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RESEARCH ARTICLE

Pedigree selection in pea (Pisum sativum L.).

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Abstract

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Two pea populations (Alaska X little Marvel) and (Alaska X Dwarf Grav Sugar) were used to improve green pod yield and some yield components trait by pedigree selection for several generations (F₃, F₄ and F₅) with check cultivar (Markado), during three winter seasons. Highly significant differences between F₃ families in both populations were detected, genotypic coefficient variation were detected for selection of green pod yield per plant. After two cycles of pedigree selection the criterion of selection was increased in population 1 and 2 by 4.98, 31.53, 32.72% and 6.23, 21.49, 20.36% compared with the bulk sample, check cv., and the best parent, respectively. Heritability in broad sense in F3 populations and two pedigree selection cycles were 96.02, 95.04, 98.38 and 96.83, 88.7, 94.17 respectively, for green pod yield per plant. Families No. 1, 10, 5, 8 and 6 had a heaviest green pod weight per plant in population 1. While, families No. 1, 5 and 10 in population 2 were attained the superiority of green pod yield per plant, compared to the bulk sample, check cv. and the best parent. Therefore, these families were recommended for use as new promising lines of pea but need more field experiments to evaluating them.

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Introduction:

Garden pea (*Pisum sativum* L.) is one of the most important favorable legume crops grown in Egypt, during the winter seasons. The green pod and dry seed consider essential sources for protein and vitamin which used for human food as well as animal. Increasing yielding of the unit area and the pods quality could be gained by growing new and heavy pod yield cultivars and/or improving the cultural practices. In breeding program for increasing productivity, three important decisions that faced breeder to achieve (**Tammam 1995**). Firstly, is to identifying germplasm for desired characteristics. Secondly, is to good choice for prospective parents should be used for hybridization. Finally, the breeder must limit which method could be used in handling the resulting segregating populations. The right decisions were easily made, when the breeding goals are to improving qualitative traits. On the other hand, seed yield controlled by multiple genes, different environmental limitations and how to handle segregating populations. Pea breeders therefore, have permission from their nations for increasing crops productivity. (**Kumaran et al., 1995 and Singh, 1995**).

Increasing pod yield of peas, is one of the most important aims (Nayak and Baisakh, 1990, Simakov 1989), regardless the main purpose of any breeding program. Genetic variability for quantitative and qualitative characters in pea and relationships among them would facilitate the breeding improvement of the crop. (Kumar et al., 1999) found that significant differences among pea genotypes. They also, reported that the differences in genotypic and phenotypic coefficients of variation (GCV and PCV) were higher in traits of plant height, biological yield, seed and number of pods/ plant. This results indicates that selection of these traits would be more effective for further breeding improvement.

Yield as being the end trait of large number of attributes, is a complex trait, it has long recognized in legume crops (Adams, 1967, Coyne 1968, Singh and Urrea 1995, Oliveira et al., 1996, Abd-Elhady 1998 and El-Ameen

2012), that low heritability, large genotypic \times environmental interaction. Selection in early segregation population can be useful than wild type cultivars (**Vikas et al., 1996**). Selection within local and exotic population may due to improving crops performance (**Qasim et al., 2002**). (**Kuo 1999**) using bulk and pedigree selection for developed a new green pea line with 90.7 cm for plant height and weight average 7.8 g per pod. (**Mital and verma 1991**) suggested that most effective selection in peas should consider days to flowering, pod length, number of seeds/pod and 100-seed weight.

The efficient of selection between and within segregating generations varied from case to another (Abd-Elhady 2003). Genetic variability, character association and component analysis in F_4 generation of field pea were studied by (Garima and Groopa 2012). Selection for characters viz. plant height, days to 50% flowering, number of pods/plant, pod length and days to maturity have a good impact in field pea yield enhancement. There are many other factors are held stable, an increase in these traits individually would reflect an increase in seed yield.

Mass selection for traits can be done and will be more effective if it begin in later hybrid generations (F_6 - F_7) or through individual selection (**Valentin 2014**). Seed yield in field pea can be improved by selection of genotypes having more number of pods/plant and number of seeds/pod (**Brijendra et al., 2013**). Breeding efforts have been employed in pea for combining genes for adaptability, earliness and high yield (**Abdou 1990**). The present investigation was conducted to determine the effective selection for improving productivity of peas yield and to estimate some genetic parameters in two populations of *Pisum sativum L*.

Materials and methods:-

Experimental material and design:-

This study was conducted at the Experimental Farm at Faculty of Agriculture, South Valley University, Qena, Egypt. The experiment was carried out during the three growing winter seasons of 2012/2013, 2013/2014 and 2014/2015 to improve the green pod yield through pedigree selection in early generations of two pea crosses. Breeding materials used in this study were 200 F_3 families traced back to random F_2 plants from the two crosses (Alaska X Little Marvel) that was considered as population 1 and (Alaska X Dwarf Gray sugar) as population 2. The name and source of the three parents and check cultivar (Markado) were shown in **table 1**:

During the first winter season 2012/2013, 200 plants were selected from each of the two F_3 populations (Base) and their parents were sown in a randomized complete blocks design with three replications. Each family was represented by one row 3 m long and 60 cm apart and 20 cm between plants. The best of 30 plants from the best 30 families of both populations for each of the selection criteria, weight of green pod yield/plant were saved to give the F_4 families. Winter season 2013/2014, 30 F_3 Bulk sample (F_4 non selected families) and the check cv. were sown in two separate experiments in a randomized compete blocks design with three replications. Each family was a single row 3 m long, 20 cm between plants. 30 families for each selection criterion were analyzed separately. The best 10 families for each selection criterion were saved to give the 10 families. During winter season 2014/2015, the 10 F_5 families for each selection criterion with the parents, check cv. and F_5 Bulk sample of both populations were sowing in two separate experiments.

Statistical procedures:-

Data were recorded for individual plants on a random sample of ten plants from each family in F_3 , F_4 and F_5 generations. The means of the ten plants were subjected to the statistical and genetic analysis for the following characters (green pod yield/ plant, 100 green seed (g), number of seeds/ pod and pod length cm).

The genetic parameters were estimated in F_3 , F_4 and F_5 generations. Estimates ($\sigma^2 p$) and ($\sigma^2 g$) variance and heritability (H^2) estimated were calculated from estimates of mean square of variance components of the select traits. The ($\sigma^2 p$) and ($\sigma^2 g$) variance as given by Al-Jiburi et al., (1958). The phenotypic (PCV) and genotypic (GCV) coefficients of variability were estimated as outlines by Burton (1952).

Results and discussion:-

Analysis of variance and means:-

The analysis of variance for each of the two population F_3 families and their parents, data for four traits studied are presented in table (2). Highly significant differences were detected among the two population F3 families and their parents. Means for green pod yield per plant (g) ranged from 92.66 for P_2 to 125.95 (g) for F_3 families with average 115.23 (g) in population 1 and ranged from 100.5 (g) for P_2 to 115.9 (g) for F_3 families with average 107.83 (g). The trait 100- green seeds (g) ranged from 30.66 (g) for (P_1 and P_2) to 39.91 (g) for F_3 families with average 34.07 (g) in population 1, and 30.55 for P_2 to 33.33 for F_3 families with average 31.44 (g) in population 2. Number of seeds per

pods ranged from 5.66 for P_2 to 7.42 for F_3 families with average 6.69 in population 1, and from 5.77 for P_2 to 6.99 for P_1 with average 6.3 in population 2. Pod length trait ranged from 5.7 for P_1 to 8.95 for P_2 with average 7.85 in population 2. Data are shown in table (3). Similar results were previously obtained by Singh (1995), Mehta (2002), Mahmoud (2004), Abdou (2005), Guleria et al. (2009), Bakheit and Metwali (2011), Garima and Groopa (2012), and Valentin (2014).

Response to selection and genetic parameters:

The genetic variability measured as genotypic coefficient of variability, the data are presented in table (4) in both populations was sufficient for selection in the base population for the two selection criteria green pod yield per plant (g). This may be due to it is easily to identify the highest green pod yield/ plant (g) genotypes. These findings are in agreement with the reports of Guleria et al. (2009) and Jitendra et al., (2010) with respect to seed yield/ plant. Another study by Brijendra et al., (2013), they found that high estimates of GCV and PCV were recorded for seed yield/ plant (32.08 and 35.28%), indicating the presence of high amount of variation and role of environmental on the expression of this trait.

The calculated values of heritability in broad sense were found highly for green pod yield per plant in two cycles for two populations 95.04, 98.83 and 88.17, 94.17, are presented in table (4), respectively. The data are shown in table (4) revealed that green pod yield per plant was mostly controlled by genetic factors. On the other side, the environmental variation hasn't had the same effects on this trait. These results were in line with those obtained by Abdou (1999), Tyagi and Srivastava, (2003), Mahmoud (2004), Abdou (2005), Abd-Elhady and Hussein (2008), Rashwan (2010), Bakheit and Metwali (2011), Garima (2012), Brijendra et al. (2013), and Fares et al.(2013). High estimates of coefficients of variation were obtained for selection of green pod yield per plant. The results indicated that after the two cycles of pedigree selection increased the criterion of selection in population 1 by 4.98, 31.53 and 32.72% compared to the bulk sample, check cultivar and the best parent respectively. While, population 2 the resulting families showed realized response to selection of 6.23, 21.49 and 20.36% compared with the bulk sample, check and best parent.

Results illustrated in table (4), indicated that mean of weight green pod yield per plant over all selected families in two cycles for both populations gave the highest value, 134.48, 141.01 and 123.49, 130.4, respectively. Compared with the bulk sample, best parent and check cv. The realized response to selection measured as the deviation percentage of the over all cycles mean from the bulk sample, best parent and check cv are presented in table (5). The results indicated that selection for green pod yield/ plant after two cycles of pedigree selection increased the criterion of selection in population 1 by 4.73, 29.68, 22.03% and 4.98, 31.53, 32.72%, and number of seeds/pod by 10.62, 24.64, 30.14 and 3.20, 17.74, 22.94% from the bulk sample, check cv and the best parent in table (5) in the two cycles, respectively. Also, in population 2, selection towards increasing of green pod yield per plan (g) by 4.38, 19.08, 21.66 and 6.23, 21.49, 20.36% and 100-seed weight by 10.27, 9..28, 24.10 and 19.75, 21.9, 25.76% in tow cycles, respectively. In population 2 compared to the bulk sample, check cv. And the best parent, and decreased by 6.19 % and 10.00 % in trait of number of seeds and pod length (cm), respectively. Compared by the check cv. Data are shown in table (5).

With regard to population 2, after the second cycles in table (5), Pedigree selection for green pod yield per plant in family no 1, 5 and 10 were higher than the bulk sample, check cv. and best parent by 13.54, 23.27, 31.05 % and 10.54, 26.48, 25.31% and 8.40, 23.97 and 28.82%, respectively. These results indicated that selection would be more effective to improve all studied traits between two populations. Finally, the high heritable for green pod yield per plant trait ($h^2 > 75$) was indicated that the effectiveness of selection for these trait.

Conclusion:-

The pedigree selection revealed that three families under the same selection criterion of green pod yield per plant, no. 1, 5 and 10 which evaluated in this investigation are promising lines due to higher seed yield per plant than other families.

 Table 1:- Source, plant height, seed color, seed texture and flower color of three parents and check cultivar used in this study.

Genotype	Source	plant height	seed color	seed texture	Flower color
Alaska	USA*	Medium	Green	Smooth	White
little Marvel	USA*	Short	Green	Wrinkled	White
Dwarf Gray Sugar	USA*	Medium	Mottled	Wrinkled	Purple
Markado	Netherland*	Short	Green	Wrinkled	White

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Table 2:- Analysis of variance of all studied traits in the F₃ families and their parents of the two pea populations.

Character	Mean squares									
		Popula	tion 1		Population 2					
	Green pod 100- Number Pod				Green pod	100-	Number	Pod		
	yield/plant	yield/plant green of seeds/ length				green	of seeds/	length		
S.O.V	(g)	seed (g)	pods	(cm)	(g)	seed (g)	pods	(cm)		
Rap.	27.438	200.96	162.99	2.668	49.50	142.80	74.20	4.40		
Families	257.14**	221.58**	1079.73**	272.10^{**}	630.40**	196.8**	833.93**	548.33**		
Error	3.5	9.56	6.02	0.354	7.25	16.80	9.60	1.09		

* and ** indicated significant at 0.05 and 0.01 levels of probability, respectively.

Table 3:- Mean of the four traits and mean squares in the F₃ families and their parents of the two pea populations.

Item		Popul	ation 1		Population 2			
Character	P ₁	P ₂	\mathbf{F}_3	Average	P ₁	P ₂	F ₃	Average
Green pod yield/plant (g)	107.1	92.66	125.95	108.57	107.1	100.5	115.9	107.83
100-green seed (g)	30.66	31.66	39.91	34.07	30.66	30.55	33.13	31.44
Number of seeds/ pods	6.99	5.66	7.42	6.69	6.99	5.77	74.20	6.30
Pod length (cm)	8.37	6.85	8.95	8.05	8.37	7.50	7.70	7.85

Table 4:- genotypic (GCV) and genotypic (PCV) coefficient of variability, heritability in broad sense (H) and Means of green pod yield/ plant over all selected families in two cycles in both populations.

Genotypes	Grain pod yiel	d/ plant		Population 1			Population 2			
	Population 1	Population 2	Genotypes	GCV %	PCV %	Н	GCV %	PCV %	Н	
Cycle 1	134.48	123.49	Base	7 20	7 4 4	96.02	12.57	12.77	96.83	
Bulk	128.40	118.30	population F ₃	1.29	/.44					
Best parent	110.20	110.20	Cyclo 1	4.56	4.61	95.04	2.00	2.13	88.17	
Check cv	103.70	103.7	Cycle I							
L.S.D 0.05	1.35	2.91	Cyclo 2	14.39 14	14 51	08 38	3.35	3.64	94.17	
L.S.D 0.01	1.95	4.19	Cycle 2		14.51	90.50				
Cycle 2	141.01	130.24	Base	8.46	8.62	96.60	10.20	10.57	93.10	
Bulk	134.20	122.60	population F ₃							
Best Parent	106.20	108.2	Cycle 1	0.71	0.01	06.00	3 77	1 16	71 91	
Check cv	107.20	107.2	Cycle I	9.71	9.91	90.00	5.77	4.40	/1.01	
L.S.D 0.05	2.37	3.35	Cyclo 2	6.84	6.96	97.35	3.44	3.51	96.62	
L.S.D 0.01	3.39	4.79	Cycle 2	0.04						

Table 5:- Direct and correlated gained for grain pod/ plant (g) in two cycles of pedigree selection in both populations
in percentage compared to the bulk sample, the check "Markado" and the best parent.

			Populati	on 1		Population 2			
Selection criterion	Genotypes	Green pod yield/plant (g)	100- green seed (g)	Number of seeds/ pods	Pod length (cm)	Green pod yield/plant (g)	100- green seed (g)	Number of seeds/ pods	Pod length (cm)
	Bulk sample	4.73	7.89	10.62	9.88	4.38	10.27	7.41	6.15
Cycle 1	Check cv	29.68	25.61	24.64	7.5	19.08	9.28	- 6.91	- 10.00
	Best parent	22.03	33.58	30.14	17.73	21.66	24.10	17.87	11.14
Cycle 2	Bulk sample	4.98	36.27	3.20	14.10	6.23	91.75	10.15	6.19
	Check cv	31.53	45.92	17.74	16.12	21.49	21.90	0.84	- 4.08
	Best parent	32.72	59.42	22.94	26.04	20.36	25.76	27.85	14.35

Table 6:- Means of tow populations after the second cycle for all studied traits.

		Populat	ion 1		Population 2				
Family No	Green pod	100-	Number	Pod	Green pod	100-	Number	Pod	
Failing No.	yield/plant	green	of seeds/	length	yield/plant	green	of seeds/	length	
	(g)	seed (g)	pods	(cm)	(g)	seed (g)	pods	(cm)	
Bulk	134.2	42.20	8.10	9.50	122.60	36.40	6.50	8.40	
Check cv	107.2	32.60	7.10	9.30	107.20	32.60	7.10	9.30	
B ost nonont	106.2	29.80	6.80	8.60	108.20	21.20	5 60	7.80	
best parent	149.63	46.96	8.00	10.36	108.20	51.20	5.00	7.60	
1	136.07	47.86	8.33	10.75	141.80	39.96	7.33	9.40	
2	138.03	47.20	8.33	10.53	121.00	39.18	7.00	8.76	
3	138.25	47.45	8.33	10.91	129.00	39.5	6.66	9.00	
4	143.93	48.03	8.66	10.95	130.76	39.13	7.33	8.33	
5	137.33	47.08	8.33	10.75	135.59	39.93	7.00	9.03	
6	141.33	47.96	8.00	10.91	126.11	39.86	7.33	9.45	
7	137.50	47.73	8.66	10.93	122.20	39.15	6.66	8.53	
8	140.76	46.26	8.66	10.90	127.60	39.88	7.33	8.96	
9	146.26	48.70	8.33	10.83	128.90	39.58	6.66	8.56	
10	140.97	47.50	8.36	10.83	132.90	40.18	7.33	9.38	
Average	2.01	0.89	0.37	0.51	129.68	39.18	7.06	8.94	
L.S.D. 0.05	3.18	1.26	0.51	0.65	2.30	0.56	0.30	0.31	
L.S.D 0.01	1.40	1.50	0.40	2.30	4.15	1.20	0.61	0.60	

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