

## **GENETIC ANALYSIS AND SELECTION OF SOME AGRO-ECONOMIC CHARACTERISTIC AND ITS COMPONENT IN COWPEA *VIGNA UNGUICULATA L WALP* UNDER DROUGHT CONDATION**

**Rashwan A.M.A**

**Dept. of Hort. (Vegetable crops), Fac. Of Agric., South Valley Univ., Qena, Egypt**

### **ABSTRACT**

The climate is changing all over the world, particularly in sem-arid and arid regions. This changing climate could strongly affect cowpea production worldwide. As the world population continues to grow, and water resource for crop production decline and temperature increase, so the development of heat and drought tolerance cultivars is an issue of global concern. In this context, two cycles of selection were employed in the  $F_2$  generation of a cross between to assess the impact of selection on seed yield in response to drought. Family selection and within-family selection were adopted in the second cycle of selection. The observed response to selection for dry seed yield was 4.27% in the  $F_2$  generation and 4.09 and 19.82% in the  $F_3$  generation for family and within family selection, respectively. The main dry seed yield of  $F_2$  generation exceeded that of two standard cultivars ("Cream 12" and "Azmerly") by 20.62 and 10.04%, respectively. While the mean of  $F_3$  selection exceeded that of the two standard cultivars by 39.60 and 26.46%, respectively. Significant positive correlations were obtained for weight of 100-seeds (2.8), Pod length (3.91) and number of seeds/pod (3.29) in the  $F_2$  generation but not in the second cycle of selection. Generally, the observed response to selection were greater than the predicted response indicating the presence of dominant gene affects for the trait studied.

### **INTRODUCTION**

Cowpea *Vigna unguiculata L walp* is one of the most important vegetable crops grow in Egypt. In this context it is one of the major grain legumes in the third world and provides major of portion of dietary protein for the people. In Egypt, cowpea is a popular vegetable crop. The total cultivated area of this crop was estimated at 8381 feddans for dry seed in 2010 with a mean production 1088 kg/fed. Also, the area that produced green pods was 6940 feddans with a mean of 3.676 ton/fed. (Dep., Agric. Statistics Ministry of Agriculture, Giza, Egypt).

Climate change is going to have a drastic impact on dry land ecosystems and its almost 2.6 billion inhabitants (Anderson and Morton 2008). All the climate models used by the IPCC suggest that the dry area will become dryer and more water stressed (IPCC, 2007) due to increasing temperature, decreasing rainfall and humidity.

The dry land areas (4% of world land surface) are home to over 2 billion people, accounting for 30% of the world's population, some 80% of dry land inhabitants live in rural areas, more than 90% of dry land inhabitants are in the developing world and 40% rural areas while approximately half of the

poorest people in the world live in dry areas (Millennium Ecosystem assessment 2005). The direct effects of climate change will be through changes in temperature, rainfall, length of growing season and timing of extreme and critical threshold events relative to crop development. In the dry land of tropics and subtropics, where crops are near their maximum temperature tolerance level, yield will decline (El-Beltagy and Madkour 2012).

Desertification and climate change will greatly impact plant biodiversity. Traditionally, gene bank in different institutions have collected, evaluated and conserved plant germplasm under short- and long-term storage conditions (El-Beltagy and Madkour 2012).

The development of new plant varieties with low- water requirements, better water use efficiency and the production of drought-tolerant varieties and the production can help increase food production. Newly reclaimed soils in these deserts suffer from various stresses such as drought, salinity, nutrient deficiency, etc. (El-fouly *et al.* 1984).

Therefore, it is imperative to increase the yield per unit area of various crops by developing high-yielding cultivars suitable for sowing on poor soils and under stress conditions as well as the development and application of improved cultural practices.

Cowpea has been reported to be more drought tolerant than other crop species (Ehlers and Hall, 1997 and Singh *et al.* , 1999a). The tolerance has been attributed to several drought deep rooting. Strong stomatal sensitivity, reduced growth rate, leaf area reduction (Lawn 1983; Mai-kodomi *et al.* , 1999a, Singh *et al.* 1999a; Turk and Hall 1980 a,b). However, the crop still suffers considerable yield reduction when exposed to severe drought stress during flowering and Pod filling is particularly important since it impacts negatively on flower development, Pollination (Boyer and McPherson, 1975), pod setting and grain filling leading to reduced number of pods per plant and seed weight, and consequently low seed yield. Genetic variability of cowpea for drought tolerance that could be utilized in breeding programmes has been reported from various parts of the world (Hall, 2004; Itan *et al.* , 1992 a,b; Singh and Matsui 2002; Singh *et al.* 1999 a,b ; Muchero *et al.* 2008).

Progress in cowpea breeding for improved drought tolerance will depend mainly on the availability of genetic variability for the traits conferring drought tolerance, adequate screening methods and knowledge of genetic control of the trait conferring drought tolerance. Therefore, the aim of the present study was to identify cowpea lines which are suitable for cultivation in drought conditions by understanding genotypic and phenotypic variation through genetic analysis and selection.

## **MATERIALS AND METHODS**

### **Field trials**

The experiment was conducted over two summer seasons (2012 and 2013) at the research farm of South Valley University, Qena, Egypt to observe the genotypic and phenotypic variation of cowpea under drought

stress. The plant material used in this study consisted of 100 F<sub>7</sub> plants derived from across established between (Cream 1 × Blackeye crowder). The name and source of the base population selection and two cheek cowpea cultivars is presented in (Table 1).

**Table 1: The pedigree and origin in the base population selection and two cheek cowpea cultivars .**

Name	Source
Base population selection (Cream 1 × Blackeye crowder) *	**local, Egyptian Agricultural, organization, Egypt.
Cheek cultivar - Cream 1*	* Prof. Dr. A.M. Damarany, Hort. Dep., Faculty of Agric., Sohag Univ.
- Azmerly **	

In the 2011 summer season, seeds of 100 plants were sown on 30 April of the experimental farm of South Valley University. Stress conditions were imposed by 16.5% moisture deficient in Sandy calcareous and infertile soil. Soil salinity before planting was 4.5 ds/m and after planting it was 5.2 ds/m. The PH of the soils was 8.5. Single plants were grown the ridge at 3m length 10 cm wide and plants spaced 20 cm from each to other. The eight highest yield segregates were selected because the predicted response to selection depends upon small selection intensity and high heritability, on the other hand, when selection intensity was small, the predicted response was greater to from F<sub>7</sub> selected families with a selection intensity 0.08 (calculated by number of selected plants/ all plants), and an equal number of seeds were pooled from plants so as to from the F<sub>7</sub> Bulk. The 8 F<sub>7</sub> selected families, together with the F<sub>7</sub> Bulk and two cheek varieties namely, Cream 1 and Azmerly were sown on 30 April in the next season. Each family was represented in each block by 10 plants with the ridge at 3m length 10 cm wide and plants spaced 20 cm from each to other.

Six highest families from 8 F<sub>7</sub> selected for seed yield were saved for the next season as family selection. Meanwhile, 0.02 plants were selected based on yield (individual selection) to from F<sub>8</sub> selected families in the next season (an intensity of 2.0%). In the 2012 summer experimental season, seeds of the F<sub>8</sub> selected families along with their relevant F<sub>8</sub> bulk and two cheek varieties were planted on the sowing date, i.e., 30 April. Each family was represented in each block by 10 plants with the ridge at 3 m length 10 cm apart and plants spaced 20 cm from each two other. Experiments were conducted by randomized complete block design (RCBD) with three, replications, in both seasons.

**Data collection:**

At fully maturity, dry seed yield kg/Fed. (DSY), 100-seed weight (100-sw), Pod length (cm) and number of seeds /pod (Ns) were recorded for each individual plant according to standard methods,

**Statistical procedure:**

Character are often correlated, i., the phenotypic value of one character in an individual is correlated with the phenotypic value of another character on that individual. These correlations can also be due to environmental affects or genetic effects. The genetic causes of correlation

are pleiotropy (genes affect more than one character) and genetic linkage. This needs not be constant across genes: some genes can cause positive pleiotropy and others negative pleiotropy; the balance determines the genetic correlation of two characters. These genotypic and phenotypic variations, due to the effect of the environment, can be identified by the following ways:

1- **Expected response to selection in this present research, expected response to selection (Rx) was estimated by the following equation, stated by plomin et al. (1989):**

$$R_x = ih^2 \sigma_p$$

Where  $i$ =standardized selection differential;  $\sigma_p$ = phenotypic standard deviation;  $h^2$  = heritability.

2- **Correlated response to selection**

Selection of one trait will often result in the response of another trait. This is genetic correlation. It is caused by changes in the breeding value of the selected trait being correlated with changes in the breeding value of the other trait. Selection of one trait can cause an apparent selection differential of another trait, because of both genetic and environmental correlations. This is a particularly huge problem when studying natural selection in natural conditions.

In this present research, the indirect response to selection (cRx) was calculated accurately according to the formula of (Falconer 1989):

$$CR_x = ih^2 \sigma_p r_{xy}$$

Where  $r_{xy}$  is the genetic correlation between the selected trait and unselected trait;  $i$  = standardized selection differential;  $\sigma_p$  = phenotypic standard deviation;  $h^2$  = heritability.

3- **Heritability (brood sense)**

Heritability determined according to (Mather and Jinks 1971) as following formula:

$$H^2 = \sigma_g^2 / \sigma_p^2 \text{ where:}$$

$\sigma_g^2$  = the genetic variance

$\sigma_p^2$  = phenotypic variance

4- **Genetic correlation and phenotypic correlation  $r_g$  and  $r_p$  were estimated according to Miller et al. (1988).**

$$R_g = \sigma_{g_{1,2}} \sqrt{\sigma_{g_1}^2 \times \sigma_{g_2}^2}$$

Where  $\sigma_{g_{1,2}}$  is the genetic covariance between traits 1 and 2 and  $\sigma_{g_1}^2$  x  $\sigma_{g_2}^2$  are the genetic variation of 1 and 2, respectively.

$$R_p = \sigma_{p_{1,2}} \sqrt{\sigma_{p_1}^2 \times \sigma_{p_2}^2}$$

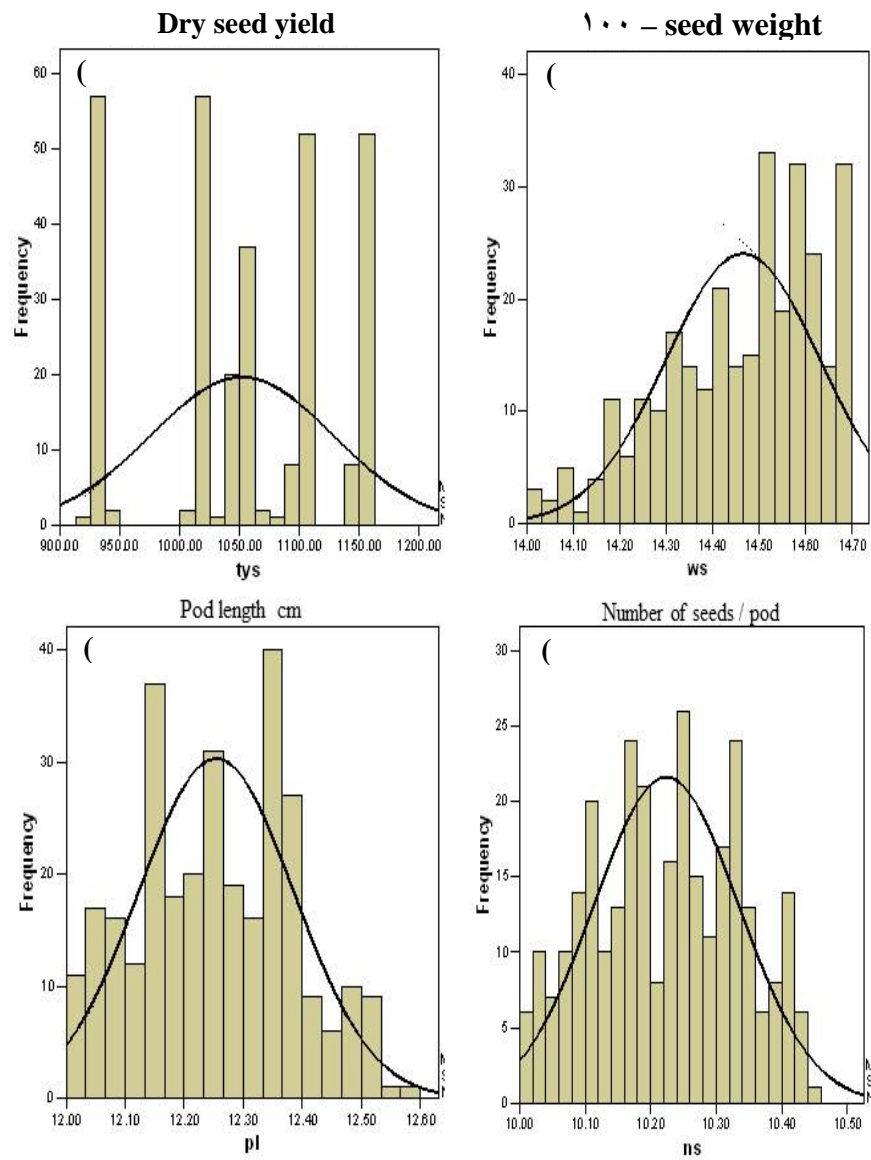
Where  $\sigma_{p_{1,2}}$  is the phenotypic covariance between traits 1 and 2 and  $\sigma_{p_1}^2$  x  $\sigma_{p_2}^2$  are the phenotypic variation of 1 and 2, respectively.

5- **Student's t-test**

A student's t-test was calculated according to the formula stated by Gosset (1896):

$$T = \frac{\bar{X} - u}{s / \sqrt{X}}$$

## RESULTS AND DISCUSSION



**Fig. 1.** Distribution of 100  $F_7$  plants for (A) dry seed yield, (B) 100-seed weight, (C) pod length cm, (D) number of seed/pod. Mean = (A) = 105.1, 29; (B) 12.22; (C) 12.22; (D) 14.35.

**Variation in agronomic characters and its components:**

**١- Dry seed yield (DSY) Kg/ Fed.**

Based on DSY of ١٠٠ F<sub>٧</sub> plants, the distribution was continuous and normal, indicating the quantitative and polygenic nature of the system controlling that character (Fig. ١A). The range of DSY of the F<sub>٧</sub> plants ranged from ٩٠٠ to ١٢٠٠ kg/fed. With an average of ١٠٥١,٧٢٩ kg/feddan. However, the t-test (Table ٢) was highly significant indicating that genetic variation among F<sub>٧</sub> plants was operating. Significant and high genetic variation was observed between F<sub>٧</sub> plants for DSY trait. Similar results were reported by Abd-Elhady (١٩٩٨), Rashwan (٢٠٠٢) and El-Ameen (٢٠٠٨).

**٢- ١٠٠ – seed weight**

The distribution of ١٠٠ F<sub>٧</sub> plants was continuous with skewness to the right indicating an abundance of very high ١٠٠-sw among that array (Fig. ١B). The ١٠٠-sw of the F<sub>٧</sub> plants ranged from ١٤,٠ to ١٤,٧٠ (g). The differences between F<sub>٧</sub> plants were significant according to the t-test (Table ٢). These are in accordance with the findings of Abo-Baker *et al.* (١٩٨٨), they found that weight of ١٠٠ seeds fitted and additive dominant genes positive effects and recessive genes having negative effects and such trait exhibited mainly dominant effects.

**٣- Pod length (pl)**

The distribution of the ١٠٠ F<sub>٧</sub> plants for PI was continuous and normal indicating a polygenic type of genetic control for this character (Fig. ١c). PI ranged from ١٢,٠ to ١٢,٦٠ cm with an average of ١٢,٢٥ cm. The t-test revealed highly significant differences between F<sub>٧</sub> plants (Table ٢). These results are in with those obtained by Hall (١٩٩٢), Singh *et al.* (١٩٩٢), Damarany (١٩٩٤) and Rashwan (٢٠١٠)

**٤- Number of seeds (Ns)**

The distribution of ١٠٠ F<sub>٧</sub> plants for Ns was continuous and normal indicating a polygenic type of genetic control (Fig. ١c). the mean of Ns ranged from ١٠,٠ to ١٠,٥٠ seeds with an average of ١٠,٢٢ seeds. According to the t-test, differences among entries were highly significant (Table ٢). Similar results were reported by Moalafi *et al.* (٢٠١٠) and El-shaieny (٢٠١٢).

**Table ٢: t-value for studied traits of F<sub>٧</sub> plants**

Traits	T	d.f	Standard error	Significant
Dry seed yield kg/fed.	١٧,٥	٩٩	٤,٣٩	٠,٠٠
١٠٠-seed weight (g)	١٨,٤٣	٩٩	٠,٠٠٩	٠,٠٠
Pod length (cm)	١٨,٨١	٩٩	٠,٠٠٧	٠,٠٠
Number of seeds/pod	١٨,٤٤	٩٩	٠,٠٠٦	٠,٠٠

**Response to selection of the F<sub>٧</sub> families for dry seed yield.**

The means of dry seed yield of the F<sub>٧</sub> selected families, F<sub>٧</sub> random families and the two cheek varieties with observed response to selection are described in Table ٣. ANOVA revealed significant differences between the entries as well as significant differences between F<sub>٧</sub> selected families. A significant positive response to selection was obtained in the F<sub>٧</sub> selected

families for DSY (Table 4). The observed response to selection was 4.27%, the observed response to selection for DSY was lowest than the predicted response (16.00), indicating that dominance gene effects are involved in the inheritance of that trait. The means of the high selections exceeded those of "Cream 12" and "Azmerly" by 20.62 and 10.04% on average, respectively. The heritability in broad sense estimate was 0.68. These results were in agreement with those obtained by Mehta (2000).

#### **Correlated response to selection for dry seed yield kg/fed.**

##### **1- 100 – seed weight (100-SW)**

Generally, the correlated response to selection for DSY in SW, PI and NS was positive and significant (Table 3). The observed correlated response for 100-SW was equal to the predicted response indicating that additive gene effects are involved in the inheritance of 100-SW. For SW, the  $F_7$  selections exceeded those of "Cream 12" and "Azmerly" by 3.16 and 2.43%, respectively. The significant positive correlated response in the  $F_7$  generation of 100-seed weight could be attributed to the positive genetic correlation between DSY and SW ( $r=0.99$ ). The heritability estimate was 0.64. These results are in same with those reported by Rashwan (2002), Indra et al. (2006) and Ishiyaku and Aliyu (2013)

##### **2- Pod length cm (PI)**

The observed correlated response was 3.91% on average. The significant positive correlated response in the  $F_7$  generation could be attributed to the positive genetic correlation between DSY and PI ( $r=0.99$ ). The observed correlated response in 100-SW was equal to the predicted correlated response indicating that additive gene effects were operating (Fig. 1c). For PI, the  $F_7$  selections exceeded those of "Cream 12" and "Azmerly" by 0.1 and 2.07%, respectively. The heritability estimate was 0.09. These results have been promoted by Abd-Elhady (1998), Abd-Elkader (2006) and Alidu et al. (2013)

##### **3- Number of seeds/pod (NS)**

Here too, a significant positive correlated response to selection for DSY and NS was obtained 3.29% (Table 3). The observed correlated response in NS was equal to the predicted response indicating that additive gene effects are involved in the inheritance of NS. For NS, the  $F_7$  selection exceeded those of "Cream 12" and "Azmerly" by 0.42 and 6.26%, respectively. The genotypic correlation between D and Ns was high and positive ( $r=0.99$ ). The heritability estimated was 0.61. These results are in same with those reported by Abd-Elhady (2002), Indra et al. (2006), Dahiya et al. (2007), El-Ameen (2008) and Manggoel et al. (2012)

**Table ٣: Means of dry seed yield( kg/Fed)., ١٠٠-seed weight(gram), pod length and number of seeds/pod of F<sub>r</sub> selected and random and to cheek cultivars with heritability.**

Generation	dry seed yield ( kg/Fed).			١٠٠-seed weight(g)			Pod length (cm)			Number of seeds/pod		
	Mean	Ob%	P%	Mean	C.R%	P%	Mean	C.R%	P%	Mean	C.R%	P%
Cream ١٢	٩٢١,٠			١٤,١٢			١٣,٤٧			١٠,٠٥٧		
Azmerly	١٠٠٥,٠			١٤,٣٥			١٢,٥٢			١٠,٠٠٣		
F <sub>r</sub> random	١٠٣٥,٦٣			١٤,٢٨			١٢,٢٨			١٠,٢٨		
F <sub>r</sub> selected	١١١٠,٩٣	٧,٢٧	١٦,٥٥	١٤,٦٨	٢,٨٣	٢,٨٣	١٢,٧٨	٣,٩١	٤,٠١	١٠,٦٣٠	٣,٢٩	٢,٥٤
H <sup>١</sup>		٠,٦٨			٠,٦٤			٠,٥٩			٠,٦١	

**Table ٤: The analysis of F<sub>r</sub> random and selected families in the ٢٠١٢ summer season.**

Items	dry seed yield kg/Fed.	١٠٠-seed weight	Pod length	Number of seeds/pod
Among entries	٦٠٠,٥٠**	٢٠,٤**	٥٠,٥٠**	١٨,٤**
Among selected F <sub>r</sub>	٣٨٩,٢١**	١٠,٧٠**	٣٨,٨**	٩,٦**
Error	٨٠,٤٠	٣,٢٠	١٠,٢	٣,٢٠

\* significant at ٥% level probability.

\* significant at ١% level probability.

**Response to selection of the F<sub>٤</sub> families dry seed yield kg/Fed**

The means of DSY of the F<sub>٤</sub> selection families, random families and the two cheek varieties with observed correlated response are given in Table ٤. The data in table ٦ reveals significant differences between the entries, while between F<sub>٤</sub> selected families, differences, differences were not significant. The observed response to selection for DSY was ٢٠,٤١ in the F<sub>٤</sub> family selection, while the F<sub>٤</sub> individual selection, it observed response to selection was greater to than the predicted response, confirming the predominance of dominant gene effects. In this research, F<sub>٤</sub> family selection "Cream ١٢" and "Azmerly" was exceeded by ٣٩,٦٠ and ٢٦,٤٦%, respectively. While individual selection was exceeded by ٢٥,٨٩ and ١٤,٠٤%. These finding indicate that family selection might be more profitable in effecting a direct response for DSY. Broad sense heritability was ٠,٧٨. The above findings of our present study was similar to Indra et al. (٢٠٠٦), they stated that the plant breeding selection has increase weight of seeds/plant, number of pods/plant and ١٠٠ seeds weight. According to Dahiya et al (٢٠٠٧) seed yield /plant showed significant and positive association with pod length , ١٠٠ seeds weight and number of seeds/plant. In another study, Eswaran et al. (٢٠٠٧), mentioned that seed yield/plant had high significant positive correlation with total dry matter

**Correlated response to selection for dry seed yield kg/fed.**

**١- ١٠٠-seed weight (١٠٠-SW)**

The CR for selection of DSY was positive (Table ٥). In the second cycle, for the family selection, the observed correlation response was ١١,٦٠, but within family selection it was ٣,٤٩% (Table ٥). The observed selection response was higher than the predicted response (٠,٣١) in the family selection indicating the presence of non-additive gene effects, also, in the



same direction, was true within family selection. The  $F_2$  selections (family selection) exceeded those of "Cream 12" and "Azmerly" by 13.1 and 11.29%, respectively, while the selection in the  $F_2$  generation within family selection exceeded those of "cream 12" and "Azmerly" by 4.89 and 3.20%, respectively. The heritability estimate was 0.71. Similar results were obtained by Abd-Elhady (1998), Thiaw and Hall (2004), Nwofia et al. (2007), El-Rawy et al. (2010), and Oyiga and Uduru (2011)

**2- Pod length (cm)**

The observed correlated response in PI ranged from 9.77 for within family selection to 11.29% for the family selection in the  $F_2$  generation (Table 3). Generally, the observed response (ob) was higher than the predicted response (P), indicating that non-additive gene effects were operating. In the  $F_2$  generation, the  $F_2$  selection exceeded that of "Cream 12" and "Azmerly" by 3.11 and 1.94%, respectively with the family selection while the individual selection was exceeded by 4.76 and 9.42%, respectively. The heritability estimate was 0.52%. These results are in same line with those obtained by Eswaran et al. (2007), Adewal et al. (2010) and Alidu et al. (2013).

**2- Number of seeds/pod (NS)**

In the  $F_2$  generation, the observed response was 4.42 with family selection and 1.92% with individual selection. Across the board, the observed response was greater than the predicted response confirming the presence of non-additive gene effects. Board sense heritability was 0.57% genetic improvement of DSY was obtained after tow cycles of selection. These results are in agreement with the findings of Adewal et al. (2010), who found that number of seeds/pod and weight seed/plant had significant direct effect on DSY. Several workers have estimated the correlation between different yield attributing characters and their direct and indirect effects on yield in cowpea Nakawuke and Adipala (1999), Venkatesan et al. (2003), Omoigui et al. (2006), Reksen (2007) and Umare et al. (2010).

**Table 2: Means of dry seed yield( kg/Fed)., pod length(cm) and number of seeds/pod of  $F_2$  selected random and to cheek varieties with heritability.**

Generation	dry seed yield kg/Fed.			100-seed weight(g)			Pod length (cm)			Number of seeds/ pod		
	Mean	Ob%	P%	Mean	C.R%	P%	Mean	C.R%	P%	Mean	C.R%	P%
$F_2$ random	10.63,07			14.31			12.48			10.41		
$F_2$ selected (F)	12.80,72	20.41	4.09	10.97	11.70	0.31	13.89	11.29	10.26	10.87	4.42	0.28
$F_2$ selected (i)	1104.80	8.08	19.82	14.81	3.49	1.48	13.70	9.77	1.20	10.71	1.92	1.36
Cream 12	917.33			14.12			13.47			10.00		
AZmerly	1012.66			14.30			12.02			10.03		
$H^2$		0.76			0.71			0.52			0.57	

**Table 3: Pertinent Ms of the different items of the analysis of variance of the  $F_2$  families with two varieties in the 2013 summer season.**

Items	dry seed yield kg/Fed.	100-seed weight	Pod length	Number of seeds/pod
Among entries	384.67**	0.100**	40.2**	8.21**
Among $F_2$ selected (F)	36.30	3.14**	12.70	4.90*
Among $F_2$ selected (i)	39.08	0.24	11.09	1.8
Error	30.04	0.9	9.2	1.7

\*significant at 5% level probability.

\*significant at 1% level probability.

Ns non significant

**Effect of drought stress on genotypic and phenotypic characters of cowpea .**

Combined analysis variance indicated that there were significant differences among the genotypes in their DSY, 100-seed weight, pod length, number of pods/plant, weight of seeds/plant, weight of pods/plat, plant height (cm) and number of branch/plat. Kwaye *et al.* (2008). Under normal irrigation no significant correlation was observed between the DSY and other morphological characters, but under the drought stress conditions there were positive highly significant correlations between the DSY and the 100-seed weight and number of pods/plat (El-shaieny 2012). Results showed that in comparison with other drought treatments, imposing drought stress at the start of stem elongation stage through the ripening stage had most impact on reducing the yield of cowpea cultivars. In different growth stages, different genotypes respond to moisture stress and irrigation discontinuance differently (Patil and Gosavi 2007). In another study 100-seed weight, weight of pods/plat and DSY were decreased by water limitation.

Despite of their significant differences ( $p < 0.05$ ) in 100-seed weight, pod length, number of pod/plant, weight of pods/plat and number of seeds/plant, but DSY of cowpea cultivar was not significantly different. Pedigree selection for the two cycles ( $F_7$  and  $F_8$  generations) in each environment showed a 20 and 20.04% increase in grain yield over the bulk samples for normal and drought stress conditions, respectively, as compared to 22.6% for selection over environments (Ali 2011). Several studies have been conducted to assess the variability of cowpea genotypes for drought tolerance. Significant differences in drought tolerance have been reported and could be utilized in breeding programmes (Turk *et al.* 1980 a,b; Itan *et al.* 1992 a,b; Mai-Kodomi *et al.* ; Watanabe and Terao, 1998; Matsui and Singh 2002; Chiulele and Agenbag 2004 and Muchero *et al.* 2008). In these studies genotypes were evaluated at different crop growth stages using different physiological, morphological traits. Comparatively, terminal drought or reproductive stage drought has received more attention given its direct negative impact on seed yield (Turk *et al.* , 1980; Hall, 2004).

## **CONCLUSION**

From the results obtained in this work, it can be concluded that selection was effective in improving the dry seed yield under drought conditions has always been important target for enhancing productivity. Also, selection was effective to produce new lines with highest yield resistant to drought.

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## التحليل الوراثي والانتخاب في بعض صفات المحصول الاقتصادية ومكوناته في اللوبيا تحت ظروف الإجهاد البيئي (الجفاف)

أيمن محمد عبد النبي رشوان

قسم البساتين (خضر) - كلية الزراعة بقنا - جامعة جنوب الوادي .

أجريت دورتين من الانتخاب الموجه لصفة المحصول وبعض مكوناته في عشيرة من نباتات الجيل الثاني في اللوبيا ناتجة من التهجين بين الصفتين (كريم ٧ x بلاك أي كرودر)، بمزرعة الخضر - بكلية الزراعة بقنا - جامعة جنوب الوادي. بهدف دراسة الاختلافات الوراثية والمظهرية تحت ظروف الإجهاد البيئي، حيث تمت الزراعة في (رطوبة تربة ١٦,٥%، وتربة رملية غير خصبة) وكانت ملحوظة التربة قبل الزراعة (٨,٤ ds/m) وأصبحت بعد الزراعة (٤,٢ ds/m) وحموضة ٨,٤.

في عام ٢٠١١ تم زراعة نباتات العشيرة القاعدية (F<sub>٠</sub>) تحت ظروف الإجهاد البيئي، حيث زرعت في خطوط بطول الخط ٣ متر وعرضه ٧٠ سم والمسافة بين النباتات ٢٠ سم. تم انتخاب أعلى ٨ عائلات عالية المحصول Family selection (شدة الانتخاب ٨%)، وانتخاب ٥ عائلات مجمعة Bulk selection. في موسم صيفي ٢٠١٢ تم زراعة ٨ عائلات المنتخبة (F<sub>١</sub>)، و ٥ عائلات مجمعة (F<sub>٠</sub>) بالإضافة إلى الصنفان القياسيان كريم ١٢ والأزميرلي، حيث زرعت المنتخبات في خطوط بطول ٣ متر وعرض ٧٠ سم والمسافة بين النباتات ٢٠ سم. تم انتخاب أعلى ٦ عائلات عالية المحصول من الـ ٨ عائلات انتخاب بين العائلات Family selection (F)، ٥ عائلات عالية المحصول من الـ ٢٤٠ عائلة (انتخاب داخل العائلات) within family selection (i) (شدة الانتخاب ٢,٠٨%).

في موسم صيفي ٢٠١٣ تمت زراعة العشائر المنتخبة في الجيل الـ (F<sub>٢</sub>) ٦ عائلات انتخاب من العائلات، ٥ عائلات انتخاب داخل العائلات، ٥ عائلات مجمعة، والصنفان القياسيان.

### أظهرت النتائج:

- أظهر منحى التوزيع وجود اختلافات مستمرة لنباتات الجيل الثاني (F<sub>٢</sub>) لصفة المحصول، وطول القرن، وعدد البذور القرن، مما يؤكد وجود موديل فعل الجين (الإضافي - السيادة) لهذه الصفات، أما في صفة وزن الـ ١٠٠ بذرة فإن منحى التوزيع الطبيعي يميل ناحية اليمين مما يشير إلى وجود فعل الجين السيادة لهذه الصفة، وتراوح المدى لصفة المحصول من ٩٠٠-١٢٠٠ كجم/فدان بمتوسط قدرة ١٠٥١,٢٩ كجم/فدان، ولصفة طول القرن ١٢-١٢,٦ سم بمتوسط قدره ١٢,٢ سم، ولصفة عدد البذور/بالقرن ١٠-١٠,٢٢ بذرة بمتوسط قدره ١٠,٢٢ بذرة ولصفة وزن ١٠٠ بذرة ١٤,٧-١٤ جم بمتوسط قدره ١٤,٣٥ جم.

- أظهر اختيار ٤ معنوية عالية لكل الصفات قيد الدراسة، مما يشير إلى وجود اختلافات وراثية فعالة في نباتات الجيل الثاني.

### الدورة الانتخابية الأولى:

- كانت الاستجابة المشاهدة للانتخاب (obs%) لصفة المحصول في الجيل الثالث (F<sub>٢</sub>) في الانتخاب العائلي Family selection (F) ٢,٢٧% وكانت الاستجابة المتوقعة لهذه الصفة (p%) ١٦,٥٥% وهذا يشير إلى وجود فعل السيادة لهذه الصفة، وكانت الزيادة الناتجة عن الانتخاب مقارنة بالصنفان كريم ١٢، الأزميزلي هي ٢٠,٦٢، ١٠,٥٤% وبلغت درجة التوريث ٠,٦٨%.

- صفة وزن ١٠٠ بذرة: كانت الاستجابة المرتبطة للانتخاب (CR%) ٢,٨% والاستجابة المتوقعة للانتخاب ٢,٨٣%، مما يشير إلى وجود فعل الجين الإضافي لهذه الصفة، كما زاد متوسط الجيل الثالث المنتخب بمعدل ٣,١٦، ٢,٤٣% عن متوسط الصنفان القياسيان، وجود ارتباط معنوي موجب (r= ٠,٩٩) مع صفة المحصول الكلي، وبلغت درجة التوريث عن النطاق الواسع ٠,٦٤%.

- صفة طول القرن: كانت الاستجابة المرتبطة للانتخاب (CR%) ٣,٩١%، والاستجابة المتوقعة للانتخاب ٤,٠١% وهذا يشير إلى وجود فعل الجين الإضافي لوراثية هذه الصفة وكانت الزيادة الناتجة عن الانتخاب في الجيل الثالث (F<sub>٢</sub>) في العائلات المنتخبة ٥,٠١، ٢,٠٧% بالمقارنة بالصنفان القياسيان وجود ارتباط معنوي موجب (r=٠,٩٩) مع صفة كمية المحصول، وبلغت درجة التوريث ٠,٥٩%.

- صفة عدد البذور: كانت الاستجابة المرتبطة (CR%) ٣,٢٩% والاستجابة المتوقعة للانتخاب (P%) ٢,٥٤% وهذا يؤكد فعل الجين لوراثية هذه الصفة، وكانت الزيادة الناتجة عن الانتخاب في الجيل الثالث (F<sub>٢</sub>) في العائلات المنتخبة ٥,٤٢، ٦,٢٦% بالمقارنة بالصنفان القياسيان، وجود ارتباط معنوي موجب (r=٠,٩٩) مع صفة كمية المحصول، وبلغت درجة التوريث ٠,٦١%.

### الدورة الانتخابية الثانية:

-وجود اختلافات معنوية في عشائر الجيل الرابع (الانتخاب من العائلات، الانتخاب داخل العائلات، الانتخاب المجمع)

-**صفة المحصول:** كانت الاستجابة المشاهدة (obs%) للانتخاب في الجيل الرابع (الانتخاب بين العائلات) ٨٢٠,٤١، والاستجابة المتوقعة للانتخاب (P%) ٤,٠٩%، وهذا يشير إلى وجود فعل الجين السادي لهذه الصفة. وكانت الاستجابة المشاهدة (obs%) للانتخاب داخل العائلات ٨,٥٨%، والاستجابة المتوقعة (P%) ١٩,٨٢%، وهذا يشير إلى وجود فعل الجين السادي في وراثته هذه الصفة.

-وكانت الزيادة الناتجة عن الانتخاب بين العائلات في الجيل الرابع ٣٩,٦%، ٢٦,٤٦%، وكانت الزيادة الناتجة عن الانتخاب داخل العائلات ٢٥,٨٩%، ١٤,٠٤% بالمقارنة بالصفان القياسيان، وكانت درجة التوريث عن النطاق الواسع ٠,٧٨%.

-**صفة وزن ١٠٠ بذرة:** كانت الاستجابة المرتبطة (CR%) للانتخاب في الجيل الرابع (الانتخاب بين العائلات) ١١,٦%، وكانت الاستجابة المتوقعة للانتخاب ٠,٣١%، وهذا يشير إلى وجود فعل الجين السادي لهذه الصفة، وكانت الاستجابة المرتبطة (CR%) للانتخاب (داخل العائلات) ٣,٤٩% والاستجابة المتوقعة للانتخاب ١,٤٨% مما يشير إلى وجود فعل الجين السادي.

-كانت الزيادة الناتجة عن الانتخاب بين العائلات في الجيل الرابع ١٣,١%، ١١,٢٩% وكانت الزيادة الناتجة عن الانتخاب (داخل العائلات) ٤,٨٩%، ٣,٢٥% وذلك عن الصفان القياسيان. درجة التوريث ٠,٦١%.

-**صفة طول القرن:** كانت الاستجابة المرتبطة (CR%) للانتخاب (بين العائلات) ١١,٢٩%، وكانت الاستجابة المتوقعة للانتخاب ٠,٢٦% وهذا يؤكد وجود فعل الجين الغير إضافي. بينما كانت الاستجابة المرتبطة (CR%) للانتخاب (داخل العائلات) ١٣,٧٠% والمتوقعة (obs%) ٩,٧٧%، وكانت الزيادة الناتجة عن الانتخاب بالمقارنة بالصفان القياسيان هي ٣,١١%، ١٠,٩٤% (انتخاب بين العائلات)، وكانت الزيادة ٨,٧٦%، ٩,٤٢% (داخل العائلات)، درجة التوريث ٠,٥٢%.

-**صفة عدد البذور:** كانت الاستجابة المرتبطة (CR%) للانتخاب بين العائلات ٤,٤٢%، والاستجابة المتوقعة للانتخاب ٠,٢٨%.

وكانت الاستجابة المرتبطة للانتخاب داخل العائلات ١,٩٢%، والاستجابة المتوقعة ١,٣٦%.  
وهذا يشير إلى وجود فعل الجين الغير إضافي لهذه الصفة، كانت الزيادة الناتجة عن الانتخاب بالمقارنة بالصفان القياسيان ٨,١٥، ٨,٣٥ في الانتخاب بين العائلات، ٥,٥٧، ٥,٧٨% في حالة الانتخاب داخل العائلات. وكانت درجة التوريث على النطاق الواسع ٠,٥٧%.