Genetic Evaluation of Some Quantitative Characters in Some Cowpea Crosses

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Abstract : This investigation was conducted to study the performance of developmental and yield characters and the type of gene action of five cowpea (*Vigna sinensisL*) parental genotypes and their $F_1, F_2,$ and F_3 generations . The five generations, P_1, P_2, F_1, F_2 and F_3 were grown in 2006 season and data were recorded on the means of all generations. The F_1 "VR$_4$ X VR$_3$" was higher than both parents for all characters except for number of leaves and branches per plant and pod weight ,while the F_2 and F_3 means were higher than their parents for stem length ,number of leaves per plant ,pod weight per plant, number of pods per plant and 100 seeds weight . All of F_1, F_2 and F_3 in the cross " VR$_6$ X VR4 "were higher than both parents for stem length, pods weight per plant, number of pods per plant, seed weight per plant and 100 seed weight .Highest mean values were observed for pods weight per plant, no of pods per plant, seeds weight per plant no. of seeds per pod and 100 seeds weight in the cross "Dokki331 X VR$_4$". In the cross "Dokki331 X VR$_{14}$" , the F$_1$ had the highest mean values for number of branches per plant , pods weight per plant , number of pods per plant , seeds weight per plant , number of seeds per pod and seeds weight per pod . Significant values of the scaling test indicated the presence of non-allelic interaction in almost all characters of the four crosses. Both positive and negative significant additive gene effects were observed in most characters of the four crosses. Eight characters of the two crosses "VR$_4$ X VR$_3$" and "Dokki331 X VR$_4$" and seven characters of the cross "Dokki331 X VR$_{14}$" showed a negative and significant additive gene effects. The dominance gene effects were significant for number of branches in cross "VR$_4$ X VR$_3$", stem length, number of branches per plant and number of pods per plant in the cross VR$_6$ X VR$_4$, weight of seeds per plant and length of pod in the cross Dokki 331 X VR$_4$ and for pod length in the cross Dokki331 X VR$_{14}$. Non-allelic interactions of the types "additive X additive" and "dominance X dominance" were found to be controlling the inheritance of most characters in all the four crosses.

Keywords: Cowpea Crosses, Genetic Evaluation

INTRODUCTION

Cowpea (Vigna unguiculata (L.) Walp.) and the other main legume crops are considered the most important source of protein foods for Egyptians . Increasing area unit productivity through utilizing improved varieties is considered an important aim of cowpea breeders. Pod characters, (i.e. length, diameter and weight of pod and both number and weight of seeds, seed index) are considered the most important components affecting seed yield (Gad El-Hak *et al.*, 1988).

Many investigators studied the inheritance of morphological and yield characters in cowpea the reported models included additive, dominance, maternal and epitasis effects, (Bieri and Kawecki, 2003). Genetic information about the nature of different types of gene action and various relationships between different genes and alleles controlling every trait are of great importance for improving this crop.

The presence of the three types of gene effects in most crosses of cowpea indicated the importance of both additive and non-additive gene action in controlling most of these characters. The three types of gene interactions were important in the inheritance of the number of pods per plant and pod yield per plant, while the additive gene effect mainly governed the inheritance of pod weight and seed weight (Rahman and Saad 2000; Pooran *et al.* 2002; Lopes *et al.*, 2003; Hooda *et al.*, 2003 and Suzan Swidan, 2005).

MATERIALS AND METHODS

This investigation was carried out at the Experimental Farm of the faculty of agriculture Suez Canal University, Ismailia, during the seasons of 2003, 2004, 2005 and 2006, using five cowpea (*Vigna sinensis L*) parental genotypes. VR$_3$ as (P$_1$), VR$_4$ as (P$_2$), VR$_6$ as (P$_3$), VR$_{14}$ as (P$_4$) and the local variety Dokki 331 as (P$_5$).The five genotypes were obtained from the Horticultural crops research institute.

In the growing season 2003, the five parental genotypes were crossed as follows, cross 1 (VR$_4$ X VR$_3$), cross 2 (VR$_6$ X VR$_4$), cross 3 (Dokki 331 X VR$_4$) and cross 4 (Dokki 331 X VR$_{14}$) to produce the F$_1$ hybrid seeds. In March 2004, seeds of the parents and (F$_1$'s) were sown. The F$_1$ hybrids were self-pollinated to produce F$_2$ population seeds. Self-pollination was made for some parental plants to get parents' self seeds. While some other parental plants were re-crossed to produce more F$_1$ hybrids seeds. In March 2005 a randome sample of seeds produced by F$_2$ plants were sown to get F$_3$ seeds.

In March 2006 the parents, F$_1$ hybrids F$_2$ and F$_3$ were planted in the field using a randomized complete blocks design with four replications. Each replicate included two rows of each of the parents and F$_1$, in addition eight rows of the F$_2$ andeight rows of the F3 populations. Two seeds per hill were sown, the hills were 30 cm apart and the rows were 1 m. in width. Each plot was 6 m^2. The agricultural treatments were similar for all entries under study.

Ten plants from each entry over all replications were randomly chosen for measuring all developmental, and yield characters. The developmental characters recorded were stem length (cm), number of leaves per plant and number of branches per plant. The dry yield characters were weight of dry pods per plant (g.), number of dry pods per plant and dry seed weight per

plant (g.). Pod quality characters which included average pod weight (g), number of seeds per pod, seeds weight per pod (g) and pod length (cm) beside weight of 100 dry seeds (g.).

Statistical Procedures:

Scaling tests which provide information about the absence or presence of gene interactions were carried out according to Mather (1949).

$C = 4 F_2 - 2 F_1 - P_1 - P_2$

$D = 4 F_3 - 2 F_2 - P_1 - P_2$

Significance of the scaling test were obtained by utilizing their standard error. The values of C, D should be equal to zero within the limits of their standard errors. The significance of any one is taken to indicate the presence of nonallelic interaction.

C provides a test of dominance X dominance type of interaction. D provides a test of additive X additive type of gene interaction.

Gene effects, were estimated by using the five parameter model suggested by Mather and Jinkes (1971) and Singh and Chaudhar (1977) as follows,

F_2 mean $m = F_2$

Additive effects $(d) = 1/2 P_1 - 1/2 P_2$

Dominance effects $(h) = 1/6 (4F_1 + 12 F_2 - 16 F_3)$

Dominance X dominance effect $(L) = 1/3 (16F_3 - 24F_2 + 8F_1)$

Additive X additive effect $(i) = P_1 - F_2 + 1/2 (P_1 - P_2 + h) - 1/4 L$

Significance of the estimates of genetic effects were obtained by utilizing their standard errors and t- values.

RESULTS AND DISCUSSION

The mean performance of the studied populations:

Tables (1 and 2) show the performance of the five populations for eleven developmental and yield characters, in the four crosses. Data in table 1, showed that the means of F_1 cross "VR_4 X VR_3" were higher than both parents for the pod's weight per plant, number of pods per plant, seed's weight per plant, number of seeds per pod, weight of seeds per pod, pod length and weight of 100 seeds. F_2 were higher for stem length, number of leaves and number of branches per plant, pod's weight per plant, number of pods per plant, seeds weight per plant and 100 seeds weight, meanwhile, the F_3 exhibited the second highest values for stem length, number of leaves per plant, weight of pods per plant, number of pods per plant, weight of seeds per plant, and weight of 100 seeds.

In the cross (VR_6 X VR_4) the performance of F_1 showed the highest values for stem length, weight of pods per plant, number of pods, weight of seeds per plant, weight of seeds per pod and weight of 100 seeds, while the F_2 had the second highest values for stem length, number of branches per plant, number of pods per plant, weight of seeds per plant, length of pod and weight of 100 seeds.

Data in Table (2), showed that the means of the F_1 in the cross " Dokki331 X VR4" were the highest mean values for pods weight per plant, number of pods per plant , seeds weight per plant, number of seeds per pod

and 100 seeds weight , while it was the second one for number of branches per plant, number of pods per plant and seeds weight per plant .

The F_1 of the cross "Dokki 331 X VR_{14}" had the highest mean values for all characters except for the stem length, number of leaves per plant and pod length, in the same time ,F2 was the second one for number of pods per plant , seeds weight per plant and seeds weight per pod .

Scaling test:

The results of scaling tests C and D are presented in Table (3). In cross "VR_4 X VR_3", the C and D values were significant or highly significant for stem length, number of leaves per plant and weight of 100 seeds; these results indicated the presence of both" additive X additive "and "dominance X dominance" non-allelic interaction for these characters. Only C test was significant or highly significant for weight of pod, number of seeds per pod and weight of seeds per pod suggesting the presence of "dominance X dominance" genic interactions for these characters. Meanwhile only D test was significant or highly significant for both weight and number of pods per plant and weight of 100 seeds indicating that the "additive X additive" non-allelic interactions are governing these characters. The two scaling tests C and D did not significantly differ from zero indicating that the additive dominance model could be adequate to interpret the gene effects for length of pod.

Cross "VR_6 X VR_4" showed that the C and D tests were highly significant for stem length and weight of pod per plant suggesting the presence of both "additive X additive" and "dominance X dominance" genic interactions for the two characters. However, only C test was significant or highly significant for the number of leaves, number of pods per plant , weight of pod and weight of 100 seeds indicating that the "dominance X dominance " genic interactions are governing these characters. But D were significant or highly significant for number of branches per plant, weight of seeds per plant, number of seeds per pod, weight of seeds per pod and length of pod indicating the presence of "additive X additive" genic interactions for these characters.

In cross "Dokki 331 X VR_4" the significance of both C and D test for stem length, number of leaves and length of pod indicated the presence of the two types of non-allelic interactions for the two characters. Meanwhile only the of C values was significance for the number of seeds per pod and weight of seeds per pod indicating the presence of "dominance X dominance" interaction for these characters.Also the D value was only significant for the weight of pods per plant and weight of 100 seeds. These results indicated the presence of "dominance X dominance" genic interactions for these characters.

Cross "Dokki 331 X VR_{14}" showed that both C and D tests were highly significant for the number of leaves per plant and length of pod. This indicated the presence of "additive X additive" and "dominance X dominance"

genic interactions for these characters. In the same time C test was only significant or highly significant for stem length and pods weight per plant , suggesting that the two characters are controlled by "dominance X dominance" non- allelic interactions, also D test was only significant for seeds weight per plant, indicating that this character is governed with "additive X additive" non- allelic interactions. The two scaling tests C and D did not significantly differ from zero for the number of branches per plant, number of pods per plant, pod weight, number of seeds per pod, seeds weight per pod and weight of 100 seeds. This indicates the absence of genic interaction for these characters.

These results are in common agreement with those obtained in Cowpea and other legume crops, by Oommen-A *et al.*, (1999), Paralkar, *et al.* 1997; Patil and Patil (1986); Bieri and Kowecki (2003), and Ojod *et al.* (2006).

Types of gene action:

Data in Table (4) and (5) showed the types of gene action and the epistatic effects using generation means for all characters for the four crosses.

In the cross "VR$_4$ X VR$_3$" (Table 4) the additive gene effects (d) were significantly negative for stem length, number of branches, weight of pods per plant, number of pods per plant, length of pod and weight of 100 seeds but significantly positive for the number of leaves per plant, weight of pod and number of seeds per pod .Meanwhile the dominance gene effects (h) were significant for the number of branches per plant only , suggesting that these characters are mainly controlled by additive genes . Among the epistatic components the significance of both "additive X additive" (i) and "dominance X dominance" (L) for stem length , number of leaves per plant , number of branches per plant, weight of pods per plant , number of pods per plant and seeds weight per plant showing the presence of the two types of interactions for these characters , while the significant of "additive X additive"(i) for the number of seeds per pods indicates the presence of "additive X additive" (i) interactions only for this character.

In the cross "VR$_6$ X VR$_4$" (Table 4) the additive gene effects (d) were highly significant and positive for all studied characters except for pod weight and seeds weight per pod, while dominance gene effect (h)were significant for stem length, number of branches per plant and number of pods per plant. These results indicated the presence of the two types of gene action (d) and (h) for these three characters and the presence of the (d) type i.e additive gene effects for the other characters. However "additive X additive " effects (i) were significant and negative for number of branches per plant and pod length but significant and positive for 100seesds weight, while "dominance X dominance" effects (L) were positive significant for the number of leaves per plant and pod length , but negative significant for the number of branches per plant , suggesting the

presence of the types of inter actions for the number of branches per plant and pod length and the presence of "additive X additive" only for the 100 seeds weight and the presence of dominance X dominance" genic interactions only for number of leaves per plant.

In the cross "Dokki 331 X VR$_4$"(Table 5) additive gene effects (d) were highly significant or significant and negative for stem length, number of leaves, number of branches per plant, weight of pods per plant number of pods per plant, weight of seeds per plant, seeds weight per pod and highly significant or significant positive for weight of 100 seeds and length of pod. Dominance gene effects (h) were significant or highly significant and positive for seeds weight per plant and pod length. These results indicated that additive (d) and dominance (h) gene actions were quite considerable for the two characters i.e. seeds weight per plant and pod length while the other significant (d) values for other characters were mainly controlled by additive gene effects. Additive X additive (i) type of digenic epitasis was found to have significant or highly significant negative values for stem length , number of branches per plant , pods weight per plant , number of pods per plant and pod weight, while dominance X dominance (L) type of digenic epitasis was found to have highly significant negative values for stem length only suggesting that additive X additive (i) type of interactions are a major factor in determining the inheritance of the number of branches per plant , weight of pods per plant, number of pods per plant and seeds weight per plant , while the two types of interactions (i) and (L) both were present in controlling the number of leaves per plant .

Cross "Dokki 331 X VR$_{14}$" (Table 5) showed that the additive gene effects (d) were highly significant or significant and negative for the number of leaves, weight of pod, length of pod and weight of 100 seeds. But highly significant or significant and positive for stem length, number of branches per plant and weight of pods per plant. Meanwhile the dominance gene effect (h) was highly significant and positive for pod length only. These results indicated that these characters were mainly affected by additive gene action. Additive X additive gene effects (i)were highly significant or significant and negative for the number of leaves per plant , pods weight per plant , seeds weight per plant , pod weight , number of seeds per pod , seeds weight per pod and 100 seeds weight, while the dominance X dominance gene effects were highly significant or significant for the number of leaves per plant and pod length only , suggesting the prevalence of additive X additive genic interactions for these characters.

Similar trends of genic interactions were obtained in Cowpea and other legume crops by Rahman and Saad (2000); Pooran *et al.* (2002); Lopes *et al.* (2003); Bieri and Kawecki (2003); Hooda-JS (2003) and Ojod *et al.* (2006); Suzan (2005) and Sheela, and Gopalan (2006).

Table (1): Means of P_1, P_2, F_1, F_2 and F_3 and standard error for developmental and yield characters in two cowpea crosses.

Genotypes	Stem length (cm)	No. of leaves/ plant	No. of branches/ plant (cm)	Yield/plant			Pod characters				Weight of 100 seeds (g)
				Pods wt. (g)	No. pods	Wt. seeds (g)	Wt. pod (g)	No. seeds	Wt. seeds (g)	Length (cm)	
				(VR$_4$ X VR$_3$)							
P_1	34.0±1.0	30.0±2.9	3.3±0.3	47.7±3.0	15.3±0.9	31.0±2.0	3.1±0.1	14.2±1.0	2.0±0.6	12.0±0.6	14.0±0.4
P_2	111.7±1.7	95.7±2.9	8.0±0.6	103.7±3.0	40.7±0.3	82.0±4.0	2.6±0.1	11.0±0.4	2.0±0.1	13.7±0.3	17.0±0.2
F_1	117.3±1.5	81.7±5.9	5.7±0.3	296.0±12.0	73.0±4.7	164.0±13.0	3.1±0.4	14.5±0.4	2.2±0.04	14.3±0.3	18.0±0.2
F_2	124.9±0.9	144.7±1.7	9.3±0.3	144.0±8.0	51.7±1.06	104.0±6.0	2.8±0.04	12.8±0.2	2.0±0.04	11.7±1.2	18.0±0.2
F_3	119.0±2.3	123.3±4.4	7.3±0.3	164.0±4.0	61.7±4.4	128.0±9.0	2.7±0.2	13.4±0.4	2.0±0.6	12.3±0.9	17.0±0.3
				(VR$_6$ X VR$_4$)							
P_1	111.7±1.7	95.7±1.2	8.0±0.06	104.0±3.0	40.7±0.3	82.0±4.0	2.6±0.1	11.0±0.3	2.0±0.3	13.7±0.3	17.0±0.2
P_2	35.3±1.8	23.3±0.3	3.3±0.3	58.0±4.0	32.3±1.5	38.3±3.0	1.8±0.6	8.0±0.3	1.2±0.02	8.0±0.05	14.0±0.2
F_1	156.3±4.9	83.0±1.2	6.0±0.6	117.0±2.0	46.3±0.9	99.0±5.0	2.5±0.1	11.0±0.4	2.1±0.1	9.7±0.3	22.0±0.2
F_2	141.7±4.4	65.0±2.9	7.0±0.6	111.0±3.0	45.0±0.6	89.0±4.0	2.5±0.04	10.3±0.4	2.0±0.04	10.7±0.4	18.0±0.2
F_3	137.3±4.3	66.0±4.5	5.4±0.3	112.0±2.0	44.3±2.3	87.0±2.0	2.5±0.2	11.3±0.6	2.1±0.1	9.7±0.3	18.0±1.1

Table (2): Means of P_1, P_2, F_1, F_2 and F_3 and standard error for developmental and yield characters in two cowpea crosses.

Genotypes	Stem length (cm)	No. of leaves/ plant	No. of branches/ plant (cm)	Yield/plant				Pod characters			Weight of 100 seeds (g)
				Pods wt. (g)	No. pods	Wt. seeds (g)	Wt. pod (g)	No. seeds	Wt. seeds (g)	Length (cm)	
					Dokki331 X VR$_4$						
P_1	69.7±2.4	76.3±3.0	4.3±0.3	86.0±4.0	35.0±2.9	54.0±2.0	2.4±0.1	11.4±0.2	1.6±0.1	14.7±0.3	18.0±0.3
P_2	111.7±1.7	95.7±1.2	8.0±0.6	104.0±13.0	40.7±0.3	82.0±4.0	2.6±0.4	11.0±0.4	2.0±0.1	13.7±0.3	17.0±0.2
F_1	72.3±1.5	68.3±4.4	4.7±0.3	140.0±12.0	54.0±4.6	105.0±8.0	2.6±0.6	11.7±0.1	2.0±0.02	13.5±0.3	20.0±0.1
F_2	62.0±1.2	63.3±2.7	5.3±0.3	107.0±8.0	44.3±2.3	91.0±1.0	2.5±0.1	10.4±0.5	1.6±0.1	12.7±0.6	18.0±0.6
F_3	60.0±2.9	62.3±3.7	5.0±0.6	114±5.0	42.7±1.5	82.0±5.0	2.7±0.2	11.1±0.3	1.7±0.1	11.3±0.3	17.0±0.5
					Dokki 331 X VR$_{14}$						
P_1	43.0±1.5	38.3±1.7	6.0±0.6	68.0±7.0	37.0±1.5	47.0±4.0	1.9±0.6	10.8±0.4	1.1±0.4	13.7±0.3	16.0±0.2
P_2	69.7±2.4	76.3±3.0	4.3±0.3	86.0±4.0	35.0±2.9	54.0±3.0	2.4±0.1	11.4±0.2	1.6±0.1	14.7±0.3	18.0±0.3
F_1	37.7±1.2	31.3±1.3	8.3±1.7	91.0±5.0	40.0±1.5	71.0±5.0	2.3±0.04	12.1±0.2	1.8±0.04	14.3±0.7	18.0±0.3
F_2	60.3±2.6	32.7±1.5	5.7±0.3	76.0±1.0	39.7±0.9	67.0±2.0	2.0±0.04	11.9±0.03	1.7±0.2	15.7±0.3	17.0±0.5
F_3	62.3±3.7	31.0±2.1	6.0±0.6	76±3.0	39.3±1.5	66.0±3.0	2.0±0.1	12.0±0.3	1.6±0.1	13.7±0.3	17.0±0.3

Table (3): Scaling tests (C and D) and their standard errors for developmental and yield characters in four cowpea crosses.

Scale test	Stem length (cm)	No.of leaves/ plant	No.of branches/ plant	Yield/plant			Pod characters				Weight 100 seeds (g)
				Pods Wt (g)	No. pods	Wt. seeds (g)	Wt. pod (g)	No. seeds	Wt. seeds (g)	Length (cm)	
				$(VR_4 \times VR_3)$							
C	119.3$\pm$4.9**	287.7$\pm$14.2**	14.5$\pm$1.5**	-27.2$\pm$41.0	4.8$\pm$11.5	-24.8$\pm$35.3	-0.7$\pm$0.3*	-3.0$\pm$1.5*	-0.4$\pm$0.2*	-7.5$\pm$5.1	3.1$\pm$0.8**
D	80.5$\pm$9.57**	76.9$\pm$18.4**	-0.7$\pm$1.5	219.8$\pm$21.8**	87.4$\pm$18.0**	191.6$\pm$39.5**	-0.5$\pm$0.6	2.8$\pm$1.8	-0.9$\pm$0.7	0.1$\pm$4.4	2.5$\pm$1.3*
				$(VR_6 \times VR_4)$							
C	107.2$\pm$19.6**	-25.0$\pm$11.8*	4.7$\pm$2.5	47.9$\pm$13.2**	14.4$\pm$3.3**	35.9$\pm$20.5	0.6$\pm$0.3*	0.1$\pm$1.5	0.6$\pm$0.6	1.7$\pm$2.0	-3$\pm$0.9**
D	118.8$\pm$6.1**	15.0$\pm$19.3	-3.7$\pm$1.8*	61.9$\pm$11.2**	14.2$\pm$8.7	48.1$\pm$13.9**	0.6$\pm$0.8	5.5$\pm$2.3*	1.2$\pm$0.6*	-4.3$\pm$1.6*	6$\pm$4.2
				Dokki 331 X VR_4							
C	-78.0$\pm$6.1**	-55.4$\pm$14.2**	-0.5$\pm$1.5	43.9$\pm$41.7	6.5$\pm$12.8	18.2$\pm$16.3	-0.2$\pm$0.6	-4.2$\pm$2.2*	-1.2$\pm$0.4**	-4.6$\pm$2.3*	-1.8$\pm$2.6
D	-60.4$\pm$12.1**	-49.4$\pm$16.1**	-2.9$\pm$2.5	54.5$\pm$24.9*	6.5$\pm$7.7	8.6$\pm$19.3	0.8$\pm$0.9	1.2$\pm$1.7	0.8$\pm$0.5	-8.6$\pm$1.7**	4.6$\pm$2.2*
				Dokki 331 XVR_{14}							
C	53.3$\pm$11.1**	289.7$\pm$14.2**	-4.1$\pm$3.7	-32.6$\pm$14.01*	6.8$\pm$5.3	23.4$\pm$14.5	-1.0$\pm$0.2	1.2$\pm$0.7	0.5$\pm$0.7	5.8$\pm$1.9**	-1.8$\pm$2.3
D	15.9$\pm$16.0	78.1$\pm$18.4**	2.3$\pm$2.3	-1.8$\pm$14.1	-2.2$\pm$6.9	27.2$\pm$12.3*	-0.2$\pm$0.5	2.0$\pm$1.3	0.3$\pm$0.5	-5.0$\pm$1.4**	-0.2$\pm$1.6

*, **: significant at 5% and 1% levels, respectively.

Table (4): Mean estimation of five parameter model of gene effects for developmental and yield characters in two cowpea crosses.

Parameter	Stem length (cm)	No. of leaves/ plant	No. of branches/ plant	Yield/plant			Pod characters				Weight 100 seeds (g)
				Pods wt. (g)	No. pods	Wt. seeds (g)	Wt. pod (g)	No. seeds	Wt. seeds (g)	Length	
				(VR$_4$ X VR$_3$)							
m	124.9±0.86**	144.7±1.7**	9.3±0.33**	144±8.0**	51.7±1.6**	104.3±5.6**	2.8±0.04**	12.8±0.14**	2.02±0.04**	11.7±1.2**	17.5±0.17**
d	-2.7±0.97**	32.9±2.0**	-4.7±0.33**	-28±3.2**	-12.7±0.47**	-25.7±2.1**	0.3±0.1**	1.6±0.52**	-0.02±0.12	-0.9±0.33**	-1.7±0.2**
h	10.7±6.4	15.1±12.8	2.9±1.13*	-0.9±20.4	-12.5±12.6	-24.2±28.9	0.5±0.4	-0.5±1.1	0.2±0.5	0.13±3.4	1.0±0.88
l	-155.2±14.6**	-282.1±31.2**	-20.3+3.31**	329.3±78.2**	110.1±27.1**	288.5±76.4**	0.3±0.9	7.7±2.5**	0.04±1.0	10.1±10.9	-1.04±2.2
i	-173.9±5.3**	176.0±10.9**	-32.4±1.2**	-206.2+23.7**	-70.4±9.5**	-159.0±24.8**	0.24±0.36	1.35±1.4	-0.2±0.4	-31.±3.5	-8.9±0.8**
				(VR$_6$ X VR$_4$)							
m	141.7±4.4**	65.0±5**	7.0±0.6**	111.03+2.8**	45.0±0.6**	88.6±4.4**	2.5±0.4**	10.33+0.4**	2.0±0.1**	10.7+0.4**	17.9±0.2**
d	38.2±1.2**	36.2±0.6**	2.35±0.3**	22.7±2.7**	8.4±0.7**	22.1±2.3**	0.4±1.05	1.5±0.24**	0.42±0.5	5.7±0.33**	1.8±0.1**
h	23.7±14.9**	9.3±13.5	3.6±1.5*	2.8±7.9	16.4±5.8**	12.5±11.4	0.1±0.55	-2.2±1.8	-0.2±0.4	2.0±1.2	1.8±2.6
l	15.5±44.2	53.3±33.7	-11.2±5.2*	19.2±25.6	-0.8±12.4	16.3±39.5	02±1.19	7.2±4.4	0.9±1.1	-8.0±3.8*	12.1±5.9*
i	0.3±14.2	49.0±11.2**	-4.4±1.7*	9.2±9.0	-0.1±4.4	5.5±12.9	0.5±0.44	1.5±1.5	0.3±0.48	6.85+1.3**	-2.7±2.1

*, **: significant at 5% and 1% levels, respectively.

Table (5): Mean estimation of five parameter model of gene effects for developmental and yield characters in two cowpea crosses.

Parameter	Stem length (cm)	No. of leaves/ plant	No. of branches/ plant	Yield/plant			Pod characters				Weight 100 seeds (g)
				Pods wt. (g)	No. pods	Wt. seeds (g)	Wt. pod (g)	No. seeds	Wt. seeds (g)	Length	
				Dokki 331 X VR$_4$							
m	62+1.1**	63.3+2.7**	5.3+0.33**	106.6+8.1**	44.3+2.1**	19.25+0.8**	2.5+0.1**	10.4+0.3**	1.6+0.09**	12.7+0.6**	18.4+0.6**
d	-5.5+1.5**	-9.7+1.6**	-1.9+0.33**	-.8.9+2.5**	-2.9+1.5*	-14.0+2.2**	-0.1+0.2	0.19+0.2	-0.23+0.08**	0.5+0.2*	0.6+0.2**
h	-12.2+8.1	6.0+11.6	0.4+1.7	2.0+20.0	10.7+6.5	33.9+13.6*	-0.5+0.6	-1.0+1.3	0.007+0.35	4.3+1.5**	1.3+1.8
l	50.+18.3**	8.0+31.4	-3.2+4.1	131.2+77.6	17.3+22.3	-12.4+32.9	1.3+1.3	7.2+4.5	1.3+0.94	-5.3+5.0	-3.7+5.6
i	-19.9+6.8**	1.4+10.7	-3.9+1.5*	-73.4+24.2**	-21.8+7.3**	-64.7+11.2**	-0.3+0.5	-0.1+1.4	-0.6+0.35	1.7+1.6	1.0+1.8
				Dokki331 X VR$_{14}$							
m	141.7+4.4**	32.7+1.4**	5.7+0.33**	75.8+1.3**	39.7+0.9**	66.7+2.1**	2.0+0.04**	11.9+0.03**	1.7+0.17**	15.7+0.33**	16.9+0.52**
d	38.3+6.1**	-19.0+1.7**	0.8+0.33**	8.9+3.9*	3.0+1.6	-3.5+2.4	-0.3+0.08**	-0.3+0.22	-0.22+0.12	-0.5+0.23*	-1.3+0.18**
h	21.5+14.9	-3.6+6.3	0.9+2.0	9.9+8.8	6.6+4.3	5.8+8.9	0.14+0.3	-0.13+0.81	0.33+0.4	4.4+1.2**	0.13+1.3
l	15.5+44.2	-38.4+16.4*	8.5+6.1	41.1+23.2	-12.0+10.9	5.1+22.3	1.04+0.6	1.1+1.7	-0.21+1.36	-14.4+3.7**	2.1+4.5
i	-4.4+14.2	-21.2+9.2*	-1.4+2.0	-31.9+10.5**	-2.0+4.2	-27.6+9.5**	-0.7+0.24**	-1.6+0.75*	-0.9+0.43**	-1.1+1.2	-2.9+1.4*

*, **: significant at 5% and 1% levels, respectively.

REFERENCES

Bieri, J. and T.J. Kawecki (2003): Genetic architecture of differences between populations of cowpea weevi (Callosobruchus maculates) evolved in the same environment. Evolution, 57: 2, 274-287.

Gad El-Hak, S.H.; M.N.M. Hassan and S.H. Mahmoud (1988): Yield component analysis in cowpea (Vigna unguiculata (L.) Walp.). Minia J. Agric. Res. Dev., 10:1469-1479.

Hooda-J.S.; Y.S. Tomer, B.P.S., Malik and R.S. Khatri (2003): Genetic analysis of seed and important traits in pigeon pea. Environment and Ecology, 21: (1), 37-40.

Lopes-FC-da-C; R.L.F. Gomes, Friere-Filho-FR, da-c-Lopes-FC (2003): Genetic control of cowpea seed sizes. Scientia-Agricola. 60:2, 315-318.

Mather, K. (1949): Biometrical Genetics. 1st ed. Methuem, London.

Mather, K. and Jinks, J.L. (1971): Biometrical Genetics Chapman and Hall Ltd., London.

Ojod K.;J.G. Bounde; S.A. Ogunbayo and A.F. Akinwale (2006): Genetics evaluation of phosphorus utilization in tropical cowpea (Vigna unguiculata (L) Walp.African J. of Biotechnology, 5(8): 597-602.

Oommen, A.; K.M.N. Namboodiri and V.K.G. Unnilhan (1999): Genetic analysis of yield and yield components in pigeon pea. J. Tropical Agr. 37: 1-2, 12-16.

Paralkar, R.M.; J.G. Patil; R.B. Deshmukh and S.S. Mehetre (1997): An analysis of degree of dominance for yield and its components in blackgram (Vigna mungo (L.) Hepper). Legume Res. 20: 3-4, 165-169.

Patil, S.B. and R.S. Patil (1986): Genetic studies in cowpea. J. of Maharashtra-Agr. Univ. 11: 1.51-53.

Pooran-Chand, C.R. Rao and P. Chand(2002): Studies on gene action in a biparental cross in blackgram [Vigna mungo (L.) Hepper]. Indian J.of Genetics-and Plant-Breeding. 62:4, 347-348.

Rahman, M.A. and M.S. Saad (2000): Estimation of additive, dominance and digenic epistatic. Euphytica, 114:1, 61-66.

Sheela Mary S. and A. Gopalan (2006): Dissection of genetic attributes among yield traits of fodder cowpea in F_3 and F_4. J. Applied Sci. Res. 2 (10): 805-808.

Singh, R.K. and Chaudhar, B.D. (1977): Biometrical Methods in quantitative Genetic Analysis, Kalyani Publishers, Delhi.

Suzan, A. Swidan (2005): Genetic evaluation of developmental and yield characters and isozymes polymorphism in some pea crosses. J. Agr. Sci. Mansoura Univ., 30(9) 5243-5260.

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التقييم الوراثي لبعض الصفات الكمية في بعض تلقيحات اللوبيا

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تمت هذه الدراسة أثناء مواسم ٢٠٠٣, ٢٠٠٤، ٢٠٠٥، ٢٠٠٦ في المزرعة التجريبية لكلية الزراعة جامعة قناة السويس بالاسماعيلية ، وقد استهدفت دراسة أداء صفات النمو والمحصول لخمس تراكيب وراثية أبوية لنبات اللوبيا والجيل الأول والثاني والثالث،للتهجين منها وأيضا لدراسة الفعل الجيني. تم زراعة الأجيال الخمسة الآباء والجيل الأول والجيل الثاني والجيل الثالث معا أثناء الموسم ٢٠٠٦، وقد سجلت البيانات على متوسطات كل الأجيال. كان الجيل الأول للهجين "VR4 X VR3" أعلى في متوسطاته عن كلا الأبوين في جميع الصفات ما عدا صفات عدد الاوراق و عدد الفروع في النبات و وزن القرون في النبات. بينما كان الجيل الاول و الثاني و الثالث أعلى في متوسطاتها عن كلا الابوين في صفات طول النبات،وزن، و عدد القرون و وزن البذور في النبات و وزن ال ١٠٠ بذرة في الهجين "VR6XVR4". و أظهر الجيل الأول للهجين "Dokki 331XVR4" أعلى قيم متوسطات بالنسبة لصفات وزن المحصول و عدد القرون و وزن البذور في النبات و وزن البذور في القرن و وزن ال ١٠٠ بذرة كما كانت اعلي قيم متوسطات للجيل الاول في الهجين"Dokki 331XVR14" بالنسبة لصفات عدد الافرع و وزن القرون و عدد القرون و وزن البذور في النبات و كذلك عدد و وزن البذور في القرن. أشارت القيم المعنوية لاختبارات نموذج توريث الصفات عن طريق الإضافة والسيادة إلى وجود تفاعل غير اليلي تقريبا يتحكم في توارث كل الصفات في الأربعة تلقيحات. لوحظ تاثيرات الإضافة المعنوية سواءا السالبة أو الموجبة في معظم الصفات في التلقيحات الأربعة و كانت التأثيرات الجينية السائدة معنوية بالنسبة لصفة عدد الأفرع في النبات في الهجين "VR4 X VR3" و صفات طول الساق، عدد الأفرع للنبات، عدد القرون للنبات.في التلقيح"VR6XVR4" و صفتي وزن البذور للنبات وطول القرن في النبات في التلقيح "Dokki331XVR4" كما كانت أيضا معنوية بالنسبة لصفة طول القرن في الهجين"Dokki331XVR14". وقد وجد أن التفاعل غير الأليلي من النوع "مضيف × مضيف" و"سائد × سائد" تتحكم في وراثة معظم الصفات في التلقيحات الأربعة.

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