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Estimation of Some Genetic Parameters using Six Populations of Two Cowpea Hybrids

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Abstract: The present experiment was carried out at South Valley University, Experimental Farm, during the three summer seasons of 2007, 2008 and 2009. The objective of this work to estimate of some genetic parameters to understand the inheritance of yield and its components of cowpea crosses (Azmerly × IT 82C-16 and Azmerly × IT 81D-1137). The results showed significant deviation from zero for values of A, B and C for all studied traits, indicating the in adequacy of the additive dominance model and the presence of non-allelic gene interaction. The additive and dominance gene effects and the types of epistasis, i.e., additive × additive, additive × dominance and dominance × dominance were important in the genetic system controlling for all studied traits in the two crosses. Dominance gene action (h) was the main types of gene effects for all studied traits in both crosses. The additive gene effects were found to be significant positive for days to flowering, number of pods/plant in the (cross 1), weight seeds/plant (g), total seed yield/kg feddan in the (cross 2), suggesting the potential for obtaining further improvements of these traits by using pedigree selection program. Duplicate epistasis was found for all studied traits in the two crosses. Heterosis % over mid-parent value ranged from - 4.45% for days to Flowering to 23.75% for number of seeds/pod trait in the (cross 2). The inbreeding depression % value ranged from -12.87% for days to flowering to 17.02% for number of pods/plant in the (cross 1).

Key words: Cowpea, scaling tests, gene effects, inbreeding depression, heterosis

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp.) is considered to be one of the most important legume crops grown in the summer season in Egypt. Cowpea is well adapted to stress and has excellent nutritional qualities (Sherif and Damarany, 1992; El-Ameen, 2008). The total cultivated area of this crop in Egypt was estimated at 9155 feddan for dry seed production in the year of 2008 with a mean 980 kg feddan^{-1}. Also, the estimated area for fresh pods was 10064 kg feddan^{-1} with a mean production of 5.19 ton/feddan (Dep. Agric. Statistics, Ministry of Agriculture, Giza, Egypt, 2008). According to Rachie (1985), worldwide production levels may approach or exceed 25 million tons of dry seed every year on about 9 million hectares. Cowpea is grown extensively in 16 African countries; Nigeria and Niger together produce 49.3% of the world crop. The third largest cowpea producing country is Brazil; where 26.4% of the worldwide total is produced (Som and Hazra, 1993). Cowpea can be used at all stages of its growth as a vegetable crop. The tender green leaves are an important food in Africa and prepared as a potherb, like spinach (Mroso, 2003). Immature snapped pods are used in the same way as snap beans, often being mixed with other foods.

Green cowpeas are boiled as a fresh vegetable, or may be canned or frozen. Dry seeds are also suitable for boiling and canning.

The partitioning of the genetic variance is of great importance to the breeder to choice the appropriate breeding program. Breeding procedures for improving cowpea is mainly dependent on the type of gene action and relative amount of the genetic variance components in the population. However, the improvement of both quantities and qualitative traits of cowpea depends on the presence of genetic variability that permits effective selection. It is assumed in most analysis that non-allelic interaction are absent although these analysis rarely provide a valid test of this assumption. Also, the tests of epistasic gene effects are very important for plant breeder along with the other two types of gene effects i.e., additive and dominance. Much work has been done towards understanding the inheritance of yield and yield components in cowpea, Sherif and Damarany (1992), Abd-Elhady (1998), Rashwan (2002), Adeyanju and Ishiyaku (2007) and El-Ameen (2008). Gene action of some characters in cowpea was studied by Bhor and Dumber (1998). They found that the magnitude of additive (d) gene effects was predomenent in most of the crosses for days to flowering. Dominance (h) gene effects were observed in all crosses. The additive x additive (i) epistasis was of a higher magnitude in most crosses for days to maturity. In anther study, Sangwan *et al.* (1998), stated that gene effects were predominantly, but additive and dominance x dominance epestatic effects were also significant in some crosses.

Comstock (1955) has shown how the presence of epistatic gene effects will cause an upward bias in the estimates of both the additive and dominance genetic variance. Perhaps, inclusion of epistasis in the model to be analyzed would decrease the amount of additive genetic variance, but this dose not appears to be the complete explanation. Hayman (1958) described parameters related to those of Anderson and Kempthorne (1954) which permit estimation of the additive, dominance, additive x additive, additive x dominance, dominance x dominance gene effects with less difficulty their interpretation. Estimation of additive, dominance and digenic epistatic interaction effects for certain yield characters was studied by Rahman and Saad (2000). They found that the importance of dominance (h) gene effects for pod yield/plant and pods/plant as compared to additive (d) gene effects. Significant and positive additive effects were noticed for pod yield/plant, pods/plant, pod weight and seed weight in different crosses. Among the digenic epistatic interactions, both additive x additive (i) and dominance x dominance (l) contributed more for pod yield/plant and pods/plant, however, it varied among the crosses. Duplicate type of epistasis was found for all traits in the two crosses. These results disagree with Sherif and Damarany (1992) and El-Ameen (2008). They found that two types of non-allelic gene interaction (duplicate or complementary types).

Heterosis depends on the non-additive gene effects, therefore, the nature of gene action was studied. The estimate of heterosis % over mid-parent and inbreeding depression were applied by Zaveri *et al.* (1983), Patil and Shete (1987), Sawant *et al.* (1994) and Abd-Elhady (1998), found that heterosis % over mid-parent ranged from -0.48% for days to flowering to 22.2% for weight of seeds/plant. Inbreeding depression% ranged from -22.01% for weight of seeds/plant to 4.07% for days to flowering.

The aim of the present study to estimate some genetic parameters, heterosis and inbreeding depression using six populations of tow cowpea hybrids.

MATERIALS AND METHODS

The present study was conducted the summer seasons of 2007, 2008 and 2009 at the experimental farm of the Faculty of Agriculture, South Valley University, Qena governorate,

Table 1: The name and source of two cowpea population

Name	Source
Population 1	
Azmerly** × IT 82C-16*	**Local, Egyptian Agricultural organization, Egypt
Population 2	
Azmerly** ×IT81D-1137*	*Prof. Dr. A. M. Damarany, Hort. Dept., Faculty of Agric., Sohag Univ

Egypt. The soil in the experimental site was clay loam. The name and source of the three parents is presented in Table 1.

In the first summer season 2007, three parental genotypes were grown and two cowpea crosses were made by hand, i.e., Azmerly × It82C-16 (cross 1) and Azmerly × IT81D-1137 (cross 2). In the second season, 2008, seeds of two F_1's were planted to produce F_2 and it were backcrossed to both parents to produce Bc_1 ($F_1 \times P_1$). In the third summer season, 2009, the obtained seeds of the six populations (P_1, P_2, F_1, F_2, Bc_1 and Bc_2) of both crosses were sown on first April and evaluated using a randomized complete block design with three replications. Each replicate consisted of 30 ridges, the ridge was 3 m length 70 cm apart and plants spaced 20 cm from each to other. The experimental plot consisted of four ridges for each parents, F_1 and back-crosses as well as 10 ridges for F_2 generation. The recommended agricultural practices of cowpea production were applied at the proper time.

Recorded Data

Data were collected on competitive plants of each population for days to flowering, pod length (cm), number of seeds/pod, number of pods/plant, weight of pods/plant, weight of seeds/plant (g), weight of 100 seeds (g) and total seed yield kg/fedden, one feddan = 4200 m^2.

Statistical Procedures

The (A, B and C) scaling tests as outlined by Mather and Jinks (1982) were used to test for epistasis. The six-parameter genetic model of Jinks and Jones (1958) was applied to separate out the components of genetic variance to its main effects additive and dominance and their respective first order interactions i.e., additive × additive, additive × dominance and dominance× dominance. Heterosis as a percentage of mid-parents (Singh and Khanna, 1975) and inbreeding depression value (Mather and Jinks, 1982).

RESULTS AND DISCUSSION

Mean Performance

Means and standard errors of the six populations (P_1, P_2, F_1, F_1, Bc_1 and Bc_2) of the two cowpea crosses for the studied traits are given in Table 2.

The F_1 was earlier than the earliest parent in two crosses. The F_1 surpassed its high performing parent for weight of pods/plant and weight of seeds/plant traits for two crosses and pod length (cm) for (cross1) and number of pods/plant and total seed yield kg Fed^{-1}. for (cross 2). These results provided evidence for the presence of heterotic effect. These results are in agreement with those obtained by Damarany (1994), Rashwan (2002), Abd-Elkader (2006) and El-Ameen (2008), Hussein and El-Dakkak (2009).

Scaling Test

The results of scaling test (A, B and C) in (Table 3) were significant for all studied traits in two crosses. This indicates the failure of a simple genetic model to explain the genetic system controlling the studied traits in the two crosses and suggests the presence of epistasis in all traits.

Table 2: Mean±SE for six population of the tow cowpea crosses for all studied traits

	Days to flowering		Pod length (cm)		No. of seeds/pod		No. of pods/plant	
Population	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$
P_1	72.00±0.83**	92.00±0.83**	13.11±0.05**	13.11±0.05**	9.14±0.01**	19.14±0.01**	55.86±1.38**	55.86±1.38**
P_2	72.96±0.80**	69.43±1.07**	17.21±0.03**	19.74±0.09**	11.10±0.03**	15.10±0.54**	36.16±1.17**	47.86±0.86**
F_1	70.16±0.91**	67.56±0.97**	17.86±0.07**	19.26±0.09**	10.90±0.02**	15.00±0.11**	50.96±1.32**	57.10±0.88**
F_2	79.2±1.02**	73.25±1.27**	16.21±0.05**	18.91±0.20**	9.83±0.03**	14.37±0.08**	42.29±1.29**	50.02±1.31**
Bc_1	70.90±1.29**	70.10±1.11**	15.04±0.11**	13.81±0.13**	9.92±0.07**	10.06±0.06**	48.58±1.34**	59.08±1.46**
Bc_2	72.6±1.09**	67.78±1.02**	18.24±0.26**	20.01±0.17**	11.25±0.11**	15.61±0.12**	58.26±1.23**	54.25±1.28**
HMP(1)	-3.19	-4.45	17.80	7.66	17.25	23.75	10.75	10.08
I. D.(2)	-12.87	-8.41	9.25	1.83	9.79	4.20	17.02	12.39
	Weight of pods/plant (g)		Weight of seeds/plant (g)		Weight of 100 seeds (g)		Total seeds yield kg feddan^{-1}	
Population	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$
P_1	71.01±0.21**	71.01±0.21**	543.58±0.63**	45.58±0.63**	19.17±0.16**	19.17±0.16**	1289.99±1.44**	1289.99±1.44**
P_2	73.03±0.50**	87.13±0.61**	49.31±0.45**	60.06±0.80**	17.54±0.18**	16.54±0.11**	1140.04±0.83**	1350.06±3.08**
F_1	81.12±1.13**	90.16±0.49**	55.46±0.62**	62.28±0.79**	18.27±0.17**	17.27±0.45**	1270.29±1.05**	1390.84±2.93**
F_2	73.55±0.68*	84.66±0.73**	50.36±0.44**	58.29±0.94**	17.38±0.34**	16.16±0.63**	1150.33±1.11**	1297.96±15.13**
Bc_1	76.70±1.26**	68.30±1.41**	55.59±1.13**	60.45±1.44**	19.51±0.18**	20.02±0.12**	1301.55±2.40**	1340.26±1.95**
Bc_2	78.52±1.32*	92.5±1.40**	52.92±1.12**	64.39±1.35**	18.58±0.21**	16.81±0.09**	1250.81±2.21**	1370.66±1.95**
HMP(1)	12.63	14.02	6.76	8.65	-0.48	-3.25	4.54	5.36
ID(2)	9.33	6.10	9.19	6.40	4.88	6.45	9.44	6.67

(1): Heterosis over mid- parent (%); (2): Inbreeding depression (%), * and ** significant at 0.05 and 0.01 levels of probability, respectively; Mean±SE

Table 3: Six parameter genetic model and type of epistasis for studied of two cowpea crosses

	Days to flowering		Pod length (cm)		No. of seeds/pod		No. of pods/plant	
Estimates	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$
Scaling tests								
A	-0.37±0.40	0.63±0.37	-0.986±0.034**	-4.76±0.04**	-0.19±0.02**	-4.02±0.01**	-9.67±0.49**	5.2±0.48**
B	2.07±0.36**	-1.43±0.37**	1.39±0.70**	1.01±0.05**	0.50±0.03**	1.11±0.11**	29.40±0.45**	3.53±0.40**
C	31.5±0.54**	16.43±0.64**	-1.21±0.04**	4.25±0.09**	-2.72±0.02**	3.24±0.11**	-24.8±0.75**	-17.83±0.62**
Gene effects								
Mean (m)	79.2±0.09**	73.25±0.12**	16.21±0.01**	18.19±0.02**	9.84±0.002**	14.37±0.01**	42.29±0.12**	50.02±0.12**
Additive (d)	-1.7±0.22**	2.32±0.19**	-3.20±0.04**	-6.20±0.03**	-1.33±0.02**	- 5.54±0.02**	-9.68±0.24**	4.83±0.25**
Dominance (h)	-32.12±0.54**	-20.38±0.61**	41.41±0.07**	-516±0.09**	3.79±0.01**	-3.26±0.07**	49.48±0.69**	31.8±0.64**
Additive× Additive (i)	-29.8±0.58**	-17.23±0.61**	1.713±0.08**	-8.00±0.09**	3.023±0.04**	-6.14±0.05**	44.53±0.67**	26.56±0.69**
Additive× Dominance (J)	-1.22±0.24**	1.03±0.23**	-1.15±0.04**	-2.88±0.03**	-0.35±0.02**	-2.56±0.05**	-19.53±0.29**	0.83±0.29**
Dominance× Dominance(l)	28.1±1.03**	18.03±1.01**	-2.22±0.15**	11.76±0.14**	-3.329±0.07**	9.05±0.13**	-64.26±1.21**	-35.3±1.19**
Type of epistasis	Duplicat	Duplicat	Duplicat	Duplicat	Duplicat	Duplicat	Duplicat	Duplicat
	Weight of pods/plant (g)		Weight of seeds/plant (g)		Weight of 100 seeds (g)		Total seeds yield kg feddan^{-1}	
Estimates	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$	$Cross_1$	$Cross_2$
Scaling tests								
A	1.268±0.39**	11.43±0.38**	1.15±0.34**	4.04±0.42**	1.58±0.06**	3.49±0.09**	42.82±0.70**	-0.315±0.78
B	2.88±0.41**	7.71±0.39**	1.06±0.32**	6.43±0.41**	1.35±0.07**	-0.19±0.09**	91.29±0.62**	0.415±0.93
C	-12.07±0.53**	0.17±0.35**	-13.36±0.31**	-6.04±0.49**	-3.74±0.15**	-5.62±0.25**	-369.26±0.61**	229.91±5.68**
Gene effects								
Mean (m)	73.55±0.06**	84.66±0.07**	50.36±0.04**	58.29±0.09**	17.38±0.03**	16.16±0.04**	1150.33±0.10**	1297.96±1.38**
Additive (d)	-1.81±0.24**	-6.19±0.26**	2.67±0.21**	-3.93±0.26**	0.93±0.04**	3.21±0.02**	50.73±0.42**	-30.40±0.36**
Dominance (h)	25.32±0.52**	30.05±0.47**	19.09±0.38**	21.47±0.54**	6.59±0.15**	8.44±0.20**	558.66±0.77**	300.82±5.61**
Additive× Additive (i)	16.22±0.53**	18.96±0.58**	15.58±0.44**	16.51±0.62**	6.68±0.15**	9.02±0.17**	503.38±0.94**	230.01±5.57**
Additive× Dominance (J)	-0.81±0.24**	1.86±0.26**	0.04±0.22**	-1.19±0.27**	0.11±0.04**	1.89±0.03**	-24.23±0.45**	-20.37±0.47**
Dominance× Dominance(l)	-20.37±1.07**	-38.09±1.08**	-17.80±0.88**	-26.98±1.13**	-9.61±0.21**	-12.43±0.25**	-637.50±1.81**	-230.10±5.84**
Type of epistasis	Duplicat	Duplicat	Duplicat	Duplicat	Duplicat	Duplicat	Duplicat	Duplicat

*and **significant at 0.05 and 0.01 levels of probability, respectively; Effects±SE

Gene Action and Epistasis Effects

Different types of gene effects were presented in Table 3, the estimated mean effect parameter (m) was found to be highly significant for all studied traits in the two crosses. Initially, it is clear that all studied traits were quantitatively inherited.

The additive (d) gene effects were found to be highly significant positive for weight of seeds/plant and total seed yield kg/fed. traits for (cross 1), days to flowering and number of

pods/plant for (cross 2) and weight of 100 seeds (g) for two crosses, suggesting the potential for obtaining further improvement of these traits by using pedigree selection program. These results are in close agreement with those of Bhor and Dumber (1998), Sangwan *et al.* (1998), Rahman and Saad (2000) and Abd-Elhady (2003).

On the other hand, highly significant negative additive effects were obtained for days to flowering and number of pods/plant traits in the (cross 1), weight of seeds/plant and total seeds yield kg/fed in the (cross 2) and pod length (cm), number of seeds/pod and weight of pod/plant in the two crosses, indicating that the additive effects were less important in the inheritance of these traits.

The estimated of dominance (h) effects were highly significant for all the studied traits in the two crosses, indicating the importance of dominance gene effects in the inheritance of these traits. These results are in harmony with those reported by Rashwan (2002), Abd-Elkader (2006) and El-Ameen (2008). They found that dominance effect were importance in the inheritance of yield and its components.

Highly significant positive additive × additive (i) types of epitasis was detected for pod length and number of seeds/pod in the (cross 1), number of pods/plant, weight of pods/plant, weight of seeds/plant, weight of 100 seeds and total seeds yield kg/fed in the crosses. Highly significant negative additive × additive was found for pod length (cm) and number of seeds/pod in the (cross 2) and days to flowering in the two crosses.

Highly significant positive additive × dominance (J) types of epistasis was found for weight of seeds/plant in the (cross1), days to flowering, number of pods/plant and weight of pods/plant in the (cross 2) and weight of 100 seeds in the two crosses.

While highly significant negative additive × dominance for days to flowering, number of pods/plant and weight of pods/plant in the (cross 1), weight of seeds/plant in the (cross 2) and pod length (cm), number of seeds/pod and total seed yield kg Fed^{-1}. in the two crosses.

Dominance × dominance (L) epestatic types were highly significant positive for pod length (cm) and number of seeds/pod in the (cross 2) and days to flowering in the two crosses. These results showed that both additive and dominance as well as one or more of the three types of epistasis, i.e., additive × additive (i), additive × dominance (J) and dominance × dominance (L) were important in the genetic system controlling in most studied traits.

These results are in agreement with those obtained by Lodhi *et al.* (1990) Sherif and Damarany (1992), Umarahan *et al.* (1997), Abd-Elhady (1998), Bhor and Dumber (1998), Sangwan *et al.* (1998), Sangwan and Lodhi, (1999), Rahman and Saad (2000), Abd-Elhady (2003), Adeyanju and Isjiyaku (2007), Abd-Elkader (2006) and El-Ameen (2008).

Duplicate epistasis (Table 3) was observed, as revealed by difference in signs of (d) and (dd) in crosses which exhibited significant epistasis. These findings illustrated that duplicate epistasis was prevailing for all studied traits in the two crosses. This indicated that duplicate epistasis was greater and important for all studied traits. These results are in harmony with those reported by Rashwan (2002) and Abd-Elkader (2006). In contrast, Sherif and Damarany (1992) and El-Ameen (2008). Their results indicated that both complementary and duplicate type of non allelic gene interaction was found for all studied traits. In another study, Bhor and Dumber (1998), stated that duplicate type of epistasis was evident for all characters in a few crosses, while a complementary type of epistasis was observed for pod length each for one cross.

Heterosis and Inbreeding Depression (%)

Positive heterosis % over mid parent (Table 2) ranged from 4.54% in the (cross 1) for total seeds yield kg/fed. to 23.75% in the (cross 2) for number of seeds/pod trait, while negative heterosis% ranged from -0.48% in the (cross 1) for weight of 100 seeds to -4.45 in the (cross 2) for days to flowering traits. Negative value of heterosis for days to flowering is the desirable value, since earliness is an important objective for the cowpea breeder. These results are in harmony with those reported by Patil and Shete (1987), Naidu and Yana (1993), Abd-Elhady (1998), Viswanatha *et al.* (1998) and Abd-Elkader (2006). Greatest positives heterosis over mid-parent was observed for seed yield/plant and pods/plant by Sawant *et al.* (1994). In another study, Rashwan (2002), found that heterosis % over mid-parent ranged from (-3.48%) days to flowering (9.25%) for pod length (6.90%) for number of seeds/pod (10.73%) for number of pods/plant (11,36%) for weight of seeds/plant (5.59%) for weight of 100 seeds (11.9%) for total seed yield kg/fedden to (15.81%) weight of pods/plant.

The inbreeding depression % ranged from -12.87 for days to flowering in the (cross 1) to 17.02% for number of pods/plant in the (cross 2). The above finding are in agreement with those reported by Viswanatha *et al.* (1998), Mehta (2000) and Rashwan (2002), stated that inbreeding depression % ranged from (-5.99%) for days to flowering (13.33%) for total seed yield/kg feddan (4.13%) for pod length (5.88%) for number of seeds/pod (13.15%) for weight of pods/plant (12.82%) for weight of seeds/plant (7.99%) for weight of 100 seeds to (19.31%) for number of pods/plant.

CONCLUSION

The additive and dominance gene effects and the types of epistasis were important in the genetic system controlling for all studied traits in the two crosses. Heterosis % over mid-parent value ranged from -4.45% for days to Flowering to 23.75% for number of seeds/pod trait in the (cross 2). The crosses Azmerly × IT82C–16 and Azmerly × IT 81D-1137 would be of interest in a breeding program, for earliness, yield and its components of cowpea.

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