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GENETIC VARIANCE REVEALED IN COWPEA BY PARTIAL DIALLEL AND FACTORIAL MATING DESIGNS

Ameen, El. A.: W. A. Ramadan and A. Y. Elsayed
Horticulture Research Institute. Agricultural Research Center, (ARC), Giza, Egypt

ABSTRACT

Genetic variability and heritability are two important factors for plant improvement programs where the magnificence and type of this variability determine the selection criteria to be used by the breeder. This study aimed to estimate the genetic components associated with variance and covariance based on partial diallel crosses and factorial mating designs, as well as, to identify the association between yield components and other quantitative traits to extend an orientation for selection. Six cowpea varieties were used in this study. All possible crosses were done according to partial diallel mating design in addition to the F_1 hybrid which were arranged in a factorial mating design. The parents, F_1 and their F_2 generations were evaluated in a field trial experiments at El-Baramon station, Dakahlia Governerate, in a randomized complete blocks design with four replicaties. The results revealed that both two mating designs were suitable to study the genetic parameters. The means of F_1 hybrids exceeded the mid parents (MP) and the better parent (BP). Significant values of heterosis were obtained for all studied traits. The highest values were 43.84% for pod length versus MP and 15.68% for number of pods per plant versus BP. The magnitude of both additive and non-additive genetic variances were high that means the possibility to development inbred lines of cowpea through selection. The higher values of broad-sense and narrow-sense heritability indicating good genetic variability for effective selection. The following traits; pod length, pod weight, weight of 100-seeds, and number of seeds per pod could be considered in breeding for grain yield, as they contribute significantly to its improvement.

Keywords: genetic variation, heterosis, inbreeding depression, *Vigna unguiculata*

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp) is a diploid plant with 2n=22 chromosomes with a genome size of 613 Mbp (Singh *et al*. 2014). It is an important food legume cultivated in over 65 countries (Singh 2005). The grains are important source of plant protein contains in average 22.0% protein, 1.4% fat, 59.1% carbohydrate, and 3.7% ash (Ajit *et al*, 2014). The protein in cowpea seeds is rich in lysine and tryptophan amino acids compared to cereal grains (Eisa and Ali 2014). The cultivated area of cowpea in Egypt was about 4760 fed. in 2013, yielding in average about 0.85 ton (FAO 2013). In autogamous species, the selection of individual plants or mass selection can be effective if the base population exhibit sufficient genetic variability. Therefore, to improve autogamous species, the hybridization based on crossing between two or more varieties or lines previously selected by the degree of additional important characteristics, followed by selection of the segregating population, using various methods available is a common approach in self-pollinated plants like cowpea (Nass 2000). To obtain segregating populations, it is important involving high mean productivity with maximum variance. To identify segregating populations involving these two attributes, there are some methodologies. One of the most used are the diallel crosses that, besides allowing identify the most promising segregating populations, provide information about the genetic control of traits (Cruz *et al*. 2004).

Estimation of genetic variance providing information to plant breeder about the suitable program for genetic improvement. Estimation of genetic variance components is generally accomplished by the method of Cockerham (1963). A mating design is used to generate sets of relatives tested in one or more environments, besides an analysis of variance (ANOVA) can be constructed for estimating variance components. Among various mating designs, the factorial (Design II) (Comstock and Robinson, 1952; Hallauer and Miranda, 1981) and the diallel designs (Yates 1947; Hayman 1954; Griffing 1956) are most used by plant and animal breeders.

Patil and Shete (1987) obtained highest positive heterosis over the mid-parents for pod clusters/plant (158%) when they are evaluated 21 F1 hybrids of cowpea followed by seed yield/plant followed by pods/plant (89%). Similarly, Sawant *et al*. (1994) studied 10 varieties of *Vigna unguiculata* L. and 45 F_1 hybrids among them.They noticed greatest positive heterosis over mid-parents (MP). These values were for seed yield/plant (140.5%), pods/plant (132.5%), branches/plant (85.6%) and plant height (73.4%).

Sawant (1995) evaluated 10 parental varieties of *Vigna unguiculata* and 45 F_1 hybrids among them through 10 x 10 diallel crosses (excluding reciprocals). The results stated that both general combining ability (GCA) and specific combining ability (SCA) variances were highly significant for all studied yield traits. In addition, non-additive gene effects predominated, except for pod length and 100-seed weight. In this respect, Biradar *et al*. (1993) evaluated three varieties of cowpea, F_1 hybrids, F_2 generations and back crosses. They observed that additive gene effects were important for the inheritance of most studied traits. They also noticed the importance of dominance effects for numbers of pods/plant, grain yield/plant and 100-seed weight.

In similar study on cowpea consisted of 40 genotypes, Dharmalingam and Kadambavanasundaram (1984) obtained values of broad-sense heritability as 87.37%, 85.38% and 69.58% for pod length, 100-seed weight and harvest index, respectively. In the same time, Patial and Baviskar (1987) studied some important traits for cowpea for 49 genotypes and found highest heritability for 100-seed weight (90.94%) followed by days to maturity and pod length. Their results indicated that the improvement should be based on 100-seed weight, pods/plant, pod clusters/plant and seed yield/plant. Similarly Sharma *et al.* (1988) obtained heritability value ranged from 46.9% for green pod yield to 98.0% for days to 50% maturity.

Thiyagarajan (1989) evaluated seven parents and their F_1 hybrids, of cowpea and concluded that the estimates of heritability and genetic advance were high for plant height, number of seeds/pod and 100-seed weight. In the same time, Ram *et al*. (1994) studied 27 *Vigna unguiculata* varieties and concluded that the highest heritability estimates were found for plant height

(36%). Their results reflected high heritability and high genetic advance as a percentage of mean for plant height, seed yield/plant and pods/plant.

Correlation studies were important to determine the association between yield and other quantitative traits to be providing an orientation for selection, i.e, whether a given trait of interest can be indirectly selected by selection for another (Mohammed *et al*. 2010). The same authors found that the number of pods per plant, seeds per pod and seeds per plant could be used in both direct and indirect selection for grain yield in cowpea. Thaware *et al.* (1992) studied 30 genotypes of forage cowpea and mentioned that phenotypic coefficients of variation were higher than genotypic coefficients. Senanayake and Wijerathne (1988) studied 17 varieties of cowpea and found that yield traits were negatively correlated with the number of primary branches (r = -0.88) and positively correlated with 100-seed weight (r = 0.98) and pod length (r = 0.88).

Oseni *et al.* (1992) noticed the presence of positive correlations values between seed yield and pods/plant, as well as, between days to flowering and 100-seed weight. In addition, the results of the same authors appeared a negative correlation between 100-seed weight and seed yield. Naidu *et al*. (1996) found positive correlation for seed yield with number of pods/plant, seeds/pod, pod length and seed weight, when they are evaluated 48 determinate and 25 indeterminate types of *Vigna unguiculata*.

The selection in segregating population can be more effective when the base population exhibit sufficient genetic variability with high mean productivity. Thus, to development such segregating population with high mean productivity and maximum variance it is a common approach applying different mating designs in self-pollinated plants.

The objective of this study was to estimate the genetic components associated with variance and covariance based on partial diallel crosses and factorial mating designs. Furthermore, identify the association between yield components and other quantitative traits to be extended as orientation for selection.

MATERIALS AND METHODS

Materials

Genetic material

Six cowpea (*Vigna unguiculata* L.) varieties as follows; Carim 7, H8-9, H6-16, VIH-8, S12 and S18 were used in this study. The first three varieties were obtained from Vegetable Research Dept., Horticulture Research Institute, Agriculture Research Center, Giza, Egypt. The other three varieties were obtained from IITA (International Institute of Tropical Agriculture).

Methods

Experimental design

In the first growing season of 2012 all possible F_1 hybrids were made according to partial diallel crosses mating design. The F_1 hybrids were also arranged in a factorial mating design where the varieties Carim 7, H 8-9 and H 6-16 were used as a male parents and the varieties VIH-8, S12 and S18 were used as a female parents. In the same growing season, all parental varieties were selfed to obtain enough seeds. In the second growing season of 2013, the six parental varieties and their hybrids were selfed to be obtained the F_1 hybrids.

In the third growing season of 2014 all varieties, F_1 hybrids and their F_2 generations were evaluated in a field trial experiments at El-Baramon station, Mansoura center, Dakahlia Governerate. The experimental design used was a randomized complete blocks design with four replicates. Each replicate contained 36 entries in a partial diallel and 24 entries in the factorial mating design. Plots were two rows of 4.0 m. long and 50 cms wide. Hills were spaced at 35 cms apart. All field practices were followed according to the recommendations of Ministry of Agriculture for cowpea cultivation.

Vegetative traits and yield components

The following traits were estimated; number of branches per plant (NBP), number of pods per plant (NPP), number of seeds/pod (NSP), number of days to first flower (DFF), pod length (PL), plant height in cm (PH) and weight of 100-seeds in grams (WS).

Statistical analysis

Different analyses of variance were made to test for the presence of heterosis, inbreeding depression and the other genetic parameters. The partial diallel analysis was accomplished as described by Cocherham (1963). While the factorial mating design, the analysis of variances accomplished according to the factorial arrangement presented by Comstock and Robinson (1952). Genotypic (r_g) and phenotypic (r_{ph}) correlation for any pair of 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).

RESULTS AND DISCUSSION

Six parental varieties, as well as, F_1 hybrids among them (15 hybrids according to diallel crosses mating design excluding reciprocals and 9 hybrids in factorial arrangement) and their corresponding F_2 generations were evaluated to estimate heterosis, inbreeding depression, the nature of gene action, heritability and the combining abilities. The results indicated that the means of F_1 hybrids significantly exceeded the means of parental varieties (Table 1). The results cleared the presence of heterosis for all studied traits. In this respect, the obtained values of heterosis versus the mid-parents were ranged from 4.83 % to 43.84% for number of days to first flower and pod length, respectively. In addition, the means of F_1 hybrids exceeded the better parent. The values of heterosis versus the (BP) were ranged from 4.80% to 15.68% for number of seeds per pod and number of pods per plant, respectively. This finding showed that superior F_1 hybrids could be used to obtain inbred lines through selection at the segregating generations. Heterosis values in F_1 hybrids followed by inbreeding depression in the F_2 generations were expected. The values of heteresis obtained from the parental varieties depend on the relation between these varieties. The results obtained herein agreed with Gasim (2003), who quantified mid parent heterosis for yield in a similar study to be about 75%.

Concerning inbreeding depression, the results revealed that the performances of F_1 hybrids was always larger than those F_2 generations. Thus it could be noticed that inbreeding depression (I.D) took place and presence for all studied traits. The highest value of I.D was obtained for number of pods per plant with the mean of -27.6. The results reflected the greater amounts of heterosis, as well as, the greater amounts of I.D.

Evaluation of offspring obtained from both diallel crosses and the factorial mating design would provide an estimation of different genetic parameters. The results illustrated that diallel crosses appeared the relative magnitudes of mean squares for GCA variances in F_1 hybrids and F_2 generations which were larger than those of SCA for all traits (Table 2). This finding cleared the importance of additive genetic variance and peristaltic (Additive x Additive) in the inheritance of all studied traits. Similar results could be noticed from factorial mating design. The mean squares of females or males were larger than those mean squares of male x female. In contrast to our findings, Supriyo *et al*. (2010) reported that the magnitude of non-additive gene action was higher than that of additive gene action for each quantitative trait in black gram.

Table 1: Means of parental varieties, F_1 hybrids, F_2 generations and the estimated values of heterosis and inbreeding depression.

Generation	NBP	NPP	NSP	DFF	PL	PH	W/100/S
M.P.	14.31	43.60	10.23	54.67	9.74	52.06	19.61
Range	8.6-17.6	28.1-49.8	8.0-12.5	49.2-62.0	7.1-12.2	42.3-62.7	15.2-11.1
F_1	18.78	57.62	13.11	52.03	14.01	68.42	24.24
Range	11.3-22.3	33.1-64.7	12.0-14.2	50.0-60.1	12.0-16.0	52.8-70.9	16.3-28.1
F_2	16.92	41.88	11.07	59.89	10.23	57.07	21.07
Range	10.4-19.7	30.0-55.3	7.3-13.0	47.6-51.0	8.1-14.2	51.1-63.6	16.9-23.4
H (MP) %	31.2**	32.1**	28.15**	-4.83*	43.8**	31.4*	23.6**
H (BP) %	6.7*	15.6**	4.80	5.75*	14.1**	8.9*	9.53**
I.D %	-9.9*	-27.3**	-15.56**	15.1**	-26.9**	-16.5**	-13.0**

***Significant at 5% level; **Significant at 1% level; NBP: number of branches per plant; NPP: number of pods per plant; NSP: number of seeds/pod; DFF: number of days to first flower; PL: pod length; PH: plant height in cm; W100S: weight of 100-seeds in grams.**

The high values for heterosis appeared a good genetic diversity among cowpea varieties used in this study which indicating the possibility of detecting high yielding transgressive segregates from hybrid populations. However, the estimates for heterosis in most cases is from space planted F_1 hybrids, which may not be a true index of performance under normal plant populations used for commercial crops. Therefore, there is a need to estimate heterosis under recommended plant population for maximum yield of cowpea.

Table 2: Analysis of variance and mean squares obtained from two mating designs in F_1 hybrids and F_2 generations.

S.V.	D.F.	G	NBP	NPP	NSP	DFF	PL	PH	W100S
Half diallel crosses									
Rep.	3	F_1	1.13	1.141	1.011	0.914	0.811	1.271	0.041
		F_2	0.098	0.181	0.122	1.021	1.592	0.092	0.137
Crosses	14	F_1	13.07**	10.68**	19.00**	21.89**	10.25**	79.94	0.327**
		F_2	22.15**	10.86**	15.02**	21.61*	12.62*	72.08	0.701**
GCA	5	F_1	21.04**	11.71**	23.81**	21.114	14.27**	86.76**	0.719**
		F_2	28.19**	14.26**	19.20**	34.93	15.07**	72.21	1.107**
SCA	10	F_1	7.78*	10.09**	14.69**	20.09**	7.22**	68.54	0.098**
		F_2	16.92**	8.07*	11.43*	12.79*	10.13*	64.81	0.482**
Error	42	F_1	0.9	1.14	3.21	4.61	0.92	27.18	0.007
		F_2	2.319	2.01	2.72	6.03	2.08	43.06	0.091
Factorial mating design									
Rep.	3	F_1	0.902	2.91	1.001	2.43	1.09	2.97	0.726
		F_2	1.07	2.003	0.227	1.287	0.423	5.22	0.037
Male	2	F_1	7.09**	14.11**	7.98**	12.81*	5.09	67.83	0.994**
		F_2	9.11**	7.22**	4.22*	14.94**	9.92	55.22	1.003**
Female	2	F_1	6.14**	13.09**	6.87**	10.27*	7.22*	68.73*	0.986**
		F_2	10.32**	7.66**	6.03**	16.22**	11.67*	59.17*	1.307**
M x F	4	F_1	5.12**	11.73*	4.14**	8.35	3.64	64.43**	0.904**
		F_2	8.61**	6.18**	3.94*	14.43*	8.22	54.11*	0.821**
Error	24	F_1	0.96	2.04	0.77	3.92	2.07	27.14	0.192
		F_2	1.61	0.92	0.97	2.82	5.65	22.08	0.102

***Significant at 5% level; **Significant at 1% level; NBP: number of branches per plant; NPP: number of pods per plant; NSP: number of seeds/pod; DFF: number of days to first flower; PL: pod length; PH: plant height in cm; W100S: weight of 100-seeds in grams, G: generation.**

Regarding the components of genetic variance, the results indicated the relative magnitudes of non-additive genetic variances including dominance in F_1 hybrids and F_2 generations which appeared to be larger than additive genetic variances for most studied traits at two mating designs, although the additive genetic values were high and it was not be neglected (Table 3).

Table 3: Additive and non-additive genetic variance and heritability in broad and narrow sense obtained from two mating designs in F_1 hybrids and F_2 generations.

S.V.	Mating des*	Gen	NBP	NPP	NSP	DFF	PL	PH	W100S
Add.	D	F_1	1.658	0.202	1.140	0.128	0.882	2.280	0.078
		F_2	1.877	1.032	1.296	3.688	0.824	1.235	0.104
	F	F_1	0.249	0.311	0.548	0.532	0.419	0.641	0.014
		F_2	0.247	0.280	0.263	0.256	0.573	0.687	0.174
Non-add	D	F_1	1.72	2.238	2.870	2.870	1.575	10.34	0.023
		F_2	6.490	1.693	3.872	3.004	3.579	9.668	0.025
	F	F_1	1.040	2.423	0.843	1.108	0.393	9.323	0.178
		F_2	3.110	2.338	1.310	5.161	1.143	14.236	0.320
h^2_n%	D	F_1	46.02	7.41	22.47	2.48	32.82	11.74	75.88
		F_2	20.28	24.41	22.16	44.98	16.74	5.70	34.55
		F_1	16.29	9.59	34.60	20.31	31.50	3.85	5.83
	F	F_2	6.57	9.83	14.48	4.18	18.31	3.36	68.43
h^2_b%	D	F_1	93.76	89.54	79.05	77.62	91.44	65.00	98.25
		F_2	93.52	88.10	88.37	81.61	89.44	50.31	92.36
		F_1	84.30	84.28	87.82	62.60	61.60	59.49	80.00
	F	F_2	89.28	91.92	86.62	88.48	54.84	73.00	97.63

*** D: diallel crosses; F: factorial mating design; NBP: number of branches per plant; NPP: number of pods per plant; NSP: number of seeds/pod; DFF: number of days to first flower; PL: pod length; PH: plant height in cm; W100S: weight of 100-seeds in grams.**

The presence of high estimated values of dominance genetic variance would explain the highly estimates of heterosis from the mid-parents, as well as, the better parent.

Concerning heritability values obtained from diallel crosses in both broad and narrow sense, the results showed that the magnitudes of h^2_b% were larger than those h^2_n% for all studied traits. The values of h^2_b% were ranged from 65% to 50.31 for plant height and 98.25% to 92.36% for weight of 100-seeds, as well as, from 93.67 to 93.52 for number of branches per plant among the F_1 hybrids and the F_2 generations, respectively. In addition, the highest values of h^2_n% were 75.88% and 44.98% for weight of 100-seeds and number of days to first flower in F_1 hybrids and F_2 generations, respectively. Similar results were obtained in factorial mating design which indicated highest values of heritability in broad (h^2_b%) and narrow (h^2_n%) senses as follows; 87.82 (number of seeds/pod) h^2_n% in F_1 hybrids and 97.63 (weight of 100-seeds) at the F_2 generations. In addition, the highest values of h^2_n% in F_1 hybrids and F_2 generations were 34.6% and 68.43% for number of seeds/pod and weight of 100-seeds, respectively. Similar finding was reported by Seif *et al*., (2004), who found high heritability (h^2= 0.75) in faba beans.

Table 4: Genotypic and phenotypic correlation between different traits in cowpea.

	NPP	NSP	DFF	PL	PH	W100S
NBP	0.33** 0.36**	0.28** 0.29	0.13 0.16	-0.19 -0.22	0.56** 0.62**	0.23 0.27
NPP		0.34* 0.36**	0.21 0.26	0.27 0.29	0.66** 0.71**	0.19 0.22
NSP			0.20 0.23	0.56** 0.61**	0.41* 0.43**	0.20 0.25
DFF				0.31* 0.32*	-0.22 -0.23	0.17 0.19
PL					0.29* 0.33**	0.26* 0.29*
PH						0.25* 0.29*

The phenotypic correlations above and the genotypic correlations below;*Significant at 5% level; **Significant at 1% level; NBP: number of branches per plant; NPP: number of pods per plant; NSP: number of seeds/pod; DFF: number of days to first flower; PL: pod length; PH: plant height in cm; W100S: weight of 100-seeds in grams.

In the genetic improvement of cowpea, breeders handle several traits in order to identify the best lines. Some of these traits, such as; grain yield was controlled by many genes greatly influenced by the environment and usually with low heritability. However, other qualitative traits such as; grain color, seed size, color, hilum, present high heritability. The results in Table 4 showed genotypic (r_g) and phenotypic (r_{ph}) correlations among the studied traits. The results indicated that the magnitudes of genotypic correlation were very close to the corresponding phenotypic correlation. These results were expected since the magnitudes of error in the analysis of covariance were small. Similar finding was observed by Gonçalves *et al*. (2012), who found that all pairs of studied traits in sweet potato related to the genotypic and phenotypic correlations had the same sign and were similar in both magnitude and level of significance. In addition, the values of genetic (cv_g) and environmental (cv_e) coefficients of variation, and the cv_g/cv_e ratio were closed that support the results obtained herein.

The results cleared that number of branches per plant were negatively insignificantly correlated with pod length. Similarly, the number of days to first flower was negatively correlated with plant height. In the same time, plant height showed significant positive correlation with most traits, expect for, DFF. The highest values of genotypic and phenotypic correlations were 0.66 and 0.71 for plant height x number of pods per plant. It also regarded that the highest values of correlation coefficient were 0.66 and 0.71 (genotypic and phenotypic correlations, respectively) for number of pods per plant x plant height. The relation between traits would make it easier to cowpea improvement through the indirect selection. These results agreed with Lopes *et al*. (2001), who found a positive correlation between pod weight, pod length, 100-grain weight, and grain yield. In addition, Romanus *et al*. (2008) also reported positive and significant correlation values ($P \leq 0.01$) between pod length, number of grains per pod and yield of seven cowpea lines.

However, Leonardo *et al*., (2012) reported that the genotypes with high pod weight and pod length, 100-grain weight, and number of beans per pod should be used to improve grain yield in cowpea. Also, the breeder should ideally insert into his group of crosses between genotypes that have a high combining ability for pod length, number of grains per pod and yield per plot. Also, Wener *et al*. (2014) found that the number of pods per plant and the number of grains per pod were the yield components with greater direct effects on the productivity.

In conclusion, both mating designs used in this study were suitable for studying genetic parameters in cowpea. The results cleared that it could be develop inbred lines of cowpea through selection. The high values of broad-sense and narrow-sense heritability indicating a good genetic variability for effective selection. The yield component traits such as; pod length, pod weight, weight of 100-seeds and number of seeds per pod could be considered in breeding for improving grain yield, as they contribute significantly to its improvement. To increase the number of progeny that generate lines with a high combining ability and high-yielding genotypes, the breeder could include parents with high GCA for pod length, number of grains per pod and yield in different crosses conducted in breeding program of genetically improvement cowpea.

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إظهار التباين الوارثى في اللوبيا بواسطة نظام التهجين النصف دوار ونظام التزاوج العاملى

الشبراوى عبد الحميد أمين ، وهبه على السيد رمضان و أحمد يوسف عبد النبى محمد السيد
اقسام بحوث الخضر – معهد بحوث البساتين – مركز البحوث الزراعية – الجيزة – مصر.

يعتبر التباين الوراثي ومعامل التوريث من العوامل الهامة لبرامج تحسين النباتات حيث تحدد أهمية ونوع هذا التباين تحدد معايير الاختيار لاستخدامها من قبل مربى النبات. يتمثل الهدف من هذه الدراسة في تقدير المكونات الوراثية المرتبطة بالتباين والتغاير من خلال نظامين للتزاوج هما نظام التهجين النصف دوار ونظام التزاوج العاملى. تم تنفيذ التجربة في المحطة البحثية بالبرامون بمحافظة الدقهلية خلال ثلاث مواسم هى ٢٠١٢ ، ٢٠١٣ ، ٢٠١٤ لإنتاج بذور الجيل الاول والثاني ثم التقييم في الموسم الثالث على التوالى.

أظهرت النتائج أن متوسطات الجيل الأول قد أسفرت عن تفوق الهجن على متوسط الآباء وكذلك أحسن الآباء. كما تم الحصول أيضاً على قيم معنوية لقوة الهجين لجميع الصفات التى درست وكانت أعلى قيمة ٤٣.٨٤% لصفة طول القرن بالسم عن متوسط الآباء ، ١٥.٦٨% لصفة عدد القرون/نبات منسوبه لأفضل الآباء ، وفى نفس الوقت أظهرت كل الصفات المدروسة قيما معنوية للإنخفاض الناتج عن التربية الداخلية.

أوضحت نتائج الدراسة أيضاً وجود تأثير غير تجمعى للجينات بما فيه السيادة بصورة أكبر من التأثير التجميعى للجينات المؤثرة على معظم الصفات التى درست وإن كانت قيم التباين التجمعى مرتفعة ولا يمكن إهمالها ، كما كانت تقديرات قيم معامل التوريث عالية فى معظم الصفات التى درست. وكانت النتائج متشابهة فى كلا نظامى التزاوج فى قياس التباينات الوراثية مما يدل على أن تصميمى التزاوج المستخدمين في هذه الدراسة لهما نفس الكفاءة.

أشارت النتائج الى أن أزواج الصفات المدروسة كانت مرتبطة مع بعضها مشيرة إلى إمكانية تحسين الصفات المدروسة من خلال برنامج الإنتخاب ، ولذلك يعتبر برنامج الإنتخاب أكثر فاعلية لتحسين محصول اللوبيا.