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IMPROVING EARLINESS AND PRODUCTIVITY FOR PEA BY SELECTION UNDER SOHAG CONDITIONS

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Abstract

The present study was carried out at Shandaweel Research Station during the three winter seasons of 2019/20, 2020/21 and 2021/22 using two F_2 populations of Master-Hindy x Super-2 (population I) and Progress x Sweet-2 (Population II) to improve earliness, yield traits using pedigree selection for two cycles. The genetic parameters were estimated in the F_3 and F_4 generations. The main genetic parameters studied were the phenotypic (PCV) and genotypic (GCV) coefficient of variance, response to selection, selection differential and broad sense heritability. The measurements recorded were (number of days to 50% flowering, number of branches/plant, pod length (cm), number of seeds/pod, number of pods/plant, pod felling%, fresh pods weight and fresh seeds weight (g)). Results showed slight values repugnancy differences were observed between PCV and GCV in all generations, indicating the importance of the genetic effects in controlling the inheritance of the studies traits. Therefore, these traits might be more genotypically predominant and it would be possible to achieve further improvement in them. Heritability were recorded from 88.42 to 90.81% for fresh pods weight. Increasing obtained for fresh pods weight/plant by 147.27% and 132.69% over Master (better check parent) in population I and population II, respectively, and also, for fresh seeds weight/plant by 87.79 and 85.11% in population I and population II, respectively.

Keywords; *Pisum sativum*, selection parameters, heritability, genetic advance.

INTRODUCTION

Pea (*Pisum sativum* L.) is considered one of the most important legume crops grown in the winter season because of its high nutritional value. Abd El-Hady (2003) in a study of inheritance of yield and its components, found that heritability showed high values for number of days to 50% flowering, plant height, pod length, number of seeds/pod, and dry seed yield. He found that the difference between PCV and GCV was narrow with respect to heritability, calculates of broad sense heritability values were 78.91% in the F₄ and 77.50% in the F₅ generation. Hussien *et al.*, (2003) indicated that selection from F₃, F₄ and F₅ generation is an effective method to develop high yield lines of cowpea. El-Dakkak (2005) found that the genotypic coefficients of variability (GCV) were large compared to the phenotypic coefficients of variability (PCV) in all studied traits except seed set, and genotypic plays a major role in the behavior of tested genotypes for most studied characters, also, broad sense heritability was high for most studied traits. Ron *et al.*, (2005) selected some garden pea lines from single plants superior in earliness and pod quality. Nosser (2007) indicated that it is possible to select new green pea lines for high quality using pedigree selection method, indicate that dry seed yield (kg/fed.) could be increased by selection for pod length and number of pods/plant. They also showed high values for days to 50% flowering, plant height, pod length, number of seeds/pod, and dry seed yield. The estimates of the predicted response to selection were too high because heritability estimates obtained were upward. The realized gain as percentage of the mid parent was highly significant (17.74 and 36.30%) in the F₄ and F₅ generations, respectively. Also, it was highly significant (-26.85 and -2.13%) in the F₄ and F₅ generations, respectively, as percentage of the check cultivar. El-Dakkak *et al.*, (2009) indicated that Master-B cv. could be used as progenitors for studied traits in genetic improvement selection in the segregating generations. Hussien and El-Dakkak (2009) found that all traits significantly differed among the breeding lines in all studied traits except number of seeds/pod, selection for seed

yield increased seeds weight by 26.11%, pod weight by 17.63% and number of pods/plant by 7.92% over the best parent sample, also found the realized gain as percentage of the mid-parent was highly significant in studied character. Mousa (2010) indicated that broad sense heritability was high for all studied traits. Nosser (2011) selected four homogenous F₇ snap bean lines superior in the characteristics of total green yield and number of pods/plant compared with their parents using pedigree selection. Hamed (2012) estimated the actual response to selection and the expected genetic gain through selection technique and also, study the genetic variability and broad sense heritability for some economic characters (number of Days to 50% flowering, yield/plant, number of pods/plant, number of seeds/pod and pod length). Results showed that all the studied traits means increased by selection. Also, broad sense heritability was high values in all traits indicating that these characteristics can be improved through selection based on phenotypic observations in early segregating generations in garden pea except green yield/plant and number of pods/plant traits. El-Dakkak (2016) found small differences were observed between PCV and GCV for all traits with high heritability coupled with high genetic advance observed for most studied traits. The estimates of broad sense heritability after the end cycle of selection were medium for number of seeds/pod in the wrinkled (52.33%), round (50.65%) of green seed and only round of mottled seed (56.74%). Tasnim *et al.*, (2022) studied the genetic relationship between different traits for commercial cultivation and to assess selection criteria in pea breeding program in five inbred parents. Results revealed that phenotypic coefficients of variation (PCV) were close to genotypic coefficients of variation (GCV) for all the characters indicating less impact of the environment and potentiality of selection. The present study aimed to improve some local cultivars of pea by selection in the some generations using breeding programs.

MATERIALS AND METHODS

The present study was carried out during 2019/20, 2020/21 and 2021/22 growing winter

seasons, at Shandaweel Agric. Res. Stat., Agric. Res. Center, Ministry of Agric., Egypt. The basic materials used in this study consisted of two F₂ Populations stemmed from crosses between four cultivars of pea (*Pisum sativum* L.), namely; Master-Hindy, Super-2, Progress and Sweet-2. The two F₂-populations, viz. Population I (Master-Hindy x Super-2) and Population II (Progress x Sweet-2) were raised in 2019/2020 season 15 October, 2019. Each population was represented by 500 plants. In the winter season of 2020/21, 70 F₃ families of each population from the progeny of each selected plants and an equal number of seeds composited from each F₂ plants to give F₃ bulk seeds, in addition to both parents and the check cultivars were grown in three replications in a randomized complete block design with plants spaced 15 cm apart between hills and were sown in 60 cm within rows. Observations and selection were made between and within the F₃ populations to choose the best plants (early flowering, dwarf plant height, tall pod length, high fresh pod weight and fresh seed weight). In winter season of 2021/22, 13-selected F₄ families of the two populations, F₄-bulk sample, the parents, and the check cultivars were evaluated. A randomized complete block design of three replications was applied. Plants were sown in rows 60 cm apart and 15 cm between hills. The sowing date was October 20 for both F₃ and F₄ generatios and harvest date was through January (early lines) and through February and March (Medium and late lines) of the three winter seasons.

Statistical procedures:

Data were recorded for individual plants on a random sample of ten guarded plants from each family in F₃ and F₄ generations. The means of the ten plants were subjected to statistical and genetic analyses for the following characteristics (number of days to 50% flowering, number of branches/plant, pod length (cm), number of seeds/pod, pod felling%, number of pods/plant, fresh pods weight (g/plant) and fresh seeds weight (g/plant). The genetic parameters were estimated in F₃ and F₄ generations. Realized response to selection were expressed as percent change in the population mean relative to mid-parents and cultivars check (Falconer 1981). Heritability in broad sense " $H_b = \sigma^2_g / \sigma^2_p$ " The Phenotypic (PCV) and genotypic (GCV) Coefficient of variations were estimated according to Burton (1952).

RESULTS AND DISCUSSION

Mean performance:

The mean performance of the two populations, parents and check cultivars of pea in the F₂, F₃ and F₄ generations in all the studied traits is shown in Table (1). Grand mean values of selected populations in F₃ and F₄ generations were decreased compared with the previous generation in the two populations in the flowering trait, reflecting the effectiveness of pedigree selection method to improve these traits. Compared with the check cultivars, the selected generations in the two populations were earlier than cultivar Balmoral, but later than cultivar Master in all seasons.

Table 1: Mean performance of the two populations, parents and check cultivars of peas in the F₂, F₃ and F₄ generations in all studied traits.

	Population I (Master-Hindy x Super-2)	Population II (Progress x Sweet-2)	Master- Hindy	Super-2	Progress	Sweet-2	Checks	
							Master	Balmoral
Number of days to 50% flowering								
F ₂ (Base)	48.97	52.03	--	--	--	--	--	--
F ₃	45.24	46.26	51.63	48.33	62.30	50.00	35.60	55.30
F ₄	42.07	45.82	52.53	47.33	63.30	49.00	34.33	54.30
Number of branches/plant								
F ₂ (Base)	3.47	3.35	--	--	--	--	--	--
F ₃	3.46	3.29	2.67	3.67	3.33	3.00	1.80	4.30
F ₄	2.49	2.57	3.13	3.37	3.00	2.67	1.83	4.10
Pod length (cm)								
F ₂ (Base)	10.05	10.72	--	--	--	--	--	--
F ₃	10.13	11.01	9.62	10.33	9.21	10.25	9.60	8.10
F ₄	10.71	10.91	9.82	10.13	9.41	10.00	9.21	8.15
Number of seed/pod								
F ₂ (Base)	7.34	7.76	--	--	--	--	--	--
F ₃	8.80	8.15	8.67	9.13	6.23	8.12	8.20	5.60
F ₄	9.27	8.59	9.15	9.33	7.00	8.23	8.23	5.72
Pod filling %								
F ₂ (Base)	73.03	72.39	--	--	--	--	--	--
F ₃	86.87	74.02	90.12	88.38	67.64	79.22	85.42	69.14
F ₄	86.55	78.74	93.18	92.10	74.39	83.20	89.36	70.18
Number of pods/plant								
F ₂ (Base)	22.12	20.65	--	--	--	--	--	--
F ₃	25.23	24.32	22.00	32.67	28.67	26.67	13.00	31.00
F ₄	26.04	25.64	24.00	33.67	29.67	27.27	14.00	33.00
Fresh pods weight (g/plant)								
F ₂ (Base)	78.68	74.25	--	--	--	--	--	--
F ₃	112.34	105.76	77.01	104.71	91.91	77.51	44.50	73.20
F ₄	114.98	108.20	80.91	108.51	91.01	81.71	46.50	76.20
Fresh seeds weight (g/plant)								
F ₂ (Base)	72.31	69.12	--	--	--	--	--	--
F ₃	83.14	80.07	70.09	77.61	64.68	54.38	24.30	40.80
F ₄	82.25	80.08	72.09	79.61	66.68	57.38	25.70	43.80

These results again indicated that the pedigree selection method was more effective in improving fresh pods and seeds weight/plant by increasing the desired gene frequency. These results are in agreement with those obtained by Abd El-Hady (2003), El-Dakkak *et al.*, (2009), Hussien and El-Dakkak (2009) and Tasnim *et al.*, (2022).

The genetic parameters:

The estimated coefficient of variance C.V% for all studied genotypes concerning studied traits are presented in Table (2). Slight

repugnancy differences were observed between PCV and GCV in all generations, indicating the importance of the genetic effects in controlling the inheritance of the studied traits. These results are in agreement with those obtained by Hussein *et al.*, (2003), El-Dakkak (2005), El-Dakkak (2016) and Tasnim *et al.*, (2022), who reported that the difference between PCV and GCV was narrow concerning GA. However, heritability in broad sense was high for all these cases and in line with the data of PCV and GCV% for both populations.

Table 2. Genetic parameters of the two pea populations in the F₃ and F₄ generations for all studied traits.

Items	No. of days to 50% flowering				Number of branches/plant			
	Population I		Population II		Population I		Population II	
	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄
G.C.V. %	14.99	17.17	16.38	15.56	20.91	47.90	16.66	31.48
P.C.V. %	15.87	18.85	17.29	17.27	24.50	50.52	18.27	33.73
B.S.H%	89.22%	82.98%	89.72%	81.20%	72.87%	89.89%	83.12%	87.09%
	Pod length (cm)				Number of seed/pod			
	Population I		Population II		Population I		Population II	
G.C.V. %	8.04	3.21	7.40	9.23	8.67	6.13	8.02	14.47
P.C.V. %	8.68	3.60	7.89	9.65	9.45	6.67	9.35	15.34
B.S.H%	85.79%	79.19%	87.94%	91.51%	84.10%	84.32%	73.64%	89.05%
	Pod filling %				Number of pods/plant			
	Population I		Population II		Population I		Population II	
G.C.V. %	5.80	6.29	6.96	7.28	46.96	38.31	22.36	26.39
P.C.V. %	6.59	6.76	8.27	7.86	50.07	42.46	24.07	28.66
B.S.H%	77.57%	86.63%	70.81%	85.82%	87.96%	81.40%	86.25%	84.78%
	Fresh pods weight (g/plant)				Fresh seeds weight (g/plant)			
	Population I		Population II		Population I		Population II	
G.C.V. %	16.00	27.31	8.64	30.61	17.41	28.33	12.49	32.76
P.C.V. %	16.79	28.79	9.19	32.34	18.36	29.92	13.23	35.65
B.S.H%	90.81%	89.68%	88.42%	89.59%	89.86%	89.68%	89.07%	84.45%

The broad sense heritability of pod filling% and number of branches/plant were the lowest values among the other traits at the F₃ and F₄ generations. The broad sense heritability of fresh pods weight/plant and fresh seeds weight/plant were higher than the the other studies traits in the F₃ and F₄ generations. These results revealed that these studies traits were mostly controlled by genetic factors and less affected by environmental variations. These results were in line with those obtained by Hussein *et al.*, (2003), El-Dakkak (2005), Hussien and El-Dakkak (2009), Mousa (2010), El-Dakkak (2016) and Tasnim *et al.*, (2022).

Observed direct response to selection:

The realized gain as percentage were highly significant in the F₃ and F₄ generations in the most studied traits, except the number of days to 50% flowering and pod length traits for the bulk population (Table 3). The realized response to selection as a percentage of the mid-parents ranged from -18.57% to -8.24% in the two populations for number of days to 50% flowering. Meanwhile, it ranged from 22.55% to 33.47% as a percentage of the check cultivar Master. However, it ranged from -22.52% to -15.67% as a percentage of the check cultivar Balmoral.

Table 3. The realized response to selection relative to mid-parents and checks populations for all studied traits of the two populations of peas.

Items	Population I		Population II		Population I		Population II	
	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄
	No. of days to 50% flowering				Number of branches/plant			
	Realized response to selection (%) relative to:							
Mid-parents	-19.43**	-18.57**	-7.45**	-8.24**	9.26**	-12.17**	3.89	-20.92**
Bulk population	7.71**	0.17	3.72	2.74	0.58	-27.62**	-1.20	-22.82**
Master	27.08**	22.55**	29.94**	33.47**	92.19**	36.07**	82.78**	40.44**
Balmoral	-18.19**	-22.52**	-16.35**	-15.67**	-19.53**	-39.27**	-23.49**	-37.32**
	Pod length (cm)				Number of seed/pod			
	Realized response to selection (%) relative to:							
Mid-parents	4.08	10.34**	10.34**	9.34**	21.83**	21.71**	-8.44*	8.57*
Bulk population	-6.46*	-1.11	-5.98*	-6.83*	12.39**	18.39**	-11.41**	-6.63**
Master	5.52*	10.98**	14.69**	13.06**	7.32*	12.64**	-0.61	4.37*
Balmoral	25.06**	31.73**	35.93**	34.19**	57.14**	62.06**	45.54**	50.17**
	Pod filling %				Number of pods/plant			
	Realized response to selection (%) relative to:							
Mid-parents	17.47**	10.47**	-17.05**	-0.17	-8.81*	-8.52*	-11.02**	-11.08**
Bulk population	21.23**	20.79**	-5.95*	0.03	23.43**	20.33**	25.10**	28.59**
Master	1.70	1.33	-13.34**	-7.82*	94.08**	86.00**	87.08**	83.14**
Balmoral	25.65**	23.02*	7.07*	11.91**	-18.61**	-21.09**	-21.55**	-22.30**
	Fresh pods weight (g/plant)				Fresh seeds weight (g/plant)			
	Realized response to selection (%) relative to:							
Mid-parents	32.61**	33.14**	16.40**	14.24**	39.66**	34.22**	20.61**	6.89
Bulk population	27.75**	30.75**	32.75**	35.81**	23.43**	22.11**	42.83**	30.02**
Master	152.45**	147.27**	137.66**	132.69**	242.14**	220.04**	266.54**	215.49**
Balmoral	77.75**	73.69**	67.34**	63.44**	103.77**	87.79**	118.31**	85.11**

*, ** = Significant at 0.05 and 0.01% probability levels, respectively.

On the other hand, it ranged from 33.14% to 14.24% of the mid-parents, it ranged from 30.75% to 35.81% as a percentage of the bulk populations, it ranged from 147.27% to 132.69% as a percentage of the check cultivar Master. However, it ranged from 73.69% to 63.44% as a percentage of the check cultivar Balmoral for fresh pods weight/plant trait. The highly sizeable gain obtained in cycle 1 was partially lost in the last cycle. This could be due

to the large and/or the masking effects of the overall mean of the selected families, since the low means cancel the high ones and give a misleading picture of the effect of direct selection in isolating lines for one or more characters. The same results have been reported by Abd El-Hady (2003) and Hussein *et al* (2009).

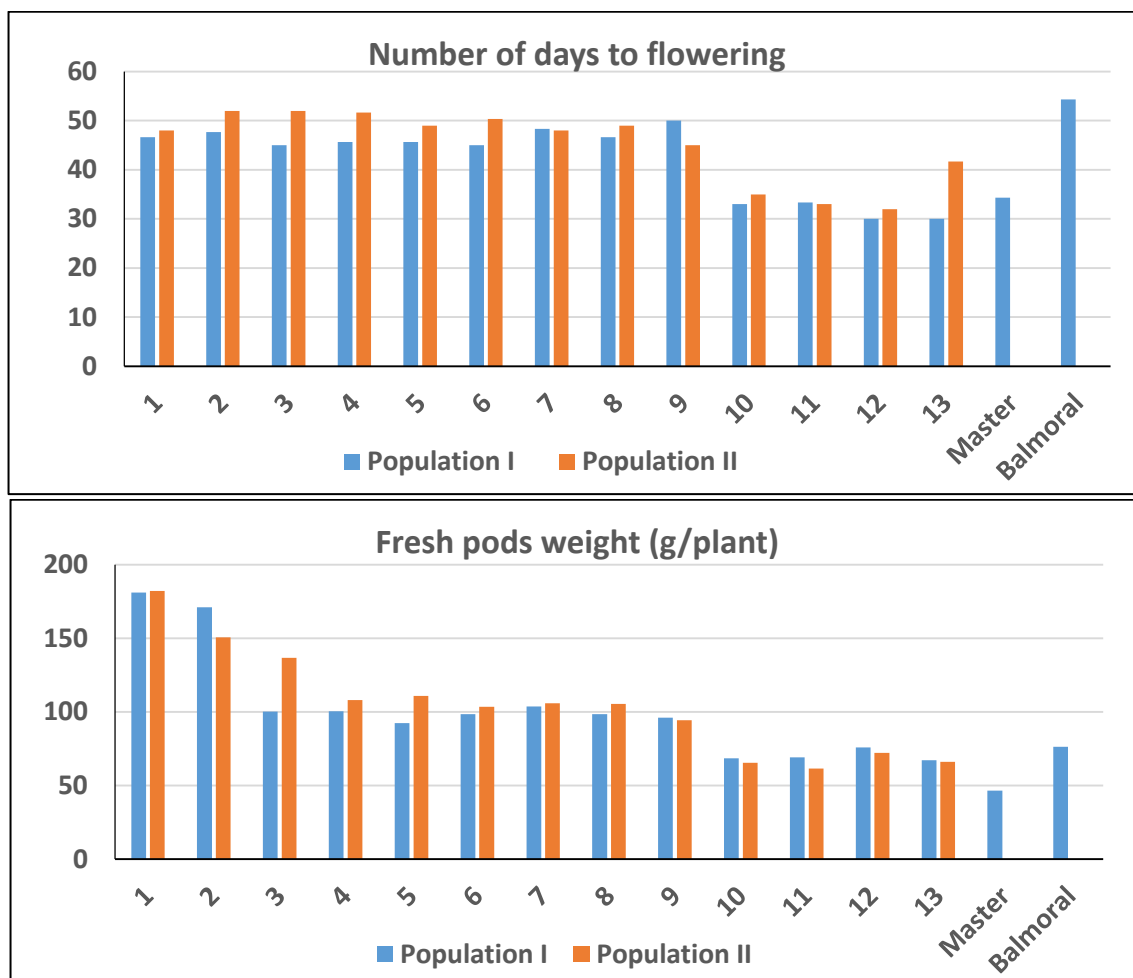


Figure 1. Comparison between promising lines and Master and Balmolar cultivars in terms of number of days to 50% flowering and fresh pods weight (g) in the two populations.

Figure 1 show the most important results of our study, where four promising early pea lines were obtained with higher fresh pod yield than the early comparison cultivar Master, and ten lines were the promising medium-early lines with higher fresh pod yield than the control cultivars Master and Balmoral.

CONCLUSION

From the results obtained from this study, after two cycle selection in two populayions of pea, we can conclude that :

- Four promising early pea lines were obtained with a higher fresh pods yield than the early comparison cultivar Master.

- Ten promising medium-early pea lines were obtained with higher fresh pods yield than the control cultivars Master and Balmoral.

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