33	60.17**	41.00	56.00	59.00	56.25	
NB/P	3.55	2.30	3.00	3.50	4.65	0.69**	2.17	2.91	3.00	3.50	5.31	5.34**	1.80	3.00	2.50	4.56	
SL (cm)	100.7	63.00	75.79	93.49	97.50	344.23**	61.00	77.99	79.22	102.84	82.40	266.07**	62.00	79.99	86.36	97.27	
PY/P (g)	144.8	74.11	169.98	116.23	191.85	7773.15**	73.89	173.55	117.87	147.79	246.99	534.38**	73.40	175.89	119.03	186.30	
Population II																	
Traits	F₃	P₁	P₂	Check	Selected families	MS	P₁	P₂	Check	Bulk	Selected families	MS	P₁	P₂	Check	Bulk	
PL (cm)	9.52	10.4	9.98	10.00	10.84	2.04**	10.52	10.11	10.34	10.52	11.36	0.39**	10.41	10.32	10.00	10.65	
PW (cm)	1.2	1.30	1.30	1.25	1.51	0.06**	1.29	1.27	1.20	1.16	1.40	0.09**	1.30	1.30	1.30	1.45	
NS/P	7.2	7.50	8.25	8.33	7.41	1.22**	7.90	8.13	8.28	7.15	8.36	0.08**	8.10	8.65	8.00	7.42	
SP (%)	45.64	41.02	45.55	45.00	50.89	55.70**	41.61	49.17	47.00	46.61	49.76	49.09**	41.50	49.50	46.00	49.30	
100-SW(g)	38.73	50.01	43.46	44.41	59.04	243.39**	51.27	45.23	45.33	40.43	51.31	106.27**	52.22	47.00	46.67	49.04	
DF	59.12	39.67	50.00	60.00	56.38	141.56**	41.17	49.00	58.00	58.12	59.67	107.67**	41.00	51.00	59.00	57.19	
NB/P	3.5	2.30	2.50	3.50	3.918	0.87**	2.17	2.77	3.00	3.51	5.93	3.72**	1.80	3.00	2.50	3.89	
SL (cm)	105	63.00	91.89	93.49	95.35	160.23**	61.00	94.33	79.22	107.68	77.39	17.91**	62.00	97.00	86.36	96.03	
PY/P (g)	91.76	74.11	135.79	116.23	166.42	4324.64**	73.89	139.25	117.87	94.75	295.90	501.91**	73.40	142.00	119.03	161.60	

PL: Pod length, PW: Pod width, NS/P: Number of seeds/pod, SP: Shelling percentage, 100-SW: 100 Seed weight, DF: Days to 50% flowering, NB/P: Number of branches/plant, SL: Stem length and PY/P: Pod yield/plant.



2.2. Heritability and genetic advance estimates:

Heritability is one of the most important factors that determine the response due to selection and genetic improvement, especially superior plants or genotypes of the population. The results of heritability in broad sense after the second cycle (generation F₅) of selection showed that high degree of heritability for all studied traits; PY/P (99.00 and 95.30), SL (97.16 and 71.75), DF (95.33 and 97.08), NS/P (91.06 and 89.41), PW (84.21 and 93.48), SP (93.61 and 92.43), PL (95.12 and 86.14), 100-SW (84.21 and 95.48) and NB/P (79.88 and 83.48) in the 1st and 2nd populations respectively, **Table (2)**. High heritability values were found in the current study for PY/P and its components characters showed that, pedigree selection method will be more appropriate for improving PY/P while making selection. Mousa et al.(2016),

Table (2). Values of PCV, GCV, GCV/PCV%, heritability and genetic advance estimates for all characters in 1st and 2nd cycles of the two population's peas.

Population	Cycle	Item	PL	PW	NS/P	SP	100-SW	DF	NB/P	SL	PY/P
Pop. I	C ₁	GCV	8.16	11.58	7.42	6.36	14.44	7.32	10.10	10.96	26.52
		PCV	8.25	11.98	7.98	6.48	14.52	7.59	10.65	11.05	26.56
		GCV/PCV%	98.91	96.66	92.98	98.15	99.45	96.44	94.84	99.19	99.85
		h ²	97.76	93.41	86.45	96.31	98.89	93.02	89.80	98.35	99.66
		GA %	1.49	0.28	0.90	6.02	14.39	6.90	0.78	18.54	88.88
	C ₂	GCV	7.93	10.65	11.23	9.56	5.46	7.36	24.16	11.37	5.39
		PCV	8.13	11.60	11.77	9.88	5.95	7.54	27.03	11.54	5.42
		GCV/PCV%	97.54	91.81	95.41	96.76	91.76	97.61	89.38	98.53	99.45
		h ²	95.12	84.21	91.06	93.61	84.21	95.33	79.88	97.16	99.00
		GA %	1.51	0.23	1.49	7.17	3.60	7.59	2.00	16.17	23.20
Pop. II	C ₁	GCV	7.56	9.08	8.39	8.43	15.23	12.16	13.34	7.61	22.79
		PCV	7.70	9.32	9.07	8.54	15.32	12.22	14.55	7.77	22.86
		GCV/PCV%	98.18	97.42	92.50	98.71	99.41	99.51	91.68	97.94	99.69
		h ²	96.41	94.92	85.60	97.46	98.82	99.08	84.00	96.03	99.43
		GA %	1.41	0.23	1.01	7.41	15.64	11.95	0.84	12.45	66.19
	C ₂	GCV	3.10	12.10	1.90	8.02	11.51	9.99	18.17	2.97	4.34
		PCV	3.34	12.52	2.01	8.34	11.78	10.14	19.89	3.50	4.44
		GCV/PCV%	92.81	96.65	94.53	96.16	97.71	98.52	91.35	84.86	97.75
		h ²	86.14	93.48	89.41	92.43	95.48	97.08	83.48	71.75	95.30
		GA %	0.57	0.29	0.26	6.72	10.10	10.28	1.72	3.41	21.92

PCV and GCV: Phenotypic and Genotypic coefficient of variance, respectively; h²: Broad sense heritability and GA: Genetic advance.

2.3. Realized and correlated response to selection:

After two cycles of pedigree selection the realized and correlated response of selection for PY/P was increased in populations I and II by (40.42, 98.16, 32.58, 107.5%) and (108.38, 174.74, 83.11, 148.59%) compared with the best parent, mid parents, sample the bulk and check cv. (Sweet 2), respectively. Such increase accompanied by increase in NB/P by (76.90, 121.13, 16.47, 112.28 %)

Gudadinni et al.(2017), Pathak et al.(2019), Yumkhaibam et al.(2019), Pandey et al.(2023) and Kumar et al.(2024) which reported high heritability for yield/plant, supported the results of high heritability observed for yield/plant in this study.

In the present investigation, the range of genetic advance values was arranged from (0.28 and 0.23%) to (88.88 and 66.19 %) for all the characters in the 1st cycle and from (0.23 and 0.26%) to (23.20 and 21.92 %) in the 2nd cycle for population I and II respectively, **Table (2)**. The highest estimates of genetic advance were recorded for PY/P. High heritability coupled with high genetic advance was recorded for PY/P which indicates presence of additive gene action and demands for population improvement by selection. Similar results were also reported by Gudadinni et al. (2017), Bhardwaj et al. (2020), Jagadeesh et al. (2023).

and (97.77, 147.21, 52.39, 137.32%), DF by (7.74, 24.4, 7.26, 2.26%) and (16.99, 29.71, 4.33, 1.13%), PL by (-0.70, 2.97, 5.74, 11.31%) and (9.15, 9.62, 6.69, 13.62%), SP by (0.40, 3.50, -7.80, -3.64%) and (0.52, 9.36, 0.93, 8.17%) also, in PW by (5.54, 7.19, -5.38, 5.54%) and (7.62, 7.62, -3.52, 7.62%) for the 1st and 2nd populations respectively, **Table (3)**. The results were in agreement with those recorded by El-Dakkak et al. (2014) and Rashwan and El-Shaieny (2016).



Table (3). Realized and correlated response to pedigree selection for pod yield measured in percentage from best parent, mid parent, bulk and check cv. (Sweet 2) in both populations I and II of peas.

Pop. No.	Cycle	Item	PL	PW	NS/P	SP	100-SW	DF	NB/P	SL	PY/P
Population I	C1	B.P.	-4.02	12.42	-12.24	27.79	11.76	1.46	59.66	25.01	10.55
		M.P.	-1.84	18.53	-9.02	30.11	26.10	16.05	83.03	40.30	55.07
		Bulk	2.76	26.43	-1.32	27.90	62.70	5.28	32.62	-5.19	29.81
		Check	2.20	21.17	-9.90	17.32	26.40	-3.79	54.87	23.08	62.76
	C2	B.P.	-0.70	5.54	-9.81	0.40	-21.33	7.74	76.90	3.01	40.42
		M.P.	2.97	7.19	-6.07	3.50	-11.58	24.40	121.13	16.06	98.16
		Bulk	5.74	-5.38	4.71	-7.80	-4.38	7.26	16.47	-15.28	32.58
		Check	11.31	5.54	-0.79	-3.64	-11.97	2.26	112.28	-4.59	107.50
		Population II	C1	B.P.	3.01	16.37	-8.93	3.52	15.15	15.07	41.61
M.P.	5.08	17.58		-7.60	12.13	22.35	25.06	58.84	22.78	56.16	
Bulk	3.01	29.37		3.64	9.21	46.03	-2.98	11.52	-11.45	75.64	
Check	4.81	25.42		-10.54	8.29	30.23	-2.79	30.60	20.36	41.19	
C2	B.P.	9.15	7.62	-3.34	0.52	-1.75	16.99	97.77	-20.22	108.38	
	M.P.	9.62	7.62	-0.17	9.36	3.42	29.71	147.21	-2.66	174.74	
	Bulk	6.69	-3.52	12.68	0.93	4.62	4.33	52.39	-19.41	83.11	
	Check	13.62	7.62	4.51	8.17	9.93	1.13	137.32	-10.39	148.59	

3. Selected families after two cycles of selection:

Table (4) show the mean of the superior selected families after the two cycle of pedigree selection using pod yield/plant as a selection criterion with bulk sample, mid parent, the best parent and check (Sweet 2) in F₅ generation for the I & II populations. For population II, the highest superior families were S1S2*S1-21, S1S2*S1-5 and S1S2*S1-32 for pod yield Fig. (1) and Fig. (2). These families provided the best values for the majority of PY/P and outperformed than the bulk sample, the best parent, check cv. (Sweet 2) and mid parent by (121.0, 151.4, 200.0 and 231.6 %), (94.23, 121.0, 163.7 and 191.4 %) and (79.2, 103.98, 143.3 and 168.9 %), respectively. On the other hand, families S1L*L-7 and S1L*L-16 were significantly higher in pod yield/plant for population I by (43.23, 51.70, 114.1 & 124.2 %) and (34.9, 42.88, 101.61 and 111.13%) than the bulk sample, the best parent, mid parent, and check cv. (Sweet 2), respectively. According

to El-Dakkak et al. (2014) and Mousa et al. (2016) the aforementioned findings are consistent with revealed that solitary plant determination was significant in creating cultivar and that family choice technique could be utilized in early age determination for yield in pea. Kumar et al. (2013) suggested that the study showed that there was a lot of genetic variation for all characteristics, including yield per plant, which showed a wide range of genotype variation. High gauges of heritability, genotypic coefficient of variety and hereditary development were noticed for case pod length, no. of seeds and the yield per plant, which demonstrate the influence of additive gene action on these traits and may be useful for efficient selection. These results are in agreement with those obtained by Zayed 1998, Zayed et al., 1999 (a and b), Zayed et al., 2005, Hussein and El-Dakkak 2009, El-Dakkak et al., 2014, Hussein and Abd El-Hady 2015.

Table (4). Means of the best-selected families from F₅ generation based on pod yield/plant of pea populations I & II.

Pop. No.	Families	PL (cm)	PW (cm)	NS/P	SP	100-SW (g)	DF	NB/P	SL (cm)	PY/P (g)	
Pop. I (F ₅)	S1L*L-3	9.91	1.33	8.63	48.31	42.42	54.67	4.67	89.33	229.08	
	S1L*L-7	11.79	1.50	6.87	39.33	40.30	63.00	6.87	81.67	266.83	
	S1L*L-10	11.78	1.47	7.40	41.61	40.99	64.67	3.67	93.33	242.62	
	S1L*L-16	11.75	1.41	7.73	43.14	42.31	56.00	6.33	79.00	251.31	
	S1L*L-26	10.35	1.12	9.13	48.96	39.20	63.00	5.33	69.00	243.65	
	Bulk	10.53	1.45	7.58	48.07	42.97	56.25	4.56	97.27	186.30	
	MP	10.81	1.28	8.45	42.83	46.47	48.50	2.40	71.00	124.65	
	BP	11.21	1.30	8.80	44.15	52.22	56.00	3.00	79.99	175.89	
	Check (Sweet 2)	10.00	1.30	8.00	46.00	46.67	59.00	2.50	86.36	119.03	
	Pop. II (F ₅)	S1S2*S1-5	11.58	1.43	8.67	48.07	51.56	66.33	6.00	75.70	313.88
		S1S2*S1-13	11.11	1.29	8.25	51.27	47.00	66.00	6.67	76.67	265.37
S1S2*S1-16		10.92	1.18	8.45	54.99	47.66	58.00	7.33	81.00	254.78	
S1S2*S1-21		11.82	1.46	8.20	44.16	49.13	54.44	4.67	75.28	357.14	
S1S2*S1-32		11.34	1.63	8.30	50.56	61.56	54.11	5.00	78.67	289.65	
Bulk		10.65	1.45	7.42	49.30	49.04	57.19	3.89	96.03	161.60	
MP		10.37	1.30	8.38	45.50	49.61	46.00	2.40	79.50	107.70	
BP		10.41	1.30	8.65	49.50	52.22	51.00	3.00	97.00	142.00	
Check (Sweet 2)		10.00	1.30	8.00	46.00	46.67	59.00	2.50	86.36	119.03	

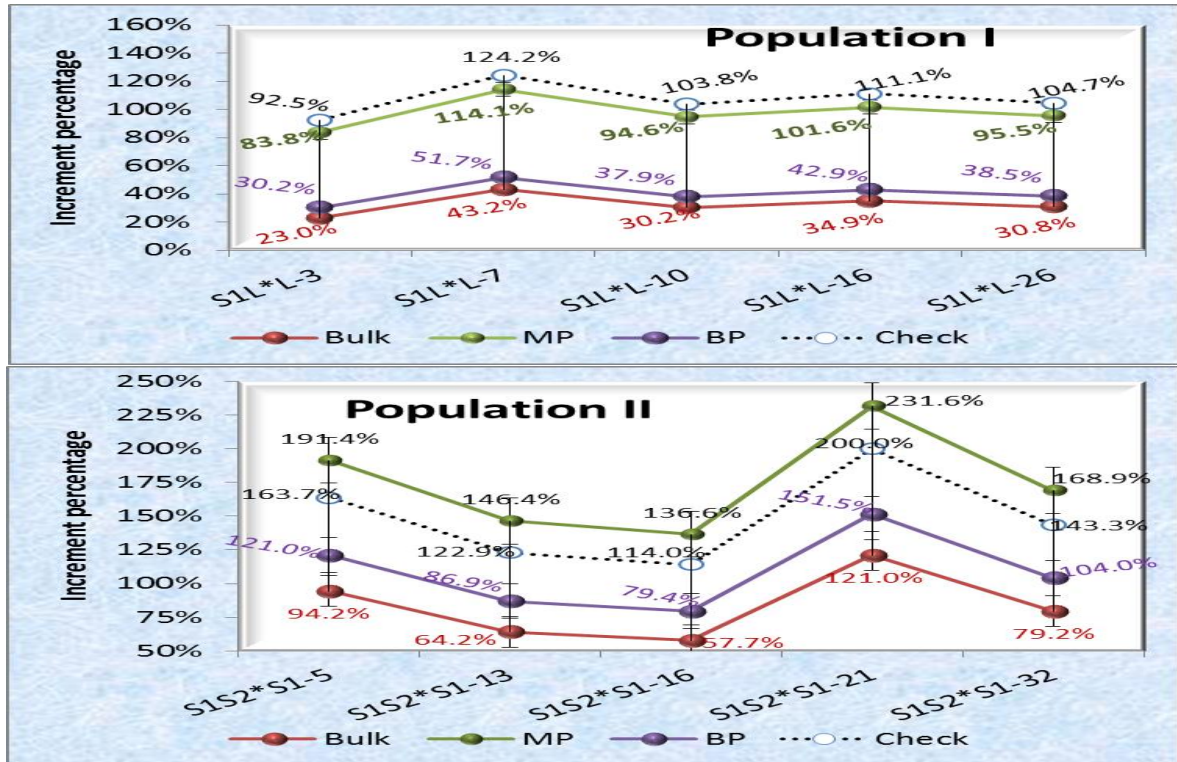


Fig. (1). Increment percentage of pod yield relative to bulck, MP, BP and the check cv. In both the studied populations

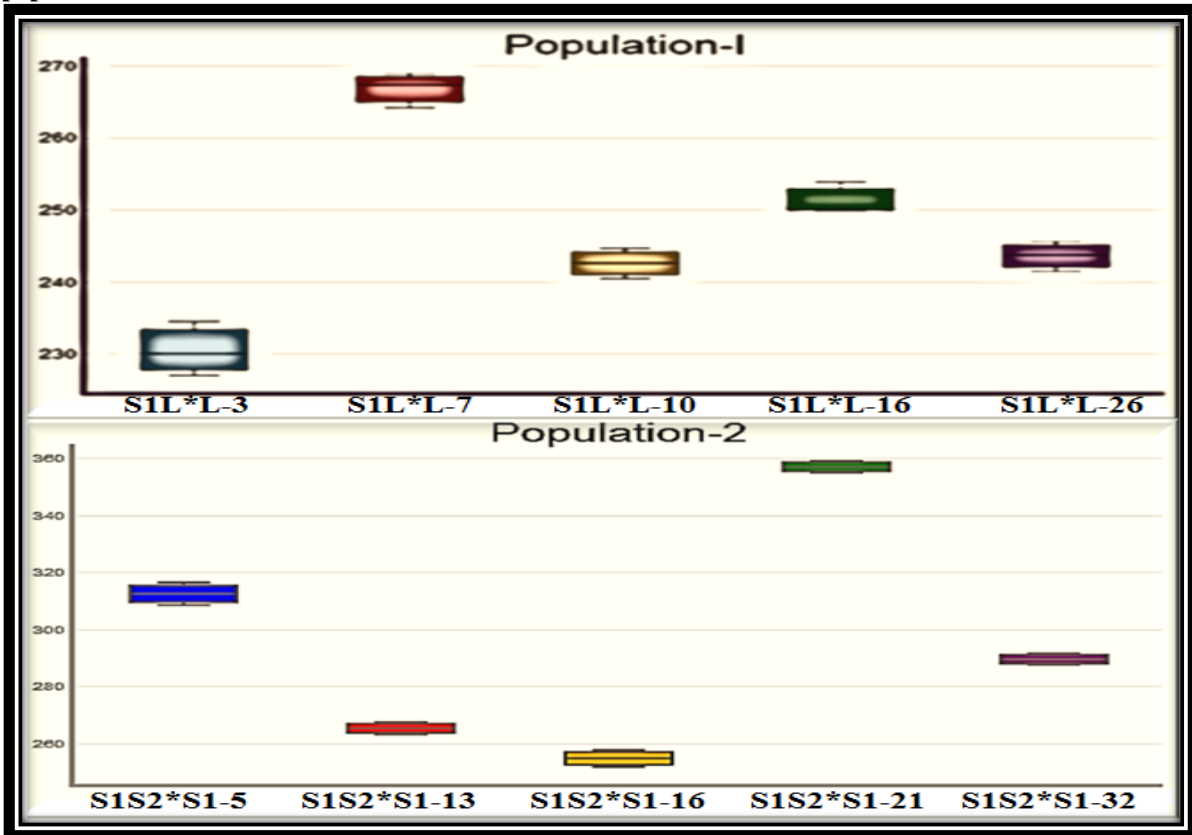


Fig. (2). Box-plot of the five selected lines of both pea populations

The results of the yield trial Table (4) and Fig. (2) revealed that line S1S2*S1-21 significantly overcome the commercial

cultivar Sweet 2 and most other new lines and produced the highest fresh pods yield (357.14 g) and surpassed the check cultivar



by 200%, and was superiority in earliness (54 days) while, the new selected line S1S2*S1-5 which no observed any significant differences with the above new line in yield (313.88 g), was superiority in NS/P and 100-SW followed by the early line S1S2*S1-32 which exhibited high yield (289.65 g) and highest both PW and 100-SW.

The promising line S1S2*S1-21 showed the highest values in most yield components i.e. pod length, pod width, 100-SW, number of seeds/pod and earliness compared with the commercial cultivar with

Table (5). Clustering patterns of new selected pea lines based on (7 vegetative and yield traits).

Clusters	Treatments			
	No.	Percentage	included	
Population I				
I	GROUP1 (Y1 >= 0, Y2 >= 0)	1	20%	S1L*L-10
II	GROUP2 (Y1 >= 0, Y2 < 0)	2	40%	S1L*L-7 & S1L*L-16
III	GROUP3 (Y1 < 0, Y2 < 0)	1	20%	S1L*L-26
IV	GROUP4 (Y1 < 0, Y2 >= 0)	1	20%	S1L*L-3
Population II				
I	GROUP1 (Y1 >= 0, Y2 >= 0)	1	20%	S1S2*S1-32
II	GROUP2 (Y1 >= 0, Y2 < 0)	2	40%	S1S2*S1-5 & S1S2*S1-21
III	GROUP3 (Y1 < 0, Y2 < 0)	1	20%	S1S2*S1-13
IV	GROUP4 (Y1 < 0, Y2 >= 0)	1	20%	S1S2*S1-16

Concerning to the population I (S1L*L), the second cluster having two selected families S1L*L-7 and S1L*L-16 accounting 40% of the best 5-selected families (20% each) beside one selected family were classified in each of 1st (S1L*L-10), 3rd (S1L*L-26) and 4th (S1L*L-3) clusters accounting 60% of total families (20% each) as shown in **Table (5)**. As for the population II (S1S2*S1), the second cluster having two selected families S1S2*S1-5 and S1S2*S1-21 accounting 40% of the best 5-selected families (20% each) beside one selected family were classified in each of 1st (S1S2*S1-32), 3rd (S1S2*S1-13) and 4th (S1S2*S1-16) clusters accounting 60% of total families (20% each). As shown in **Table (6)**, selected families of the clusters I and II of 1st population were dominant in 71 and 57% of the studied traits, respectively compared to the rest of clusters. As for 2nd population, selected families were prevalent in 85.71%, 71.43% and 57.14% of the traits in the first, second and third clusters, respectively.

no significant differences between the two new promising lines S1S2*S1-21 and S1S2*S1-32 in the earliness, NS/P, PW and NB/P. These results are in agreement with those obtained by Zayed (1998), Zayed and Faris (1998), El-Dakkak et al. (2009) and Hussein and El-Dakkak (2009).

Cluster analysis:

Cluster analysis (based on 7 vegetative and yield traits) grouped 5 selected families of peas (populations I and II) into four clusters as shown in **Table (5)** and mean value of all traits in each cluster in **Table (6)**.

Cluster I had highest in cluster means values for Pod length (11.78 and 11.34 cm), Pod width (1.47 and 1.63 cm), No. of branches (3.67 and 5) and Pod yield (242.62 and 289.65 g/plant) in 1st and 2nd population, respectively, addition to stem length (93.33 cm) in Pop.I and both No. of seeds/pod (8.3) and 100-SW (61.65 g) in Pop.II. whereas cluster II exhibited the highest cluster means values for pod length (11.77 and 11.70 cm), pod width (1.46 and 1.45 cm), No. of branches (6.60 and 5.34) and pod yield (259.07 and 335.51 g/plant) in 1st and 2nd population, respectively, addition to 100-SW (50.35 g) in Pop.II., indicating that the presence of the most promising genotypes in both clusters can be extensively used for further pea breeding to obtain high yielding new cultivars with the heaviest 100-seed weight and highest number of seeds. As for clusters II and IV, Pop.II exhibited remarkably high values for most traits comparing with Pop.I.



Table (6). Cluster-wise mean values and percentage increment over the check cv. of different characters among the selected families.

Item	based on:	PC-I		PC-II		PC-III		PC-IV	
		Value	%*	Value	%*	Value	%*	Value	%*
PL	Pop.I	11.78	17.80%	11.77	17.70%	10.35	3.50%	9.91	-0.90%
	Pop.II	11.34	13.40%	11.70	17.00%	11.11	11.10%	10.92	9.20%
PW	Pop.I	1.47	13.08%	1.46	11.92%	1.12	-13.85%	1.33	2.31%
	Pop.II	1.63	25.38%	1.45	11.15%	1.29	-0.77%	1.18	-9.23%
NS/P	Pop.I	7.40	-7.50%	7.30	-8.75%	9.13	14.13%	8.63	7.88%
	Pop.II	8.30	3.75%	8.44	5.44%	8.25	3.13%	8.45	5.62%
100-SW	Pop.I	40.99	-12.17%	41.31	-11.50%	39.20	-16.01%	42.42	-9.11%
	Pop.II	61.56	31.90%	50.35	7.87%	47.00	0.71%	47.66	2.12%
NB/P	Pop.I	3.67	46.80%	6.60	164.0%	5.33	113.2%	4.67	86.80%
	Pop.II	5.00	100.0%	5.34	113.4%	6.67	166.8%	7.33	193.2%
PL	Pop.I	93.33	8.07%	80.34	-6.98%	69.00	-20.10%	89.33	3.44%
	Pop.II	78.67	-8.90%	75.49	-12.59%	76.67	-11.22%	81.00	-6.21%
PY/P	Pop.I	242.62	103.83%	259.07	117.65%	243.65	104.70%	229.08	92.46%
	Pop.II	289.65	143.34%	335.51	181.87%	265.37	122.94%	254.78	114.05%
High	Pop.I		71%		57%		43%		43%
	Pop.II		85.71%		71.43%		57.14%		42.86%
Moderate	Pop.I		0.00%		14.29%		14.29%		42.86%
	Pop.II		0.00%		14.29%		14.29%		57.14%
Low	Pop.I		28.57%		28.57%		42.86%		14.29%
	Pop.II		14.29%		14.29%		28.57%		0.00%

* Increment percentage of selected families than the check cultivar

On the other hand, the current study found that out of the seven studied traits and their contributing, the proportionate contribution of the PY/P towards divergence was found 66.75% and 97.54% for Pop.I and Pop.II, respectively **Fig. (3)**. Therefore, this trait would be the important parameter for selecting divergent genotypes based on the

studied traits. However, the proportionate contribution of the SL towards divergence was found 31.4% in Pop.I and did not contribute more than 0.33% in Pop.II. Therefore, the fresh pod yield/plant trait would be the important parameter for selecting divergent treatments in both populations.

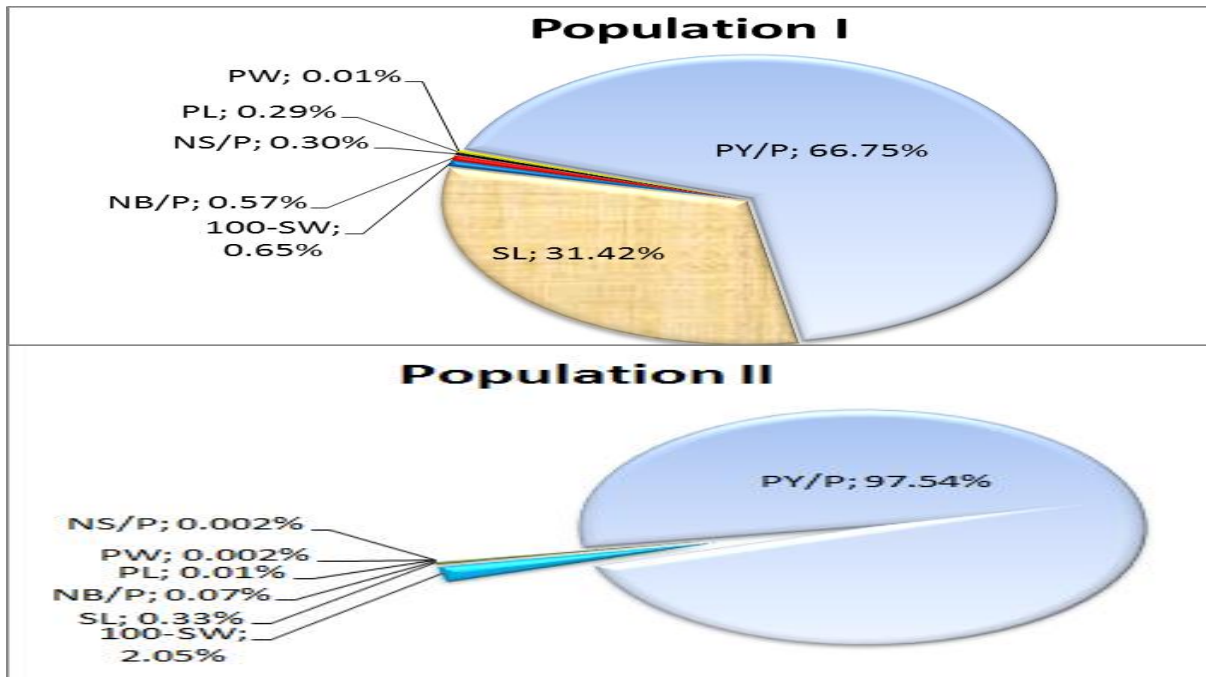


Fig. (3). Graphical representation of the proportionate contribution of studied vegetative growth and productivity traits toward different selected families in 1st (UP) and 2nd populations (Down).

Principal component analysis (PCA):



Principal components analysis (PCA) was conducted to determine which traits were the major sources of variation within the lines groups. The results of the PCA of the pea selected families based on 7 vegetative and productivity traits are presented in **Table (7)**. It is evident from **Fig. (4)** that > 96% of the total variability, (the highest variance when correlating the most relevant components), present among the new selected lines is explained by the first three principal components based on 1st or 2nd population. Out of four principal components, the first two (population I) and three (population II) components axe **Fig. (4)** in the principal component analysis had an Eigenvalue up to above 1.0, presenting 96.8% and 96.3%, respectively of the total variability. These findings are in agreement with Islam et al. (2014). Chowdhury and Mian (1996) reported a similar observation in field pea crop. **Fig. (5)** and **Table (7)** show factor loadings for various studied traits. According to **Table (7)**, the first PC was related to yield and yield traits, i.e., PL (0.48 and 0.46), PW (0.49 and 0.42) and PY/P (0.41 and 0.44), with positive loadings for Pop.I and Pop.II, respectively and exhibited negative loadings for NS/P (-0.52, Pop.I) and NB/P (-0.48, Pop.II). The second PC exhibited a positive effect on

100-SW (0.46 and 0.68) and SL (0.59 and 0.45) for Pop.I and Pop.II, respectively and a negative effect on NB/P (-0.46) and PY/P (-0.41) for Pop.I. The third PC explained variation among genotypes for 100-SW (0.54) in population I and NS/P (0.957) in population II, with a positive factor loading whereas exhibited a negative effect on NB/P (-0.60) for Pop.I. As for the fourth PC, exhibited a positive effect on PL (0.75, Pop.I) and PY/P (0.50, Pop.II) and a negative effect on SL (-0.40 and -0.77) for Pop.I and Pop.II, respectively. The positive and negative effects of factors indicate the association between components and genotypes (Kasyanenko, 1989). Therefore, the abovementioned positive and negative productivity elements also contributed to cluster formation. According to the principal component analysis, NS/P (Pop.I) and NB/P (Pop.II) was selected for the first group; SL (Pop.I) and 100-SW (Pop.II) was selected for the second group; NB/P (Pop.I) and NS/P (Pop.II) was selected for the third group as well as PL (Pop.I) and SL (Pop.II) was selected for the fourth group. During the differentiation of genotypes into clusters, it was found that the contributions of the four major components were greater than those of the other components.

Table (7). Principal component analysis for different traits in the two populations.

Variables/Factors	PC _{F1}	PC _{F2}	PC _{F3}	PC _{F4}
1st population				
PL	0.4835	-0.0582	0.219	0.7462
PW	0.4853	0.2525	-0.0325	-0.2148
NS/P	-0.5243	-0.058	-0.1164	0.1765
100-SW	0.0839	0.457	0.5393	0.3357
NB/P	0.2222	-0.4598	-0.604	-0.2749
SL	0.1804	0.5857	0.1559	-0.3953
PY/P	0.4086	-0.4077	0.0415	-0.1463
2nd population				
PL	0.4602	-0.2454	0.1381	-0.2213
PW	0.4154	0.4081	0.0857	0.2393
NS/P	-0.1179	-0.0672	0.957	-0.0652
100-SW	0.2271	0.6836	0.1794	0.1048
NB/P	-0.4783	-0.138	0.1412	0.1773
SL	-0.3556	0.4472	-0.0632	-0.7744
PY/P	0.4416	-0.2871	0.0408	0.4973

PC_{F1}, PC_{F2}, PC_{F3}, PC_{F4}: loading factors.

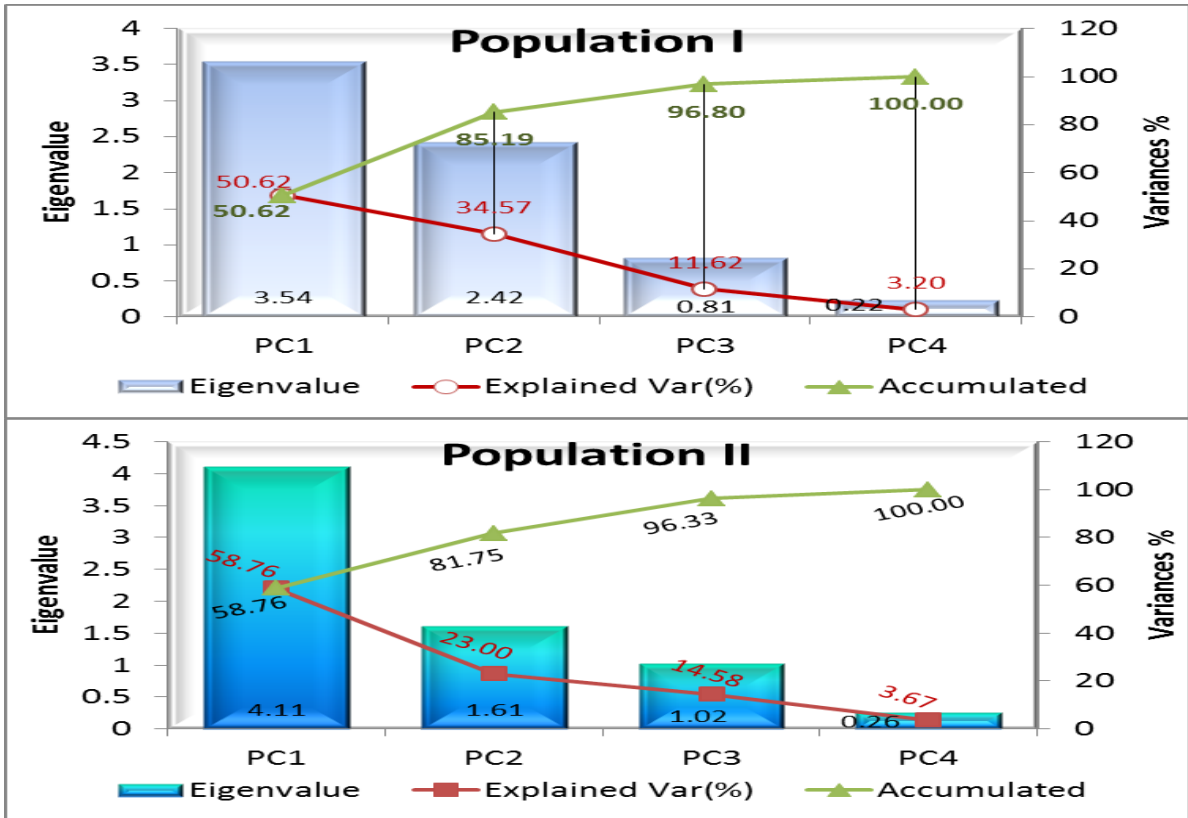


Fig. (4). Scree plot of Eigen values, explained (%) and accumulative variability (%) for 7 parameters of new 10 selected pea lines from two populations (5 lines each).

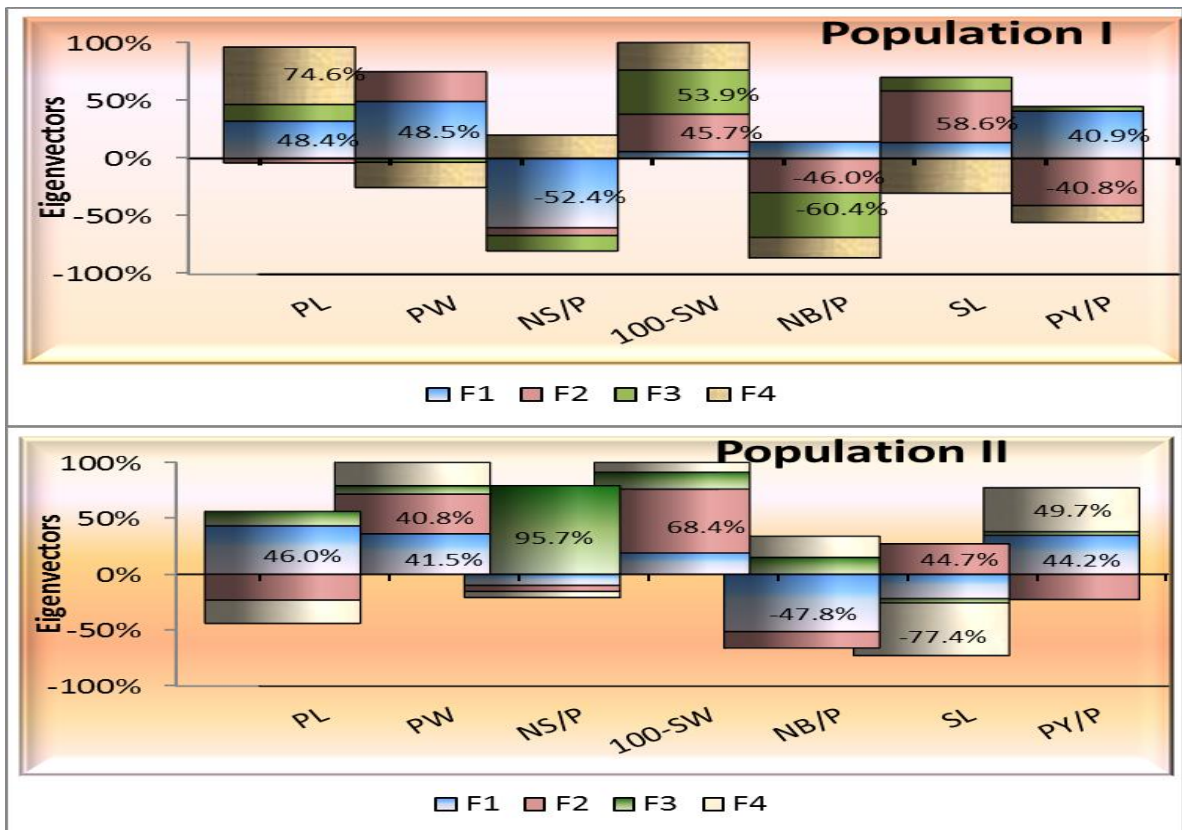


Fig. (5). Scree plot of Eigen vector for 7 parameters of new 5 selected pea families.

The results obtained from biplot-PCA Fig. (6) indicated the presence of high variations among the studied selected lines based on the two populations data of

studied traits resulting in amplitude that may appear their effects the future breeding program.

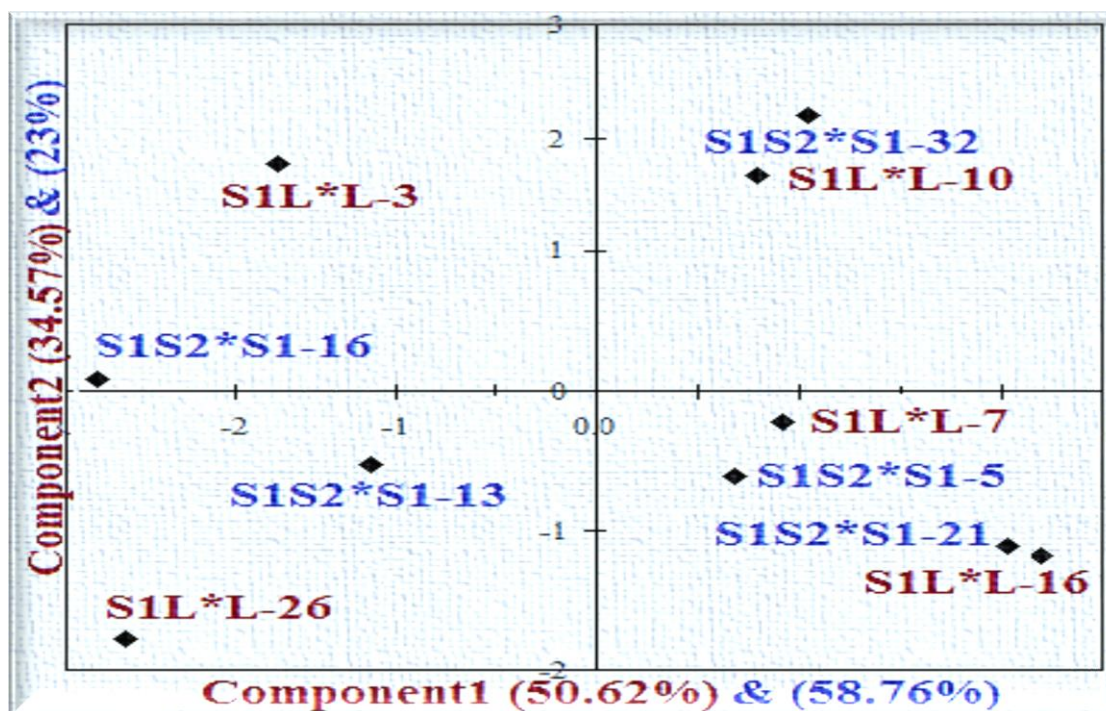


Fig. (6). Principal component bi-plot of 10 selected new pea lines from the two populations (Pop.I and Pop.II) based on 7 morphological traits (under) where, the blue color.

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تحسين بعض صفات المحصول بالانتخاب في بعض عشائر التهجين الرجعي للبسلة

هاله صدقي عبداللاه موسى وأبوبكر عبد العظيم عبده الدقاق وأحمد حلمي حسين

معهد بحوث البساتين - مركز البحوث الزراعية - الجيزة - مصر

أجريت هذه الدراسة في محطة بحوث شنديويل التابعة لمركز البحوث الزراعية بمصر. خلال ثلاث مواسم شتوية 2020/2019، 2021/2020 و 2022/2021، تم استخدام عشائر الجيل الثالث الناتجة من التهجين الرجعي بين ثلاثة أصناف من البسلة لتحسين إنتاجية محصول القرون باستخدام دورتين من الانتخاب وذلك من خلال دراسة المقاييس الوراثية الرئيسية وهي معامل الاختلاف الوراثي والمظهري ودرجة التوريث والتقدم الوراثي والاستجابة للانتخاب و تم تقديرهم في كلا من الجيل الانعزالي الرابع والخامس. ووجد ان قيم معامل الاختلاف الوراثي والمظهري كانت مرتفعة لمحصول القرون ومكوناته، مما يشير إلى وجود تباين عالي أقل تأثيراً بالبيئة. بالإضافة إلى ذلك، تم قياس درجة التوريث وكانت مرتفعة مقترنة بالتقدم الوراثي المرتفع في صفات المحصول ومكوناته مما يشير إلى أن هذه الصفات يتم التحكم فيها وراثياً من خلال الفعل الجيني الإضافي وبالتالي امكانية استخدامها لتحسين إنتاجية البسلة عن طريق الانتخاب. أوضحت النتائج أن أفضل العائلات المتفوقة لصفة محصول النبات بالنسبة للعشيرة الثانية هي العائلات رقم 21 و 5 و 32 والتي كانت اعلى من العينة المجمعَة وأفضل الاباء والصنف الاختباري (سويت 2) ومتوسط الاباء بنسبة (121.0 و 151.4 و 200.0 و 231.6%) و (94.23 و 121.0 و 163.7 و 191.4%) و (79.2 و 104.0 و 143.3 و 168.9%) على التوالي. ومن ناحية أخرى، كانت العائلات رقم 7 و 16 أعلى معنوياً في محصول النبات للعشيرة الأولى من العينة المجمعَة وأفضل الاباء ومتوسط الاباء والصنف الاختباري (سويت 2) بنسبة (43.23 و 51.70 و 114.1 و 124.2%) و (34.9 و 42.88 و 101.61 و 111.13%) على التوالي وبالتالي يمكن استخدام هذه العائلات في برامج تربية البسلة لتحسين إنتاجية القرون.