EVALUATION OF SELECTED NEW INBRED LINES IN COW PEA AND THE HYPRIDS AMONG THEM.

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ABSTRACT

The present study was conducted to investigate the nature of variability in cow pea. These variabilities could be utilize to develop new inbred lines. Pedigree selection program with self pollination was used.

Five inbred lines were obtained as a result of pedigree selection program from four cultivares (populations) of cow pea. These cultivares were: Cream 7 (A), Fetriat (B), Cyprus (C) and Dokki 301 (D).

The obtained five inbred lines were crossed in a diallel crosses mating design excluding reciprocal hybrids to obtaine 10 F_1 hybrids. The results cleared that the means of the F_1 hybrids, significantly exceeded the mid parents (M.P.) for all studied traits. The obtained heterosis values ranged from –3.42% to 45.45% for days to flowering (D.F.) and number of branches per plant (No. B./P.) traits, respectively.

The results also revealed that the magnitudes, of non-additive genetic variances including dominance (σ^2_D) were larger than those additive genetic variances (σ^2_A) for most studied traits. The obtained values of additive genetic variances could not be neglected.

The calculated values of heritability in broad sense ranged from 67.82% to 94.60% for number of seeds per pod (No. S./P.) and plant length (P.L.) traits, respectively. In the same time, the highest value of narrow sense heritability was: (49.11%) for seed yield per plant (S.Y./P.) trait.

The results illustrated the presence of genotypic (r_g) and phenotypic (r_{ph}) correlations among pairs of studied traits. The highest values of correlation coefficient were: 0.72 and 0.81, among weight of 100 seeds (W/100/S) and seed yield per plant (S.Y./P.) for r_g and r_{ph}, respectively. This investigation could be continued to improve of the studied traits through selection in segregated generations.

INTRODUCTION

Cow pea considers as one of the important vegetable crops in Egypt and other countries. Thus, this investigation was carried out to develop new inbred lines of cow pea through selection program using pedigree method. These lines could be evaluated and used to produce new hybrids or utilize as varieties. In this respect, Vgura (1996) suggested that selecting of individual plants could be effective to improve pod length, number of pods/plant, seeds/pod, 100 seed weight and total yield traits. In the same time, Ewa Ubi et al. (2001) studied the nature of segregation in some crosses at the F_3 and F_6 generations of cow pea. They cleared insignificant differences between the mean of F_3 and the corresponding F_6 mean. They suggested the existence of additive measure of gene action. They also added that the selection in early generations is feasible. Similarly, El-Sherbeny et al. (2001) studied the effect of selection program on cow pea. They obtained significant variations among F_3 families for (D.F.), (P.H.) and (S.Y./P.) traits.

Singh and Saini (1986) evaluated some different hybrids of bean. They obtained quite of estimated heterosis values from the mid-parents. These values were 76%, 35% and 8.9% for total yield, 100 seed weight and protein content traits, respectively. In this respect, Yadav and Harer (1994) evaluated six parental genotypes of bean and 15 F_1 hybrids among them. They claimed the presence of heterosis values for number of branches/plant, number of pods/plant and seed yield. They also added that the highest value was 55% for seed yield trait. At the same time, Cunha-Melo et al. (1997) evaluated 11 varieties of bean and the F_1 hybrids among them. They reported that some F_1 hybrids exhibited heterosis for many studied traits. They also mentioned that the two F_1 hybrids (A – 488 x Oura) and (Esal 591 x Oura) were the best promising hybrids. Similarly, El-Sharkawy et al. (1999) obtained highly significant estimates of heterosis against the better and the mid-parents for all studied traits.

Singh and Saini (1986) stated the importance of non-additive genetic variances including dominants and additive genetic variances for yield/plant and 100-seed weight. Similarly, Pessoni et al. (1997) claimed that both of SCA and GCA had similar importance in the inheritance of bean traits. On the other hand, Wassimi et al. (1988) cleared that the additive genetic variances were larger than the non-additive genetic variances for most studied traits of bean. Different results were obtained by Amen (1998). He evaluated three crosses of bean. He indicated that dominance effects were larger than additive effects for most studied traits and also cleared that selection programe could be effective to improve bean traits. In this respect, El-Sharkawy et al. (1999) illustrated the importance of both additive and non-additive genetic variances in the inheritance of bean traits.

Singh et al. (1991) obtained heritability values ranged from 43% to 76% for yield and 100 seed weight traits, respectively. In this respect, Ranalli et al. (1996) estimated heritability values for different traits of bean. They revealed that seeds/pod and pods/plant traits showed higher heritability estimates. Similarly, El-Sharkawy et al. (1999) regarded that the highest values of heritability were 77.82% for (No. L./P.). In the same time, Ewa Ubi et al. (2001) indicated that the values of heritability in broad sense ranged from 47.8% to 91.1% for seed weight and pod length traits, respectively. Similar results were obtained by El-Sherbeny et al. (2001). They obtained high estimates of heritability ranged from 60.4% (S.Y./P.) to 78.4% (P.H.).

Dimova et al. (1991) regarded that seed weight was closely and significantly correlated with number of fertile nods and number of pods/plant. In this respect, El-Sharkawy et al. (1999) mentioned that most studied traits of bean showed positive correlation coefficient among them. At the same time, El-Sherbeny et al. (2001) indicated the presence of correlations among pairs of studied traits of cow pea.

MATERIALS AND METHODS

In this study four cultivars of cow pea were used. These cultivars were: Cream 7, Fetriat, Cyprus and Dokki-301 named as A, B, C and D as code number, respectively. The seeds of each cultivare were cultivated

separately in the growing season of 1998 (S_0). These plants were selfed to produce the seeds of (S_1). From the S_1 plants several plants were selected from each population to be planted in the next season. The selection was made according to different favorable vegetative and yield component traits.

The selected S_1 genotypes were cultivated during the growing season of 1999. All plants were selfed to produce S_2 seed,

Accordingly, S_3 and S_4 generations were obtained through the growing seasons of 2000 and 2001, respectively. From S_4, five lines were selected from four cultivars. These lines named as PAL_1, PBL_1, PBL_2, PCL_1 and PDL_1. These selected five inbred lines were evaluated in the 2002 growing season. The experimental design was a randomized complete blocks design with three replications. Each replicate contained the selected five inbred lines of cow pea. Plots were two rows 3.0 m. long and 0.5 m. wide with spacing at 30 cm. apart. All agricultural requirements were made. This investigation was conducted at horticultural research station at Al-Bramoun Dakahlia Governorate. The analyses of variance were made as outlined by Steel and Torrie (1960).

In the same growing seasons, lines were crossed among them according to diallel crosses mating design excluding reciprocal to obtaine 10 F_1 hybrids. All lines were selfed to obtain enough seeds of parental lines. In the growing season of 2003 all genotypes, which included five parental lines, 10 F_1 hybrids were evaluated in a field trial experiments at El-Barmoun. Complete blocks design with three replications was used. Each block consisted of 15 plots. Each plot was two rows with 10 hills.

Data were recorded on plant length (P.L.), number of branches per plant (No. B/P), days to flowering (D.F.), number of seeds per pod (No. S/P), weight of 100 seeds (W/100/S) and seed yield per plant (S.Y/P.).

Several analysis of variances were made to test the significance of the differences among genotypes using L.S.D values. Heterosis values from the mid-parents (M.P) and the better parent (B.P) were determined. The form of the diallel crosses and the expectations of the mean squars were made as outlined by Cockerham (1963) in Table 1. General combining ability and specific combining ability were determined according to Matzinger and Kempthorn (1956).

Table 1: The form of the analysis of variance and expectations of the mean squares.

S.V.	d.f	M.S.	E.M.S.
Reps.	$r-1$		$\sigma^2_e + c\,\sigma^2_r$
Crosses	$c-1$		$\sigma^2_e + r\,\sigma^2_c$
GCA	$P-1$	M_3	$\sigma^2_e + r\,\sigma^2_s + r(P-2)\,\sigma^2_g$
SCA	$\dfrac{P(P-3)}{2}$	M_2	$\sigma^2_e + r\,\sigma^2_s$
Error	$(r-1)(c-1)$	M_1	σ^2_e

r: the number of replications   c: the number of crosses
P: the number of parental lines
σ^2_g: the variance of general combining ability
σ^2_s: the variance of specific combining ability

The variance components additive genetic variance (σ^2_A) and non-additive genetic variance including dominance (σ^2_D) were determined as follows:

$$\sigma^2_g = \tfrac{1}{2}\sigma^2_A, \quad \sigma^2_A = 2\sigma^2_g$$
$$\sigma^2_s = \sigma^2_D, \quad \sigma^2_D = \sigma^2_s$$

heritability values were determined as follows.

$$h^2_{b.s} = \frac{2\sigma^2_g + \sigma^2_s}{2\sigma^2_g + \sigma^2_s + \sigma^2_{e/r}} \times 100$$

$$h^2_{n.s} = \frac{2\sigma^2_g}{2\sigma^2_g + \sigma^2_s + \sigma^2_{e/r}} \times 100$$

Genotypic (r_g) and phenotypic (r_{ph}) correlations for any pair of studied traits could be estimated as outlined by Steel and Torrie (1960).

The significance of (r_g) and (r_{ph}) was tested by using the "t" test at 5% and 1% levels of significances as described by Cochran and Cox (1957) as follows:

Calculated "t" for genotypic correlation (r_g) $= \dfrac{(r_g)}{\sqrt{\dfrac{1-(r_g)^2}{n-2}}}$

Calculated "t" for phenotypic correlation (r_g) $= \dfrac{(r_{ph})}{\sqrt{\dfrac{1-(r_{ph})^2}{n-2}}}$

Where: n : is number of error degrees of freedom.

RESULTS AND DISCUSSION

This investigation was carried out to creat new inbred lines of cow pea through pedigree selection program. The obtained inbred lines could be used to improve the characteristics of cow pea or used to produce new hybrids.

In general, the five inbred lines were obtained from the four cultivars which were used as a source of selection. One of them were obtained from the first cultivare (A) and named as PAL_1, while the other three inbred lines were obtained from the other three cultivars B, C and D, and named as PBL_1, PBL_2, PCL and PDL_1 as a code number, respectively. The means and the ranges of the pedigree selection cycles on the four cultivars are cleared in Tables 2, 3, 4 and 5, respectively.

The results revealed that the five inbred lines were varied in different studied traits. The results also indicated the improvement of most studied

traits as a result of selection program. The means of selected plants were *changed every cycle* for all studied traits. Similarly, the ranges of all studied traits became narrower as a results of homogzyosity through selfing and selection program.

Table 2: The pedigree of selected lines from cultivare Cream 7 (A) depends on different traits.

	P. L.	No. B/P.	D. F.	No. S/P.	W/100/S	S.Y/P.
1997 S_0	123.4	4.4	63.5	10.1	16	74.9
	15(1)	15(1)	15(1)	15(1)	15(1)	15(1)
	120(123)126	4(4)5	62(63)65	9(10)11	15(15)17.4	73(76)77
1998 S_1	121.4	4.6	65.4	10.4	16.5	75.0
	5(3)	5(3)	5(3)	5(3)	5(3)	5(3)
	119(119)124	4(5)5	64(66)67	9(9)11	15.5(15.8)178	74(76)77
1999 S_2	123.8	4.75	63.0	10.8	16.3	76.5
	4(4)	4(4)	4(4)	4(4)	4(4)	4(4)
	122(125)125	4(5)5	62(62)65	10(11)11	15.8(16.8)16.8	75(78)78
2000 S_3	123.5	4.5	63.3	10.0	16.0	74.6
	8(2)	8(2)	8(2)	8(2)	8(2)	8(2)
	119(126)126	3(5)5	62(63)64	9(10)11	15(15.8)16.7	73(78)78
2001 S_4	121.8	4.12	62.2	10.2	15	74.3
	12(5)	12(5)	12(5)	12(5)	12(5)	12(5)
	121(125)125	4(3)5	62(63)65	9(10)11	14.9(15.3)16.2	73(76)76
PAL_1	125	5	65	10	15.3	76

Table 3: The pedigree of selected lines from the cultivare Fetriat (B) depends on different traits.

	P. L.	No. B/P.	D. F.	No. S/P.	W/100/S	S.Y/P.
1997 S_0	114.6	4.46	69.3	10.3	12.9	79.1
	15(1)	15(1)	15(1)	15(1)	15(1)	15(1)
	113(113)119	4(4)5	66(68)69	10(10)11	11.9(13.5)13.8	78(78)81
1998 S_1	114	4.2	65.8	11	12.3	80.0
	5(3)	5(3)	5(3)	5(3)	5(3)	5(3)
	110(117)118	4(4)5	65(66)67	10(10)12	11.7(12.8)12.8	78(80)81
1999 S_2	112.3	4.0	65.5	11.3	12.2	79.3
	4(4)	4(4)	4(4)	4(4)	4(4)	4(4)
	112(118)118	3(5)5	64(65)68	11(12)12		77(77)81
2000 S_3	112.8	4.12	64.6	10.1	11.55	80
	8(2)	8(2)	8(2)	8(2)	8(2)	8(2)
	109(111)115	3(4)5	63(64)66	10(10)11	11.15(12.4)12.4	78(80)82
2001 S_4	102.1	4	64.4	10.3	11.6	78.2
	12(5)	12(5)	12(5)	12(5)	12(5)	12(5)
	100(103)105	4(5)5	63.(66)66	9(10)10	10.9(12.2)12.2	77(78)79
PBL_1	103	5	66	10	12.2	79
PBL_2	105	4	64	9	11.7	79

Concerning pedigree selection in cultivare A, it could be noticed from Table 2 that the ranges of S_0 were: 120 – 126; (4 – 5); 62 – 65; 9 – 11; 15 – 17.4 and 73 – 77 for (P.L), (No. B/P), (D.F.), (No. S/P), (W/100/S) and (S.Y/P), respectively. In the same time, the ranges in S_4 were: (121 – 125),

(4 – 5), (62 – 65), (9 – 11), (14.9 – 16.2) and (73 – 76) for the same obvious studied traits, respectively. The means of the selected inbred lines (PAL$_1$) which obtained from the population A were [(125) (P.L.); (5) (No. B./P)], [(65) (D.F.)]; [(10) (No. S./P.)]; [(15.3) (W/100/S)] and [(76) (S.Y./P.)].

Table 4: The pedigree of selected lines from the cultivare Cyprus (C) depend on different traits.

	P. L.	No. B/P.	D. F.	No. S/P.	W/100/S	S.Y/P.
1997 S$_0$	152.0	4.8	44.5	12.26	20.47	81.6
	15(1)	15(1)	15(1)	15(1)	15(1)	15(1)
	150(151)156	4(5)6	42(45)48	11(12)13	18(20)21.7	80(80)83
1998 S$_1$	150.2	4.6	43.0	11.8	19.48	80.6
	5(3)	5(3)	5(3)	5(3)	5(3)	5(3)
	148(150)154	4(6)6	42(42)44	11(11)13	18.4(19.5)20.7	79(79)82
1999 S$_2$	149.5	4.25	42.5	11.00	20.05	79.8
	4(4)	4(4)	4(4)	4(4)	4(4)	4(4)
	149(149)153	4(4)5	42(42)43	10(10)12	19.5(20.2)20.7	79(80)81
2000 S$_3$	148.0	4.62	41.0	11.62	19.25	79.37
	8(2)	8(2)	8(2)	8(2)	8(2)	8(2)
	143(126)152	4(4)6	41(42)44	10(11)13	18.5(18.9)20.2	78(78)81
2001 S$_4$	148.75	4.33	39.75	10.83	17.78	80.6
	12(5)	12(5)	12(5)	12(5)	12(5)	12(5)
	147(149)150	4(5)5	39(40)41	9(12)12	14.3(18.3)18.5	79(81)83
PCL$_1$	147	4	41	9	14.3	79

In the same time, the results of the pedigree selection in the cultivare B are shown in Table 3. The results cleared that the ranges at S$_0$ were: 113 – 119; 4 – 5; 66 – 69; 10 – 11; 11.9 – 13.8 and 78 – 81 for (P.L.), (No. B./P.), (D.F.), (No. S./P.), (W/100/S) and (S.Y./P.), respectively. On the other hand, the ranges at S$_4$ were: 100 – 105; 4 – 5; 63 – 66; 9 – 10; 10.9 – 12.2 and 77 – 79 for the same studied traits, respectively. The means of the two selected inbred lines from the cultivare B were: (103 and 105), (5 and 4), (66 and 64); (10 and 9); (12.2 and 11.7) and (79 and 79) for (P.L), No. B./P, D.F., No. S./P., W/100/S and S.Y./P., respectively. The results of the pedigree selection in the cultivare C are presented in Table 4. The results indicated that the ranges at S$_0$ were (150 – 156), (4 – 6) (42 – 48), (11 – 13), (18.0 – 21.7) and (80 – 83) for (P.L.), (No. B./P.), (D.F.), (No. S./P.), (W/100/S) and (S.Y./P.), respectively. On the other hand, the ranges in the S$_4$ were (147 – 150), (4 – 5), (39 – 41), (9 – 12), (14.3 – 18.5) and (79 – 83), for the same obvious studied traits, respectively. From this cultivare one inbred lines was selected and named as PCL$_1$. The means of the selected inbred line were (147), (4), (41), (9), (14.3) and (79) for P.L., No. B./P., D.F., No. S./P., W/100/S and S.Y./P., respectively.

Concerning the pedigree selection programe in the cultivare D, the results are shown in Table 5. It could be noticed from the table that the ranges at S$_0$ were (93 – 102), (3 – 4), 42 – 47), (11 – 12), (21 – 23.5) and (73 – 77) were: (93 – 102), (3 – 4), (42 – 47) and for (P.L.), (No. B./P.), (D.F.), (No. S./P.), (W/100/S) and (S.Y./P.) traits, respectively.

Table 5: The pedigree of selected lines from the cultivare Dokki 331 (D) depend on different traits.

	P. L.	No. B/P.	D. F.	No. S/P.	W/100/S	S.Y/P.
1997 S_0	98.58	3.46	44.06	11.46	22.20	74.9
	15(1)	15(1)	15(1)	15(1)	15(1)	15(1)
	93(102)102	3(3)4	42(45)47	11(12)12	21(22.7)23.5	73(77)77
1998 S_1	96.8	3.2	42.8	11.0	21.28	75.0
	5(3)	5(3)	5(3)	5(3)	5(3)	5(3)
	95(97)99	3(3)4	42(42)44	10(11)12	20.7(21.8)21.8	74(75)77
1999 S_2	98.5	3.00	43.0	11.5	19.92	76.5
	4(4)	4(4)	4(4)	4(4)	4(4)	4(4)
	93(93)102	3(3)3	40(43)45	11(12)12	19.2(19.2)20.5	75(75)78
2000 S_3	100.0	3.25	42.25	11.25	19.17	74.6
	8(2)	8(2)	8(2)	8(2)	8(2)	8(2)
	99(99)101	3(3)4	41(42)44	10(11)12	18.5(19.7)19.8	73(78)78
2001 S_4	99.5	3.33	42.33	11.0	18.42	72.33
	12(5)	12(5)	12(5)	12(5)	12(5)	12(5)
	98(101)102	3(3)4	40(41)44	10(12)12	15.5(19)19.5	72(72)75
PDL_1	99	4	42	10	15.5	72

On the other hand, the obtained ranges in the S_4 were (98 – 102), (3 – 4), (40 – 44), (10 – 12), (15.5 – 19.5) and (72 – 75) for the same studied traits, respectively. The obtained ranges in the S_4 which were narrow illustrated that the studied traits reached a certain degree of homogeneity and small degree of variation due to inbreeding and direct selection. It was expected that during the following cycles of selection the range could be more narrower and homozygosity would be then. One inbred line: named as PDL_1 was selected with the mean of (99); (4); (42); (10); (15.5) and (72) for (P.L.), (No. B./P.), (D.F.), (No. S./P.), (W/100/S) and (S.Y./P.) traits, respectively.

Generally, the results cleared that selection was efficient and useful in recovering new inbred lines of cow pea. These inbred lines would be either used per se as a new varieties or would be used for further breeding program to produce F_1 hybrids.

In the growing season of 2002, the selected five inbred lines were crossed according to diallel crosses mating design (excluding reciprocal) to obtained 10 F_1 hybrids. In addition, the inbred lines were selfed to obtain more seeds. In the growing season of 2003, the 15 genotypes (five inbred lines and 10 F_1 hybrids) were evaluated in a field trial experiment with three replications and the results are cleared in Table 6. The results indicated that the mean squares of crosses showed highly significance for all studied traits except of (No. S./P.) which showed (only significance). In the same time, the mean squares of general combining ability (G.C.A.) and specific combining ability (S.C.A.) showed highly significance for all studied traits. These results indicated the presence of significant differences among genotypes which inturn would lead to the presence of genetic variation among them. These genotypes could be improved through suitable programme.

Table 6: The results of the analysis of variances and the mean sguares of half diallel cosses for all studied traits.

S.V.	d.f	M.S.					
		P.L.	No. B/P.	D.F.	No. S/P.	W/100/S	S.Y/P.
Reps.	2	21.71	2.03	10.02	6.09	9.22	22.1
Cross.	9	173.15**	54.16**	55.27**	13.22*	26.07**	108.49**
GCA	4	218.05**	75.33**	74.95**	18.43**	32.18**	131.9**
SCA	5	137.23**	37.22**	39.53**	9.05	21.19**	89.76**
Error	18	10.33	3.71	7.18	4.93	5.83	18.92

The means of selected parental inbred lines, the ranges, the means of the F_1 hybrids were determined and the results are presented in Table 7. Heterosis values estimated from the mid-parents (M.P.) and the better parent (B.P.) were also calculated and the results are shown in the same table.

The results revealed that the means of the F_1 hybrids always significantly exceeded the (M.P.) for all studied traits. The estimated heterosis versus the (M.P.) ranged from (-3.42%) to (45.45%) for (D.F.) and (No. B./P.) traits, respectively. In the same time, the estimated values of heterosis against the (B.P.) were: 11.76%, 28.0%, 30.98%, 1.9%, 28.76% and 7.25% for (P.L.), (No. B./P.), (D.F.), (No. S./P.), (W/100/S) and (S.Y./P.), respectively. These values of heterosis mentioned to the possibility of producing new hybrids among the obtained inbred lines. These values of heterosis explaine the presence of non-additive genetic variance including dominance. Similar results were obtained by Singh and Sainin (1986), Yadav and Harer (1994), Cunha Melo et al. (1997) and El-Sharkawy et al. (1999).

Table 7: The means and the ranges of the mid-parents and F_1 hybrids and heterosis values from the mid and the better parent.

	P.L.	No. B/P.	D.F.	No. S/P.	W/100/S	S.Y/P.
M.P.	115.8	4.4	55.6	9.6	13.8	77.00
Range	103 – 125	4 – 5	41.0 – 66	9 –10	11.7–15.3	75 – 79
F_1	139.7	6.4	53.7-59.2	10.19	19.7	84.73
Range	106.2-149.3	4.1-5.8	41.0-59.2	8.2-11.4	11.6-20.3	80.4-89.7
H(F_1, M.P)	20.64**	45.45**	-3.42**	6.15*	42.75**	10.04**
H(F_1, B.P)	11.76**	28.0**	30.98**	1.9	28.76**	7.25**
0.05 L.S.D.	6.21	0.149	1.07	0.52	2.53	2.94
0.01	8.14	0.201	1.84	0.67	3.04	3.11
0.05 L.S.D.	4.01	0.217	0.92	0.181	2.61	2.18
0.01	4.67	0.252	1.07	0.20	2.94	3.20

The additive genetic variances (σ^2_A) and the non-additive genetic variances including dominance, in addition heritability values in broad and narrow senses were estimated and the results are cleared in Table 8. The results indicated that all studied traits showed positive values for additive (σ^2_A) and non-additive genetic variances including dominance (σ^2_D). It could be noticed that the values of (σ^2_D) were larger than those values of the (σ^2_A)

for all studied traits except of (No. S./P.) and (S.Y./P.). These findings were expected and explain the values of heterosis which were obtained and described earlier. The values of σ^2_A and σ^2_D indicated the possibility of improving of these genotypes through selection program.

Table 8: The estimates of additive genetic variance (σ^2_A), non additive genetic variance (σ^2_D) and heritability values in broad and narrow senses for all studied traits.

	P.L.	No. B/P.	D.F.	No. S/P.	W/100/S	S.Y/P.
σ^2_A	17.96	8.46	7.88	2.084	2.442	27.36
σ^2_D	42.30	11.17	10.78	1.373	5.107	23.61
$h^2_{n.s}$	28.19	40.54	37.43	40.89	25.73	49.11
$h^2_{b.s}$	94.60	94.06	88.65	67.82	79.55	89.33

Concerning heritability, the results illustrated that the calculated heritability values in narrow sense ranged from (25.73%) to (49.11%) for (W/100/S.) and (S.Y./P.) traits, respectively. On the other hand, the values of heritability in broad sense were high and ranged from (67.82%) to (94.60%) for (No. S./P.) and (P.L.) traits, respectively. These results indicated the possibility of improving the genetic materials in this investigation through selection program, and explain the importance of both additive and non-addition genetic variances for all studied traits. It could be concluded that it is possible to improve cow pea traits through selection programe to obtaine new inbred lines. These inbred lines could be combined to produce superior F_1 hybrids. Many authors obtained similar results, among them Singh and Saini (1986), Pessoni et al. (1997), Amen (1998) and El-Sharkawy et al. (1999).

The associations among different pairs of studied economical traits of cow pea were studied through calculating of genotypic (r_g) and phenotypic (r_{ph}) correlations among pairs of studied traits. The obtained values of genotypic (r_g) and phenotypis (r_{ph}) correlations among pairs of traits were estimated are presented in Table 9.

Table 9: Genotypic and phenotypic correlations among pairs of studied traits of cow pea.

	P.L.	No. B/P.	D.F.	No. S/P.	W/100/S	S.Y/P.
P.L.		0.53**	-0.32**	0.27*	0.22*	0.63**
		0.51**	-0.32**	0.24*	0.19	0.51**
No. B/P			-0.33**	0.28**	0.41**	0.59**
			-0.22**	0.21**	0.30**	0.51**
D.F.				-0.46**	-0.34**	-0.51**
				-0.37	-0.30**	-0.40**
No. S/P.					0.36**	0.72**
					0.29**	0.68**
W/100/S						0.81**
						0.72**
S.Y./P.						

The results revealed that the days to flowering (D.F.) negatively correlated (r_{ph}) with number of seeds per pod (No. S./P.), weight of 100 seeds (W/100/S), seed yield per plant (S.Y./P.), number of branches per plant (No. B/P.) and plant length (P.L.). The obtained values of correlation were: - 0.46, -0.34, -0.51, -0.33 and –0.32, respectively. On the other hand, seed yield per plant S.Y./P. trait was positively correlated with plant length (P.L.) (0.63), No. B./P. (0.59), No. S.P. (0.72) and W/100/S. (0.81). Similar results were obtained for (r_g), the results also indicated that the highest values of (r_{ph}) and (r_g) were 0.81 and 0.72 among S.Y./P. and W/100/S. It could be concluded the presence of association between pairs of studied traits indicating the possibility of improving of studied traits through selection program.

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تقييم سلالات نقية جديدة منتخبة فى اللوبيا والهجن بينها .
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أجريت هذه الدراسة لإيضاح طبيعة الاختلافات ودراسة إمكانية استخدام هــذه الاختلافــات لإنتــاج سلالات جديدة من اللوبيا . وقد استخدمت خمسة دورات من الانتخاب مع تسجيل النسب فى أربع أصــناف من اللوبيا هى: Cream 7, Fetriat, Cyprus and Dokki 301 . وفى نهاية دورات الانتخاب أمكن الحصول على خمسة سلالات سميت كالآتى :-

PAL$_1$, PAL$_2$, PBL$_1$, PCL$_1$ and PDL$_1$

-   تم التهجين بين هذه السلالات الخمسة طبقا لنظام التهجين الدورى وذلك باسـتبعاد الهجــن العكسـية وبالتالى تم الحصول على عشرة هجن . ثم تم تقييم هذه الهجن مع السلالات الأبوية الخمسة .

-   أوضحت الدراسة أن متوسط الجيل الأول قد فاق معنويا متوسط الآباء وذلك لجميع الصــفات التــى درست وذلك قياسا بمتوسط الآباء وقد تراوحت قوة الهجين المتحصل عليهــا مــن – ٤٢ر٣% إلــى ٤٥ر٥% وذلك لصفتى عدد الأيام للتزهير وعدد الأفرع/نبات، على الترتيب .

-   أظهرت النتائج أيضا أن التباين الغير تجمعى والذى يضم التباين السيادى كان أعلى من التباين التجمعى لمعظم الصفات التى درست مع أن قيم التباين التجمعى المتحصل عليهــا تشــير إلــى إنهــا لا يمكــن استبعادها .

-   أظهرت هذه الدراسة أيضا وجود قيم عالية لمعامل التوريث، وقد تراوحت هذه القــيم بــين ٨٢ر٦٧% إلى ٦٠ر٩٤% لصفتى عدد البذور/قرن وطول النبات على الترتيب وذلك قياسا فــى معنــاه الضــيق ١١ر٤٩% وذلك لصفة محصول البذور/نبات .

-   أشارت النتائج أيضا لوجود ارتباط وراثى ومظهرى معنوى بين أزواج الصفات التى درست، وكانــت أعلى قيم لمعامل الارتباط هى ٧٢ر٠، ٨١ر٠ وذلك (وزن ١٠٠ بذرة × محصول البذور /المحصول) وذلك للإرتباط الوراثى والمظهرى على الترتيب .

-   هذه الدراسة سوف تستمر لتحسين الصفات التى درست وذلك من خلال الانتخاب فــى الأجيــال الانعزالية .