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Improvement of some new pea (*Pisum sativum* L.) Lines by pedigree selection

Raafat M. Galal^{1*}, Ahmed G. Mohamed², and Gamal A. Zayed²

¹Horticulture Department (Vegetable), Faculty of Agric., Beni-Suef University, Beni-Suef, **Egypt**.

²Vegetable Department, Horticulture Research Institute, Agricultural Research Center, Giza, **Egypt**

*Correspondence: drraafatgalal@agr.bsu.edu.eg, drraafatgalal@gmail.com Received 01-10-2019, Revised: 28-10-2019, Accepted: 05-11-2019 e-Published: 16-11-2019

Pedigree selection method for three pea (*Pisum sativum* L.) populations i.e. Palmoral x Jaguar (population I), Master-B x Little Marvel (population II) and Master-B x Jaguar (population III) were applied on the base populations (F3) to F6 generation across three selection cycles during four successive winter seasons from 2015/2016 to 2018/2019 at Sids Horticulture Research Station, Beni-Suef Governorate, Horticulture Research Institute, Agriculture Research Center, Egypt. Results illustrated highly significant differences among the families for all studied traits in all selection cycles. Both PJ-1 and PJ-6 developing pea lines, possessed the highest for pod yield / feddan, number of pods / plant and plant height as well as each of pod length, number of seeds/ pod and pod weight for PJ-1 line and both surpassed the highest check cultivars, Entesar 1 and Entesar 2. The pea line PL-28 have earliness for flowering and high values in each of pod length, number of seeds/ pod and pod weight with medium yield. Therefore, these lines are recommended as new cultivars. After three cycles of pedigree procedure increased the GCV/PCV% in number of seeds/pod, pod weight and seed yield /plant in pop I, pod weight in pop II and all traits in pop III except flowering and yield which slightly decreased from 91.3, 91.1 and 91 % after the first cycle to 90.4, 89.9 and 89.9% after the 3rd cycle of selection in flowering trait of Pop I, Pop II and Pop III, respectively, and from 85.1 and 87.4% in yield trait of pop II and Pop III, respectively

Keywords: Pea (*Pisum sativum* L.), yield components, pedigree selection, heritability, genetic advance.

INTRODUCTION

Pea (*Pisum sativum* L.) is considered one of the most important legume crops, in Egypt. Many researchers used selection to obtain new yielding lines of pulse crops. Stelling and Ebmeyer (1990) found that efficiency of dried pea yield selection was not significantly increased in early generations by indirect selection. Ron et al (2005) selected some garden pea lines from single plants superior in earliness and pod quality. Nossier (2007) indicated that it is possible to select new green pea lines for high yield and high quality using pedigree selection method. Hamed (2012) found that the means increased by selection for all

studied traits. Selection procedure led to increase pea traits means, i.e. number of days to flowering, green pods yield per plant, no. of pods per plant, no. of seeds per pod and pod length. Ghobary (2009) developed new lines and cultivars of pea through pedigree selection methods. The three lines i.e. MG 4-31, MG 12-19 and MG 15-1 were exceeded for the final fresh seed yield/plant above the highest check cv. (Victory Frizer) by 57.1, 55.0 and 37.0%, respectively. High significant differences among the studied lines for all studied traits. The studied lines showed pods per plant ranging from 9.0 to 35.0 pods with mean 15.1 pods. The lines 4-31, 4-29 and 11-10 possessed

the highest values for pod length and recorded 11.1, 10.1 and 9.4 cm. Lines were ranges from 6.0 to 7.8 seed with mean 6.8 seed per pod. Lines 4-29, 4-31, 11-10, 12-19 and 15-1 showed the earliest flowering plants, highest number of pods, seeds weight and fresh seed yield per plant. Bhnan (2013) used pedigree selection method for selection of some new lines of pea for high productivity and good pod characteristics, which is considered as new cultivars. Mehaet and Erean (2013) reported that number of pods/plant had the greatest direct and indirect effects on green-pod yield. Pod length showed significant direct effect on yield. Pal and Singh (2013) found that the genotype VRP-345 recorded highest values for plant height (173.50 cm), days to 50% flowering (41.70 days). The maximum pod length (9.29 cm). The genotype VRP-190 recorded maximum of number of pods /plant (47.00). Seeds number of seeds /pod was ranged from 5.60 to 8.70. Green pods yield/plant ranged from 74.48 to 240.72 g. El-Dakkak et al. (2015) found that both new pea Lines, Sh/H1/2008 and Sh/L18/2009, were distinctive in earliness and fresh pods yield compared with the other tested lines and/or check cvs across the five tested seasons. The promising line Sh/H1/2008 is earliness and the promising line Sh/L18/2009 produced the highest fresh pods yield (4.948 ton/fed.) and line Sh/H1/2008 was the earliest genotype. Elsadek et al. (2017) found that highly significant differences among genotypes for most of the studied characteristics. Selection program resulted in genotypes or lines given symbols of H3, G7, N1, N3, G2, G1 and K2 that considered promising lines. These lines have good pods traits, higher productivity and earliness of flowering.

In plant breeding, the estimation of variance components and broad sense heritability are very important in genetic analysis of quantitative traits. Shinde (2000) and Sureja and Sharma (2000) revealed that yield/plant had high heritability values coupled with high percentage of genetic advance indicating greater scope for selection in pea. In Egypt, Nosser (2002), Hamed (2005), Zayed et al. (2005), Salib(2006), Galal (2014) and El-Dakkak et al. (2014) estimated broad sense heritability in garden pea as moderate to high being 63.4% to 94.23% for number of days to flowering, 37.9% to 86.0% for number of green pods/plant, meanwhile, it was low to moderate being 14.67% to 53.6% for number of seeds/pod. Gupta et al (2006), Singh and Singh (2006), Sardana et al. (2007), Fikreselassie (2012) and Siddika et al (2013) found high heritability in most

characters studied with high genetic advance for plant height, pod length and seed yield, the phenotypic coefficients of variation were higher than genotypic coefficients of variation in all the characters studied. Broad sense heritability (BSH) of plant length was high in the broad sense (Bora et al., 2009, Kumari et al., 2009 and Galal, 2014). Also, High BSH estimates were observed for green pod yield trait (Bora et al., 2009, Choudhary et al., 2010, Singh, 2010 and El-Dakkak et al., 2014). Choudhary et al. (2010) and Singh et al. (2012) estimated high values of heritability in the broad sense indicating good scope for selection for number of pods/plant trait.

The main objective of this study was to improve garden pea cultivars by selection in early generations using breeding program such as a pedigree method. Study the genetic variability and broad sense heritability for some economic characters.

MATERIALS AND METHODS

This study was carried out at Sids Horticulture Research Station, Beni-Suef Governorate, belong to Horticulture Research Institute, Agricultural Research Center, Giza, Egypt, during four successive winter seasons of 2015/2016, 2016/2017, 2017/2018 and 2018/2019 to estimate the response of pedigree selection in early generations of pea (*Pisum sativum* L.) crosses. Three F₃ populations of pea, viz. Pop. I (Palmoral x Jaguar), Pop. II (Master-B x little Marvel) and Pop. III (Master-B x Jaguar), produced by Galal (2014), were used as the main genetic materials for this study. In the winter season of 2015/2016 (October 18th), the 500 F₃-plants from each population, in which twenty rows of 25 plants each, were sown with plants spaced 20 cm within rows set 70 cm apart. Also, the parents of each population in addition to both local check cultivars Entsar1 and Entsar2 were grown alongside in three rows for each. Pedigree selection was applied in each population. All different agricultural practices i.e. irrigation, fertilization and pest management were applied as recommended by Egyptian Ministry of Agriculture. For each population, selected the best plants out of the 500 plants (selection intensity 10%) were tagged. At the end of the growing season, selfed seeds on each selected plant (selected F₄ seeds) were picked and saved. The selfed seed of each selected plant was considered the seeds of the first cycle of pedigree selection for pod length, number of seeds per pod, average green pod weight and number of pods per plant in addition to

earliness for each population. In the winter season of 2016/2017 (October 15th), the 50 F₄ selected families of each population in addition to the parents and the check cultivars (Entesar1 and Entesar2) were sown in a randomized complete blocks design with four replications. Each family was two rows 5 m long, 0.7 m width and 0.2 m between plants. Data were recorded as mentioned previously. The 10 best F₄ plants of each selection criterion (selection intensity 20%) were saved to give seeds of the second cycle of pedigree selection. In the winter season of 2017/2018 (October 16th), the F₅-selected families for each population were sown along with the parents and both local check cultivars in a randomized complete block design of four replications. The 6 best plants were tagged and selfed to give seeds of the third cycle of pedigree selection (F₆ families). In the winter season of 2018/2019 (October 15th), the six F₆ selected families covering all populations (three for population I, one for population II and two for population III) with the parents and the check cultivars (Entesar 1 and Entesar 2) were sown and evaluated in separate experiments. A randomized complete block design of four replications was applied. Plants were sown in rows 70 cm apart and 10 cm between hills. The harvest date was about 1st week of April in the four winter seasons of 2015/2016, 2016/2017, 2017/2018 and 2018/2019.

Statistical analysis:

Data were recorded for individual plants on a random sample of ten guarded plants from each family in all generations. The means of the ten plants were subjected to the statistical and genetically analyses for the following traits: plant height, number of days to flowering, pod length, number of seeds/pod, pod weight, number of pods/plant and seed yield/plant. The collected data were statistically analyzed according to the method described by Snedecor and Cochran (1981). Means for F₆ generation were compared using Duncan's multiple range test as published by Duncan (1955). All statistical analyses were performed using analysis of variance technique by means of MSTATC computer software package (Freed et al., 1991). Broad sense heritability (h²) was estimated according to Allard (1960) and Falconer (1989). Heritability based on Stanfield (1983) $0 \leq x \leq 0.2$ = low, $0.2 \leq x \leq 0.5$ = medium and $x > 0.50$ = high. Phenotypic (PCV%) and genotypic (GCV) Coefficient of variability were calculated according to Singh and Chaudhury

(1985). Genetic advance (GA) was calculated with the method suggested by Johnson et al. (1955) as: $GA = K \times \delta^2g / \sqrt{\delta^2ph}$, where: K= 1.76 and 1.40, constant (On the basis of intensity of the selection 10 and 20%). Genetic advance as percent of mean (expected genetic advance) $GAM \% = (GA / X) \times 100$. GAM% based on Hadiati et al. (2003), 0 - 7% = low, 7 - 14% = medium and > 14,1 = high

RESULTS AND DISCUSSION

Base populations:

The overall mean of the base materials without applying any selection procedure for No. of pods /plant in the three populations were 37.0, 30.7, 28.3 in population I, II and III, respectively (Table 1)

Table 1; Mean performance of the studied traits in the base population of pea populations I, II and III.

Traits	Base materials (F ₃)		
	I	II	III
Plant height (cm)	93.67	69.67	80.67
No. of days to flowering	60.67	40.67	64.00
Pod length(cm)	7.93	8.50	6.60
No. of seeds/pod	7.63	7.33	6.03
Pod weight (g)	4.17	3.77	3.53
No. of pods/plant	37.00	30.67	28.33
Seed yield /plant (g)	47.00	38.33	39.60

Analysis of variance:

Analysis of variance for each of F₄, F₅ and F₆ families for all studied traits of the three populations are presented in Tables 2, 3 and 4. The mean squares indicated highly significant differences between genotypes for all studied characters in all selection cycles.

Mean performance:

After applying the pedigree selection, the overall mean of the selected families for no. of pods /plant ranged from 39.7, 34.3 and 30.7 in the 1st cycle to 46.0, 39.7 and 40.8 in the 3rd cycle in population I, II and III, respectively. The means performance for F₄, F₅ and F₆ families and their parents for all studied traits of the three populations are presented in Tables 2, 3 and 4.

Table 2; Analysis of variance (MS) and Mean performance of selected families in the three selection cycles along with parents and check cultivars of pea population I.

Cycle number	Traits	MS	Selected families	P ₁	P ₂	Local check cvs.	
				Palmaral	Jaguar	Entesar1	Entesar2
C ₁ (F ₄)	Plant height	658.50 **	99.00	86.67	82.67	58.00	89.00
	days to flowering	422.58 **	58.67	66.33	59.00	39.00	60.33
	Pod length	1.41 **	8.23	7.93	8.37	9.93	10.90
	No. of seeds/pod	5.21 **	7.93	7.10	7.60	8.53	8.33
	Pod weight	0.71 **	4.47	5.17	5.17	5.23	5.37
	No. of pods/plant	16.65 **	39.67	41.00	42.00	35.00	42.67
	Seed yield	36.20 **	48.27	40.33	40.17	38.33	42.00
C ₂ (F ₅)	Plant height	386.92 **	101.33	86.50	82.00	57.67	88.33
	days to flowering	335.99**	57.33	65.87	59.00	38.33	61.33
	Pod length	1.68 **	8.70	8.10	8.30	10.00	10.90
	No. of seeds/pod	5.40 **	8.23	7.40	7.67	8.63	8.30
	Pod weight	0.65 **	4.73	5.03	5.27	5.47	5.20
	No. of pods/plant	49.20 **	42.00	41.00	42.60	37.00	44.33
	Seed yield	22.50 **	50.33	40.37	41.50	37.83	43.33
C ₃ (F ₆)	Plant height	482.96 **	108.33	87.33	83.0	58.97	89.97
	days to flowering	316.08**	58.30	65.47	58.40	38.60	60.10
	Pod length	1.83 **	9.10	7.90	8.13	10.53	11.23
	No. of seeds/pod	7.40 **	8.20	7.60	7.60	8.70	8.40
	Pod weight	1.27 **	5.00	5.20	5.40	5.60	5.40
	No. of pods/plant	60.85 **	46.00	41.50	44.30	38.50	44.90
	Seed yield	12.20 **	53.00	41.43	41.73	38.50	44.20

**= highly significant at P < 0.01.

Table 3; Analysis of variance (MS) and Mean performance of selected families in the three selection cycles along with parents and check cultivars of pea population II.

Cycle number	Traits	MS	Selected families	P ₁	P ₂	Local check cvs.	
				Master-B	Little Marvel	Entesar1	Entesar2
C ₁ (F ₄)	Plant height	270.59 **	73.33	57.67	55.00	58.00	89.00
	days to flowering	283.57**	38.00	37.00	40.00	39.00	60.33
	Pod length	1.70 **	9.00	8.30	7.00	9.93	10.90
	No. of seeds/pod	5.00 **	7.80	7.77	6.10	8.53	8.33
	Pod weight	0.59 **	4.17	4.17	4.40	5.23	5.37
	No. of pods/plant	48.83 **	34.33	35.33	29.50	35.00	42.67
	Seed yield	84.00 **	40.33	34.63	28.63	38.33	42.00
C ₂ (F ₅)	Plant height	236.97 **	75.33	57.00	56.76	57.67	88.33
	days to flowering	320.23**	36.83	37.50	43.00	38.33	61.33
	Pod length	1.41 **	9.23	8.57	6.20	10.00	10.90
	No. of seeds/pod	5.30 **	8.00	7.70	6.70	8.63	8.30
	Pod weight	0.79 **	4.63	4.27	4.67	5.47	5.20
	No. of pods/plant	38.76 **	37.00	35.13	29.90	37.00	44.33
	Seed yield	16.90 **	43.00	34.73	29.00	37.83	43.33
C ₃ (F ₆)	Plant height	266.67 **	80.10	60.03	59.53	58.97	89.97
	days to flowering	305.17**	34.90	37.60	42.00	38.60	60.10
	Pod length	1.21 **	9.83	9.06	7.37	10.53	11.23
	No. of seeds/pod	6.00 **	8.30	7.90	6.50	8.70	8.40
	Pod weight	1.23 **	5.00	4.60	4.40	5.60	5.40
	No. of pods/plant	49.50 **	39.70	36.00	29.50	38.50	44.90
	Seed yield	56.90 **	45.80	35.27	30.20	38.50	44.17

** = highly significant at $P < 0.01$.

Table 4; Analysis of variance (MS) and Mean performance of selected families in the three selection cycles along with parents and check cultivars of pea population III.

Cycle number	Traits	MS	Selected families	P ₁	P ₂	Local check cvs.	
				Master-B	Jaguar	Entesar1	Entesar2
C ₁ (F ₄)	Plant height	279.98 **	84.33	57.67	82.67	58.00	89.00
	days to flowering	463.60**	62.33	37.00	59.00	39.00	60.33
	Pod length	0.74 **	7.47	8.30	8.37	9.93	10.90
	No. of seeds/pod	5.70 **	6.37	7.77	7.60	8.53	8.33
	Pod weight	0.61 **	4.00	4.17	5.17	5.23	5.37
	No. of pods/plant	14.78 **	30.67	35.33	42.00	35.00	42.67
	Seed yield	57.00 **	40.67	34.63	40.17	38.33	42.00
C ₂ (F ₅)	Plant height	270.91 **	85.67	57.00	82.00	57.67	88.33
	days to flowering	523.23**	64.83	37.50	59.00	38.33	61.33
	Pod length	0.72 **	7.80	8.57	8.30	10.00	10.90
	No. of seeds/pod	4.90 **	6.70	7.70	7.67	8.63	8.30
	Pod weight	0.70 **	4.50	4.27	5.27	5.47	5.20
	No. of pods/plant	17.87 **	35.33	35.13	42.60	37.00	44.33
	Seed yield	40.00 **	43.67	34.73	41.50	37.83	43.33
C ₃ (F ₆)	Plant height	319.05 **	89.10	60.03	83.00	58.97	89.07
	days to flowering	468.82**	63.50	37.60	58.40	38.60	60.10
	Pod length	0.96 **	8.13	9.03	8.13	10.53	11.23
	No. of seeds/pod	7.00 **	7.10	7.90	7.60	8.70	8.40
	Pod weight	0.88 **	4.90	4.60	5.40	5.60	5.40
	No. of pods/plant	21.00 **	40.80	36.10	44.30	38.50	44.90
	Seed yield	25.90 **	46.90	35.27	41.73	38.50	44.17

** = highly significant at $P < 0.01$.

For earliness, selected families of population I were earlier than parental genotypes and the check cv. Entesar2 in the 3 selection cycles, while Selected families of population II showed the earliness over parental genotypes and both check cvs (Entesar1 and Entesar2) after both 2nd and 3rd selection cycles. On the other hand, no. of pods, seed yield /plant and plant height of pop I exceeded the values of parental genotypes and both check cvs (Entesar1 and Entesar2) after 3rd selection cycle. For population II, no. of pods and plant height exceeded the values of parental genotypes and Entesar1 in addition to seed yield /plant over all parental and check genotypes. Seed yield/plant and plant height of pop III exceeded the values of parental genotypes and check genotypes. These results reflecting the effectiveness of pedigree selection method to improve these traits. After the 3rd cycle of selection, the population I gave high means of all studied traits than the 1st cycle (Table 2). The population I gave the means of F₆ generation were higher than its parents for all traits except pod weight, while was higher than check cultivars for plant height, number of pods\plant and seed yield\plant, while Entesar 1 cultivar was the best in

earliness, pod weight and number of seeds/pod. On the other hand, Entesar 2 cultivar possessed pod length. After three selection cycles, the selected families of population II (Table 3) gave the higher means than for parents in all traits, while was the best in earliness and seed yield\plant over check cultivars. While the check cultivar Entesar 1 possessed number of seeds /pod and pod weight. On the other hand, Entesar 2 cultivar possessed plant height, pod length and number of pods\plant.

As in Table 4, the population III gave the means of F₆ generation (after 3rd selection cycle) were higher for each of plant height, number of days to flowering and seed yield\plant than parents and check cultivars. While the check cultivar Entesar1 possessed both number of seeds\pod and pod weight. On the other hand, Entesar2 cultivar possessed pod length and number of pods\plant. The mean values for F₆ generation (after 3rd selection cycle) were higher than means of F₅, F₄ and F₃ generations for all traits in three populations.

Genetic parameters:

Estimates of genetic parameters like genotypic (GCV) and phenotypic (PCV) coefficient

of variability, broad-sense heritability (h^2), genetic advance as percent of mean (GAM%) from selection as percentage of mean for different characters have been presented in (Tables 5-7). Data revealed that the magnitude of phenotypic (PCV) and genotypic (GCV) coefficient of variances varied from all traits. The highest GCV and PCV were observed after the 3rd cycle of selection for all studied traits in the three populations except both pod length and number of pods/plant in the pop. I, indicating the high potential for effective selection (Burton, 1952). Hamed (2012) and El-Dakkak et al. (2014) found that most studied traits had high GCV and PCV. Small differences were observed between GCV% and PCV% in most generations of the three populations in most traits, indicating the importance of the genetic effects in controlling the inheritance of these traits. Our results showed that most studied traits had high GCV/PCV percent in all selection cycles for the three populations. After the 3rd selection cycle, such values ranged from 68.3% for pod weight (Pop III) to 96.8% for plant height of the same population (Pop III). These results indicated that about 68% 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. Generally, after three cycles of pedigree procedure increased the GCV/PCV in number of seeds/pod, pod weight and seed yield /plant in pop I, pod weight in pop II and all traits in pop III except flowering and yield which slightly decreased from 91.3, 91.1 and 91 % after the first cycle to 90.4, 89.9 and 89.9% after the 3rd cycle of selection in flowering trait of Pop I, Pop II and Pop III, respectively, and from 85.1 and 87.4% in yield trait of pop II and Pop III, respectively (Tables 5-7).

The heritable fraction of the variation provides the base of the plant breeder for selection on the phenotypic performances. Results revealed that broad sense heritability (h^2) improved considerably for all studied traits from the C₁ to C₃ selection cycles. Broad sense heritability based on Stanfield (1983), after the three cycles of selection were moderate magnitude for number of seeds/pod (48% and 48.3%) for populations II and III, respectively as well as pod weight (46.7%) for population III and high for each of all other traits in all populations. Again, the highest estimates of broad sense heritability after 3rd selection cycle were recorded for all studied traits except number of seeds/pod of pop II and both number of seeds/pod and pod weight of pop III which

exhibited moderate values. High heritability indicated rapidly progress through selection for these traits. These results indicated that the environmental factors had a small effect on the inheritance of such traits and the selection, based on mean, would be successful in improving these traits. The high heritability of these parameters indicated that selection of them would be more effective than the other parameters. The F₆ selections displayed considerable and almost comparable genetic advance in seed yield/plant which ranged from 10.9 to 14.8 % (Pop. I), from 8.3 to 17.8% (Pop II) and from 9.9 to 12.6 (Pop. III) in the three cycles of pedigree selection (Tables 5-7). Genetic advance based on Hadiati et al., (2003), after the three cycles of selection were low for both pod length (6%) and number of pods/plant (6.1%) of pop I, while it was of moderate magnitude for each of pod length (10.7 and 10.2 %), pod weight (10.3 and 9.2) and number of pods/plant (13.1 and 9.8) for populations II and III, respectively and high for each of seed yield /plant (14.8, 17.8 and 12.6 %), number of seeds/pod (18.9, 16.1 and 20.4 %), plant height (21.6, 27.9 and 25.3 %) and number of days to flowering (25.2, 41.2 and 28.0 %) for populations I, II and III, respectively (Tables 5-7). Johnson et al., (1955) reported that heritability values along with estimates of genetic advance were more useful than heritability alone in predicting the effect of selection.

Generally, high heritability was obtained for plant height, number of days to flowering and seed yield along with high genetic advance as percent of the mean (GAM%). Therefore, selection for these characters would be more effective because it has high heritability and genetic advance%. On the basis of the results obtained in the present study it can be concluded that the range of variability was quite considerable for almost all studied characters among different genotypes. These results are in agreement partially with those obtained by Shinde (2000), Sureja and Sharma (2000) Nosser (2002), Hamed (2005), Zayed et al., (2005), Gupta et al., (2006), Salib(2006), Singh and Singh (2006), Sardana et al., (2007), Fikreselassie (2012), Siddika et al., (2013), Kumari et al., (2009), El-Dakkak et al., (2014) and Galal (2014).

Selected families after three cycles of selection

The selected families mean after the third cycle of pedigree selection for selection criteria are presented in Table 8. Families PJ-1 and PJ-6

were higher in pod yield/plant by (20.0 and 14.0%), (42.93 and 35.7%) and (15.4 and 9.6%), number of pods /plant (13.5 and 7.9%), (26.5 and 20.3%) and (8.5 and 3.1%), plant height (21.7 and 27.9%), (76.1 and 85.1%) and (15.4 and 21.2%) and number of days to flowering (-11.6 and -

4.2%), (41.7 and 53.6%) and (-9 and -1.3%), than mid parent, check-1 and check-2, respectively, in population I (Table 8).

Table 5; Different genetic parameters for seven quantitative traits after three selection cycles (C) of pea population I.

Cycle number	Item	plant height	No. of days to flowering	Pod length	No. of seeds/pod	Pod weight	No. of pods/plant	Seed yield /plant
C ₁	GCV%	17.6	16.2	5.8	12.8	9.4	6.0	7.2
	PCV%	18.1	17.7	6.9	20.0	13.0	8.0	8.3
	GCV/ PCV	97.1	91.3	83.7	63.8	72.8	75.4	86.6
	h ²	94.2	83.3	70.0	40.7	52.9	57.0	75.0
	Genetic advance%	25.9	26.0	8.1	14.9	12.1	8.0	10.9
C ₂	GCV%	17.5	16.8	5.7	13.1	8.2	5.2	8.2
	PCV%	18.1	18.5	6.7	20.2	11.7	6.8	9.5
	GCV/ PCV	96.9	90.8	85.6	64.8	70.7	76.1	86.0
	h ²	93.9	82.5	73.3	41.9	50.0	58.0	73.9
	Genetic advance%	24.9	26.9	8.2	15.8	10.3	6.9	12.4
C ₃	GCV%	17.2	15.9	4.6	13.5	8.25	4.86	9.43
	PCV%	17.9	17.5	5.5	18.7	11.0	6.8	10.6
	GCV/ PCV	96.0	90.4	83.7	71.9	75.3	71.4	89.0
	h ²	92.2	81.7	70.0	51.7	56.7	51.0	79.4
	Genetic advance%	21.6	25.2	6.0	18.9	10.9	6.1	14.8

GCV and PCV = genotypic and phenotypic coefficient of variability. h²= broad-sense heritability.

Table 6; Different genetic parameters for seven quantitative traits after three selection cycles (C) of pea population II.

Cycle number	Item	plant height	No. of days to flowering	Pod length	No. of seeds/pod	Pod weight	No. of pods/plant	Seed yield /plant
C ₁	GCV%	18.5	23.4	8.4	12.7	10.7	10.3	5.6
	PCV%	19.2	25.6	9.9	18.3	15.1	14.0	6.5
	GCV/ PCV	96.6	91.1	84.7	69.4	70.7	73.7	85.1
	h ²	93.4	82.9	71.7	48.2	50.0	54.4	72.5
	Genetic advance%	32.4	37.4	10.9	17.8	13.3	13.4	8.3
C ₂	GCV%	18.7	25.8	9.1	12.4	8.1	10.7	11.6
	PCV%	19.5	28.2	10.5	16.8	11.9	14.6	13.6
	GCV/ PCV	95.9	91.5	87	73.6	68.3	73.6	85.8
	h ²	91.9	83.6	75.7	54.2	46.7	54.1	73.5
	Genetic advance%	30.7	41.5	12.0	18.5	9.8	13.9	17.6
C ₃	GCV%	19.0	26.0	8.5	11.2	8.0	10.3	12.0
	PCV%	19.7	29.0	10.1	16.1	11.0	14.2	14.2
	GCV/ PCV	96.3	89.9	84.5	69.3	73.1	72.3	84.5
	h ²	92.8	80.8	71.4	48.0	53.3	52.4	71.4
	Genetic advance%	27.9	41.2	10.7	16.1	10.3	13.1	17.8

GCV and PCV = genotypic and phenotypic coefficient of variability. h²= broad-sense heritability

Table 7; Different genetic parameters for seven quantitative traits after three selection cycles (C) of pea population III.

Cycle number	Item	plant height	No. of days to flowering	Pod length	No. of seeds/pod	Pod weight	No. of pods/plant	Seed yield /plant
C ₁	GCV%	15.2	18.2	11.3	14.6	9.7	13.0	6.4
	PCV%	15.8	20	13.1	23.1	14.8	16.9	7.3
	GCV/ PCV	96.3	91	86.2	63.3	65.4	76.9	87.4
	h ²	92.7	82.8	74.3	40.0	42.9	59.3	76.4
	Genetic advance%	30.9	29.2	14.6	19.2	11.2	17.7	9.9
C ₂	GCV%	14.7	18.3	9.8	6.8	8.9	6.5	7.5
	PCV%	15.4	20.4	11.6	9.4	14.1	8.6	8.7
	GCV/ PCV	95.5	89.6	84.7	72.0	63.3	75.5	84.1
	h ²	91.1	80.2	71.7	51.9	40.0	57.0	70.7
	Genetic advance%	28.6	28.8	12.6	10	9.9	8.7	11.0
C ₃	GCV%	14.1	17.7	7.7	14.6	7.6	7.2	8.5
	PCV%	14.6	19.7	8.9	21.0	11.2	9.3	10
	GCV/ PCV	96.8	89.9	86.5	69.5	68.3	77.3	84.8
	h ²	93.7	80.8	75.0	48.3	46.7	59.7	72.0
	Genetic advance%	25.3	28.0	10.2	20.4	9.2	9.8	12.6

GCV and PCV = genotypic and phenotypic coefficient of variability. h²= broad-sense heritability.

Table 8: Selected families mean after three cycles of pedigree selection method in the three populations.

Genotypes		Plant height (cm)	No. of days to flowering	Pod length (cm)	No. of seeds / pod	Pod weight (g)	No. of pods /plant	Pods yield (ton/feddan)
Origin	Promising							
P ₁ xP ₂	PJ-1	103.7 c	54.7 d	10.7 b	9.3 a	5.8 a	48.7 a	6.0 a
	PJ-6	109.0 b	59.3 c	8.2 ef	6.7 e	3.8 d	46.3 b	5.7 b
	PJ-12	113.0 a	63.3 b	8.4 e	8.5 b	5.3 b	43.0 cd	4.8 e
P ₃ xP ₄	ML-28	80.7 g	34.7 g	10.3 c	8.7 b	5.5 ab	41.0 de	4.7 ef
P ₃ xP ₂	MJ-36	92.0 d	60.3 c	8.1 f	7.3 d	4.5 c	41.7 de	4.7 ef
	MJ-44	86.7 ef	66.7 a	8.1 f	6.8 e	5.3 b	40.0 ef	4.4 fg
Parents	P ₁	87.4 e	65.4 a	7.9 f	7.6 cd	5.2 b	41.5 de	4.9 de
	P ₂	83.0 fg	58.4 c	8.1 f	7.6 cd	5.4 b	44.3 bc	5.1 cd
	P ₃	60.1 h	37.4 f	9.1 d	7.9 c	4.6 c	36.1 g	4.2 g
	P ₄	59.6 h	42.0 e	7.4 g	6.5 e	4.4 c	29.5 h	3.8 h
Check cvs.	Entesar 1	58.9 h	38.6 f	10.6 b	8.7 b	5.6 ab	38.5 f	4.2 g
	Entesar 2	89.9 de	60.1 c	11.5 a	8.4 b	5.4 b	44.9 bc	5.2 c
C.V. %		2.55	2.01	1.78	2.37	4.11	2.99	3.69

Palmoral: P₁ Jaguar : P₂ Master-B: P₃ Little Marvel: P₄

Means within column with different letters differ significantly at P ≤ 0.05 according to Duncan's Multiple Range test at the 5% level.

For population II, family ML-28 was significantly higher in pod yield/plant by (17.5, 11.9 and -9.6%), number of pods /plant (25, 6.5 and -8.7%), Pod weight (22.2, -1.8 and 1.9%), number of seeds/ pod (20.8, 0.0 and 3.6%), number of days to flowering (-12.6, -10.1 and -42.3%), and plant height (34.7, 37.0 and -10.2%), than mid parent, check-1 and check-2, respectively, in population II (Table 8). From population III, Families MJ-36 and MJ-44 were higher in pod yield/plant by (17.5 and 0%), (11.9 and 4.8%) and (-9.6 and -15.4%), number of pods /plant (3.7 and -0.5%), (8.3 and 3.9%) and (-7.1 and -10.9%), plant height (28.5 and 21.1%), (56.2 and 47.2%) and (2.3 and -3.6%) and number of days to flowering (25.9 and 39.2%), (56.2 and 72.8%) and (0.3 and 11%) than mid parent, check-1 and check-2, respectively (Table 8). Abdou et al. (1999 a & b) indicated that great selection gain for green pod yield (68%) was expected. Green pod yield was suggested to be the most efficient criterion to score cultivar productivity. Records on stem length should be considered independently in selection. They showed that pod yield could be efficiently selected through pod length. However, direct selection for pod yield was also effective.

The means F6 selected families (Promising lines);

their parents and the check cultivars for all studied traits of the all populations are presented in Table 8. For plant height, the lines PJ-1, PJ-6 and PJ-12 were superiority over all lines, parents and check cultivars. While the line ML-28 was the earliest genotypes followed by both Master-B and Entesar 1 cvs. Each of Entesar 2, PJ-1, Entesar1 and ML-28 genotypes were the tallest for green pod in descending order. The line PJ-1 was the greatest number of seeds per pod followed by PL-28, Entesar 1, PJ-12 and Entesar 2 genotypes. The line PJ-1 was the greatest weight for green pod followed by PL-28 and Entesar1 genotypes. The lines PJ-1 and PJ-6 were superiority in number of pods/plant and pod yield/feddan. Generally, the pea lines PJ-1 and PJ-6 possessed the highest for pod yield per feddan, number of pods per plant and plant height addition to pod length, number of seeds/ pod and pod weight for PJ-1 line. The lines PJ-1 and PJ-6 surpassed the highest parents and check cultivars (Entesar 1 and Entesar 2). The pea line PL-28 was selected for earliness over all new lines, parents and check

cvs as well as for its pod yield/plant over the average of all parents and equally for mid-check cvs. For this, the new line PL-28 have earliness for flowering and high values in each of pod length, number of seeds/ pod and pod weight with medium yield. Therefore, these lines are recommended as new cultivars. Many investigators among them Kuo Chun Yi (1998), Ghobary (2009), Pal and Singh (2013) and El-Dakkak et al., (2015) developed new lines and cultivars of pea.

CONCLUSION

In conclusion, it could be concluded that the two lines PJ-1 and PJ-6 were superior for yield of green pods compared with all lines and commercial varieties cultivated in Egypt. Also, pea line PL-28 was selected for earliness. Therefore, these lines were recommended as new cultivars.

CONFLICT OF INTEREST

The authors declared that present study was performed in absence of any conflict of interest.

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AUTHOR CONTRIBUTIONS

All authors contributed equally in all parts of this study.

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