

## Selection for productivity and earliness of (*Pisum sativum* L.) under late sowing

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**Abstract:** Productivity and earliness of pea population (Barl X Protor), under late sowing date (5<sup>th</sup> December), were studied for some quantitative characters via selection. Four field experiments were conducted at the Experimental farm of Faculty of Agriculture South Valley University, Qena Governorate, during the four winter seasons (2012/2013 – 2015/2016). Highly significant was detected among generations (F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub>), for all investigated traits. The generations were earlier than the base population (F<sub>2</sub>) by 5.7, 8.5 and 9.5 days respectively, and earlier by 3.5 and 5.5 days for average two parents and check cultivar compared to F<sub>5</sub> generation. Dry seed yield/plant, green seed yield/plant, number of pods/plant, weight of 100-dry seeds, weight of 100-green seeds, shell – out %, number of seeds/pod and pod length traits were increased by 64.15%, 42.8%, 29.14%, 44.33%, 17.65%, 17.65, 10.25% and 2.12%, respectively. In the F<sub>5</sub> generations as compared to F<sub>2</sub>, percentage of response to selection of the mid-parent showed values of -4, 84, -4.05 and -6.41 in the F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> populations, and it was value of -8.81, -11.25 and – 9.94 in F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> generations as percentage of the check cultivar in NDF trait. Slightly differences were observed between PCV% and GCV% in all populations for all studied traits. Estimates of broad sense heritability value ranged from 36.41% in the F<sub>4</sub> populations for NS trait to 99.85% in F<sub>5</sub> population for 100-WGS. These results indicating the importance of the genetic effects in controlling the inheritance of all traits compared to the environmental conditions. the genetic variation and broad sense heritability were high for number of days to flowering and green seed yield/plant in F<sub>3</sub> generation, the genetic improvement could be by selection.

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**Key words:** *Pisum sativum*, GCV%, Heritability, Late sowing date, pedigree selection.

### 1. Introduction

Breeding in (*Pisum sativum* L.) has a significant role in improvement productivity, with large genetically differences among genotypes in yield and its attributes. Generally, various factors effects on pea yielding, such as number of Pods/plant, number of seeds/ pods, weight of seeds/ plant and number of seeds/ plant. Selection one of the traits associated with yielding is the selection of the yield traits, thus contributing high varieties production, high quality, and adapted to various environmental conditions. Peas (*Pisum sativum* L.) are belonging to Fabaceae family, and consider the fourth important cultivated legumes in the world followed by soybean, groundnut, and beans (Hulse, 1994). In Egypt, the total area cultivated for pea in 2013 was 42524 feddans (fed=4200 m<sup>2</sup>) and produced total yields of 181000 tons with average 4.24 ton/fed. (Dep., Agric., Statistics, Ministry of Agriculture, Giza, Egypt). At present, the importance of pea has been increased, to the increasing the consumption of seeds that, canned or frozen. In addition to, green pods that consumption more and more in Egypt, for local consumption and exportation, and all over the world. Breeding for earliness in Peas maximize the economic value of the yield, and make it available in different regions and environments, so

the short life cycles. Genetic improvement and variability in Pea were studied by many authors in different areas of Egypt, Zayed *et al.* 1999; Nosser 2002; Hussien *et al.*, 2003; Mahmoud, 2004; Zayed *et al.* 2005; Nosser 2007; Mousa 2010; Hamed 2012 and El-Dakkak *et al.* 2014. Therefore, the aim of the present investigation to study the genetic analysis and selection for earliness and productivity of pea.

### 2. Materials and Methods

The present study was conducted in four successive seasons (2012/2013, 2013/2014, 2014/2015, 2015/2016) at the Experimental farm, Faculty of Agriculture, South Valley University. Base Population F<sub>2</sub> (Barl x Protor), two parents and check cultivar (Entsar 1) was obtained from Dr. El-Dakkak, A.A.A., Horticulture Research Institute, Agriculture Research Center, Giza, Egypt. Growing seasons, number of selected plants from each populations and steps to implement the experiment were as follows Table 1.

Late sowing date was of 5<sup>th</sup> December every season, single plant were grown on the ridge at 3m length 60 cm in width and plant spaced 25 cm between each other families, parents, check cultivar were grown with three replication in a randomized

complete block design. Data were recorded for individual plant on a random sample of ten guarded plants from population in F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> generations. The means of the ten plants were subjected to the statistical genetic analysis for the following traits:

- 1- Number of days to flowering (NDF).
- 2- Pod length (PL).

- 3- Number of seeds/pod (NSP).
- 4- Shell – out % (SO).
- 5- Weight of 100-green seeds (100-WGS).
- 6- Weight of 100-dry seeds (100-WDS).
- 7- Number of pods/plant (NPP).
- 8- Green seed yield/plant (GSYP).
- 9- Dry seed yield/plant (DSYP).

Table 1: Growing seasons, number of selected plants in different generations.

Seasons	Generations	Number of selected plants	Selection intensity %	Number of plants for every season			Spacing between hills, long row and width ridge
				Barl (P <sub>1</sub> )	Protor (P <sub>2</sub> )	Check Entsar 1	
2012/2013	F <sub>2</sub>	800	Base	-	-	-	-
2013/2014	F <sub>3</sub>	400	50%	3 rows	3 rows	3 rows	25 cm/ 3m/.7 cm
2014/2015	F <sub>4</sub>	160	40%	3 rows	3 rows	3 rows	
2015/2016	F <sub>5</sub>	24	15%	2 rows	2 rows	2 rows	

### Statistical Procedures:

Analysis of variance for randomized complete block design was carried out according to Snedecor and Cochran (1980). The genetic parameters were estimated in F<sub>2</sub>, F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> generations.

Realized response to selection were expressed as percent change in the population mean relative to mid-parent, bulk population and check (Falconer, 1981).

Heritability in broad sense =  $\sigma^2_g / \sigma^2_p$ .

The genotypic (GCV %) and phenotypic (PCV %) coefficient of variability were calculated as  $(\sigma^2_g / \bar{X}) \times 100$  and  $(\sigma^2_p / \bar{X}) \times 100$ , GCV% and PCV% were calculated by Johanson et al. (1995).

### 3. Results and Discussion

Analysis of variance (Table 2) revealed highly significant differences between selected families in F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub>. The means of selected families ranged from 34.5 to 38.3(N), while for P1 ranged from 37.3 to 40.5, and 36 to 40 for P2 see Table 3. However, the means of number of seeds of selected families' ranged 7.37 to 8.0 and from 9.20 to 10.80 for two parents respectively. As for green seed yield/plant the means ranged from 42.8 for P1 to 130.52 for selected families. The Same results were obtained from many researchers (Abdou 1999; Kou 1999; Mahmoud 2004 and El-Dakkak *et al.* 2014), They found that days to flowering ranged from 37.0 to 81.0 days. On the other hand, the results conflicted with (Ishtiaq *et al.* 2001 and Qasim 2000), they reported that earlier flowering and harvesting times (138 and 162 days), respectively.

Table 2: analysis of variance for F3, F4 and F5 populations

Mean Squares						
Families	F3		F4		F5	
Items	MST	MSE	MST	MSE	MST	MSE
1- NDF	44.662**	0.285	54.93**	0.133	130.7**	0.167
2- PL	2.513**	0.025	3.477**	0.009	0.167**	0.003
3- NSP	0.533**	0.175	0.375**	0.138	0.06**	0.015
4- SO	49.64**	0.758	47.74**	0.778	69.36**	0.035
5- 100-WGS	172.5**	0.431	186.03**	0.398	208.9**	0.105
6-100-WDS	55.71**	0.346	107.33**	0.206	211.2**	0.167
7-NPP	26.55**	0.852	41.23**	0.683	28.17**	0.667
8-GSYP	1641.2**	79.5	976.4**	28.98	240.4**	37.32
9-DSUP	79.5**	1.459	174.7**	4.805	83.63**	2.882

The mean of selected families for number of days to flowering (NDF) exceeded that of the P1 by 2.60% and by 6.33 of the mean of P2. Regard to green seed yield/plant (GSYP) the mean of selected families increased by 157.9% of mean P1 and 123.8 for P2 and by 121.56 of check cultivar see Table 4.

The genetic parameter for studied traits of selected families in generations F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> are

shown in table 5. The genetic variation for number of days to flowering ranged from 14.7 to 43.51. AS for pod length the genetic variation ranged from 0.05 for F<sub>5</sub> generation to 0.83 for F<sub>3</sub> generation. In this context, the genetic variation was highest in the F<sub>3</sub> generation compared with F<sub>4</sub> and F<sub>5</sub> generations. Uniformly, genetic coefficient variation ranged from 1.53 for number of seed/pod to 25.29 for shell –out%.

These results are in harmony with those reported by Partap *et al.* 1995; Singh 1995; Ibrahim 2002; Sharma *et al.* 2003; Mahmoud 2004; Nosser 2007; and Hamed 2012.

Estimates of broad sense heritability values were 98.11, 92.28% and 99.62%, in F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> generations for DF trait in Table 5, 97.07, 99.23, 94.8 for PL, 40.54, 36.41, 50.0 for NS, 95.55, 95.27, 99.55 for SO trait, 99.25, 99.36, 99.85 for 100-WGS, 98.16, 99.43, 99.76 for 100-WDS, 90.95, 95.19, 93.22 for 100-WDS, 86.75, 91.60, 86.83 for GSYP, 94.69, 92.18, 90.33 in F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> generations, respectively. These results revealed that all traits were controlled by genetic factors and less affected by the environmental conditions. The Same results were obtained from many researchers such as Abdou 2005; Gupta *et al.*, 1999; Tyagi and Sirvastava 2001; Nosser 2002 Rashwan 2010; Million 2012; Nosser 2007.

The realized response to selection as percentage of the mid-parent (Table 6) showed values of -4, 84, -4.05 and -6.41 in the F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> generations as percentage of the chick cultivar (Entsar 1) in DF trait, for PL showed value 17.17, 14.10, 19.20 and 8.92, 9.53, 13.24, for NS 10.83, 13.63, 14.0 and 3.8, 6.53, 0.25, for SO trait 5.28, 4.47, 3.7 and -27.1, -24.31, -27.13, for 100-WGS -7.79, -9.91, -4.87 and -17.68, -16.54, -9.88, for 100-WDS 5.51, 10.89, 28.57 and 16.67, 13.65, 21.13, for NP 108.75, 136.63, 135.22 and 138.57, 136.63, 164.63, for GSYP 157.65, 218.22, 262.50 and 134.71, 166.06, 235.14, for DSYP 103.25, 167.20, 223.5 and 45.57, 93.96, 143.12% as percentage of the mid-parent and the chick cultivar in the F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub>, respectively. These results are on line with Hamed 2012 and El-Dakkak *et al.* 2014.

Table 3: Range, average for all populations, parents and check cultivar. for all studied traits.

Items	NDF		PL		NS		SO		100-WGS	
	Range	Average	Range	Average	Range	Average	Range	Average	Range	Average
F <sub>2</sub> base population	-	44.0	-	11.97	-	7.18	-	34.80	-	42.3
Families (F <sub>3</sub> -F <sub>5</sub> )	38.3 - 34.5	36.11	11.58-12.23	11.80	7.37-8.0	7.68	44.48-44.23	44.45	48.32-51.37	49.86
P <sub>1</sub>	40.50-37.3	38.26	9.20-10.02	9.70	7.30-8.0	7.6	43.50-47.8	46.00	36.4-42.5	41.10
P <sub>2</sub>	40.0-36.0	37.66	10.6-10.80	10.61	6.0-6.0	6.0	41.0-37.5	39.1	68.4-65.5	66.76
Check	42.0-38.0	40	10.65-10.50	10.58	7.1-8.0	7.43	61.0-60.7	60	58.7-57.0	58.5
Items	100-WDS		NPP		GSYP		DSYP			
F <sub>2</sub> base populate	-	17.9	-	15.0	-	112.9	-	19.0		
Families (F <sub>3</sub> -F <sub>5</sub> )	25.9-32.43	28.33	16.7-21.17	18.93	130.52-197.4	162.87	28.08-53.0	39.76		
P <sub>1</sub>	22.6-23.3	22.73	9.0-10.0	9.33	42.8-50.6	46.6	15.35-18.40	17.01		
P <sub>2</sub>	26.4-27.1	26.43	7.0-8.0	7.33	58.5-58.3	57.13	12.30-14.37	8.89		
Check Cv.	24.7-23.7	23.96	7.0-8.0	7.66	55.6-58.9	58.3	18.18-21.8	19.89		

Table 4: Average of all studied traits for population as well as parents and check cultivar

	Population 1 (Barl x Protor)	Barl (P <sub>1</sub> )	Protor (P <sub>2</sub> )	Check (Entsar1)
No. of days to 50% flowering (DF)				
F <sub>2</sub> (Base)	44.0			
F <sub>3</sub>	38.3	40.50	40.0	42.0
F <sub>4</sub>	35.5	37.0	37.0	40.0
F <sub>5</sub>	34.5	37.3	36.0	38.0
Pod length (cm) (PL)				
F <sub>2</sub> (Base)	11.97			
F <sub>3</sub>	11.58	9.20	10.60	10.65
F <sub>4</sub>	11.61	9.90	10.45	10.60
F <sub>5</sub>	12.23	10.0	10.80	10.50
Number of seeds/ pod (NS)				
F <sub>2</sub> (Base)	7.18			
F <sub>3</sub>	7.37	7.30	6.00	7.10
F <sub>4</sub>	7.67	7.50	6.00	7.20

	Population 1 (Barl x Protor)	Barl (P <sub>1</sub> )	Protor (P <sub>2</sub> )	Check (Entsar1)
F <sub>5</sub>	8.00	8.00	6.00	8.00
	Shell-out% (SO)			
F <sub>2</sub> (Base)	34.80			
F <sub>3</sub>	44.48	43.50	41.00	61.00
F <sub>4</sub>	44.66	45.70	38.80	59.00
F <sub>5</sub>	44.23	47.80	37.50	60.70
	Weight of 100 green seeds (100-WGS)			
F <sub>2</sub> (Base)	42.30			
F <sub>3</sub>	48.32	36.40	68.40	58.70
F <sub>4</sub>	49.91	44.40	66.40	59.80
F <sub>5</sub>	51.37	42.50	65.50	57.00
	Weight of 100 dry seeds (100-WDS)			
F <sub>2</sub> (Base)	17.90			
F <sub>3</sub>	25.90	22.60	26.40	24.70
F <sub>4</sub>	26.67	22.30	25.80	23.50
F <sub>5</sub>	32.43	23.30	27.10	23.70
	Number of pods/plant (NP)			
F <sub>2</sub> (Base)	15.00			
F <sub>3</sub>	16.70	9.00	7.00	7.00
F <sub>4</sub>	18.93	9.00	7.00	8.00
F <sub>5</sub>	21.17	10.00	8.00	8.00
	Green yield/ plant (g) (GSYP)			
F <sub>2</sub> (Base)	112.90			
F <sub>3</sub>	130.52	42.80	58.50	55.60
F <sub>4</sub>	160.70	46.40	54.60	60.40
F <sub>5</sub>	197.40	50.60	58.30	58.90
	Dry seed yield (g) DSYP			
F <sub>2</sub> (Base)	19.0			
F <sub>3</sub>	28.08	15.35	12.30	18.18
F <sub>4</sub>	38.20	17.30	11.30	19.70
F <sub>5</sub>	53.00	18.40	14.37	21.80

Table 5: The genetic parameters of studied traits for F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> generations for population peas.

Items	F <sub>3</sub>	F <sub>4</sub>	F <sub>5</sub>	F <sub>3</sub>	F <sub>4</sub>	F <sub>5</sub>
	No. of days to flowering			Pod length (cm)		
Genetic Variance.	14.79	18.27	43.51	0.83	1.16	0.05
Phenotypic Variance.	15.07	18.40	43.68	0.85	1.17	0.06
P. C. V.%	10.14	12.08	19.27	7.85	9.30	1.96
G.C.V.%	10.04	12.04	19.23	7.97	9.26	1.91
Broad sense heritability %	98.11	99.28	99.62	97.07	99.23	94.8
	Number of seed/ pod			Shell-out%		
Genetic Variance.	0.12	0.078	0.02	16.29	15.65	23.11
Phenotypic Variance	0.29	0.217	0.03	17.05	16.43	23.14
P.C.V.%	7.36	6.07	2.17	9.28	9.08	10.88
G.C.V.%	4.69	3.66	1.53	9.08	8.86	10.87
Broad sense heritability %	40.54	36.41	50.0	95.55	95.27	99.85
	100-seed weight (green)			100-seed weight (g)		
Genetic Variance.	18.45	35.71	70.34	57.29	61.88	23.11
Phenotypic Variance	18.80	35.92	70.51	57.05	62.28	23.14
P.C.V.%	15.73	15.81	10.26	16.77	22.47	25.92
G.C.V.%	15.67	15.76	10.24	16.62	22.41	25.89
Broad sense heritability %	99.25	99.36	99.85	98.16	99.43	99.76
	Number of pods/ plant			Green pod yield (g/plant)		

Genetic Variance.	8.57	13.52	9.17	520.6	315.8	67.69
Phenotypic Variance	9.42	14.20	9.83	600.1	344.8	105.01
P.C.V.%	18.38	19.91	14.81	18.77	11.55	7.13
G.C.V.%	17.53	19.42	14.03	17.48	11.06	6.62
Broad sense heritability %	90.95	95.19	93.22	86.75	91.60	86.83
	Dry seed yield (g/plant)					
Genetic Variance.	26.01	56.63	26.92			
Phenotypic Variance	27.47	61.44	29.80			
P.C.V.%	18.65	20.51	10.30			
G.C.V.%	18.15	19.69	9.79			
Broad sense heritability %	94.69	92.18	90.33			

Table 6: The actual, expected and the realized response to selection relative to mid parents and check population for all studied characters of population peas.

Items	Population			Population		
	Realized response to selection (%) relative to:					
	No. of days to flowering			Plant height (cm)		
	F <sub>3</sub>	F <sub>4</sub>	F <sub>5</sub>	F <sub>3</sub>	F <sub>4</sub>	F <sub>5</sub>
P1	-5.43	-4.05	-8.04	20.00	19.85	22.67
P2	-4.25	-4.05	-4.72	37.40	47.01	40.82
Mid-parents	-4.84	-4.05	-6.41	28.11	32.05	31.12
Entsar 1	-8.81	-11.25	-9.74	31.71	28.05	28.37
Realized response to selection (%) relative to:						
	Number of branches/plant			Pod length (cm)		
P1	85.16	77.76	100.00	26.09	17.27	22.06
P2	97.93	95.53	93.75	9.43	11.10	16.48
Mid-parents	91.33	86.22	96.83	17.17	14.10	19.20
Entsar 1	81.65	83.31	87.88	8.92	9.53	13.24
Realized response to selection (%) relative to:						
	Number of seed/pod			Shell-out%		
P1	0.96	2.27	-0.25	2.25	-4.37	-7.47
P2	22.83	27.83	33.00	8.48	15.10	17.95
Mid-parents	10.83	13.63	14.00	5.28	4.47	3.70
Entsar 1	3.80	6.53	-0.25	-27.1	-24.31	-27.13
Realized response to selection (%) relative to:						
	Number of pods/plant			Green pod yield (g/plant)		
P1	85.56	110.33	111.70	204.91	246.34	290.12
P2	138.57	170.43	164.63	123.08	194.32	238.60
Mid-parents	108.75	136.63	135.22	157.65	218.22	262.50
Entsar 1	138.57	136.63	164.63	134.71	166.06	235.14
Realized response to selection (%) relative to:						
	100-seed weight (green)			Dry seed yield (g/plant)		
P1	32.75	12.41	20.87	83.06	120.87	188.04
P2	-29.36	-24.33	-21.57	128.46	238.14	268.82
Mid-parents	-7.79	-9.91	-4.87	103.25	167.20	223.5
Entsar 1	-17.68	-16.54	-9.88	45.57	93.96	143.12
Realized response to selection (%) relative to:						
	100-seed weight (g)			Pod width		
P1	14.38	19.60	39.06	45.83	32.59	42.31
P2	-2.08	3.37	19.56	-2.78	-0.56	5.71
Mid-parents	5.51	10.89	28.57	16.67	13.65	21.31
Entsar 1	4.66	13.49	36.71	9.37	15.48	23.33

## Conclusion

From the previous results in this work, it can be concluded that the genetic variation and broad sense heritability were high for number of days to flowering and green seed yield/plant in F3 generation, the genetic improvement could be by selection.

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