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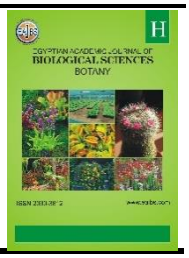

Estimation of the Coefficient of Variation and Some Genetic Parameters of Some Landraces of Cowpea

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ABSTRACT

The present investigation was carried out during two successive summer seasons of years 2019 and 2020 at the Faculty of Agriculture (Saba Basha), Alexandria University and the laboratory of the vegetable seed of Sabahya Horticulture Research Station, Alexandria Governorate, Egypt to evaluate six local cultivars and landraces of cowpea for some morphological characters, yield and its components as well as estimate some genetic parameters. Results reflected obvious differences among the six genotypes of cowpea for most of the studied characters. The coefficient of variation (C.V.) was less than 10 % for all the studied traits in all genotypes of cowpea. These results indicate that the six genotypes of cowpea are genetically identical concerning these traits. Analysis of variance showed that variances of genotypes were highly significant in all studied traits. These findings refer to that there were highly variations between genotypes under study. Generally, the data prove that all of the studied traits could be improved through the selection method, but with different degrees of the improving depending upon the amount of variation present in each population. Meanwhile, mean squares of years were significant only in height of the first flower, this can be interpreted as this property being affected by the different environmental conditions in both years of the study. Cluster analysis, based on RAPD plus ISSR analysis, divided the 6 studied genotypes into 3 major groups. The first contained Geza and Kareem7 Cvs. with similarity of (30%), the second consisted of Fowa Lr. and Kaha Cv., and the third one contained the ones of Behira Lr. and Kafr Elshikh Cv.

INTRODUCTION

According to FAOSTAT (2019), cowpea (*Vigna unguiculata* (L.) Walp.), 2n=22, is one of the most widely grown legume crops. Currently, Africa is considered the main producer of cowpea in the world, with 95.2 of the world's productions. Nigeria is the biggest country in production (3.5 million tons), Egypt produced 7180 tons. By a total area of 1853 hectares (4474 feds).

Cowpea is mainly grown for its seeds, which are high in protein, although the leaves and immature seed pods can also be consumed. The whole plant is used as forage for

animals, with its use as cattle feed likely responsible for its name (Therese *et al.,* 2019). Four subspecies of cowpeas are recognized, of which three are cultivated. A high level of morphological diversity is found within the species with large variations in the size, shape, and structure of the plant. Cowpeas can be erect, semi-erect (trailing), or climbing.

Cowpea suitable for poor soils (Moroke *et al.,* 2005). It is valued for its ability to tolerate drought, and fix atmospheric nitrogen (rhizobium bacteria) which allows it to grow and improve poor soils, these make it an important component in many cropping systems (Mahalakshmi *et al.,* 2006).

There are several diverse uses of cowpea due to which the varietal requirement in terms of plant type, seed type, maturity, the pattern of use and growth are diverse from region to region. Therefore, the cowpea breeding program becomes more complex and no single variety can be suitable for all the objectives. Thus, there is a need to develop varieties suitable for a specific region and or use. Traditionally, diversity within and between varieties was determined by assessing the difference in morphology. Cowpea is primarily a self-pollinating crop and its genetic base is considered to be narrow (Fana *et al.,* 2004). Genetic diversity plays an important role in the success of any breeding program (Ali *et al.,* 2007). Knowledge of genetic diversity in available varieties and genotypes is very useful for plant improvement all over the world, promoting the efficient use of genetic variations in breeding programs through supporting a proper selection of cross combination among large sets of parental genotypes (Mafakheri *et al.,* 2017).

For any crop improvement program, the evaluation of verities to assess the existing variability is the first step. Greater variability present in the initial material better would be the chances for evolving desired types. A clear understanding of the variability of various characters of the breeding materials is an asset to the plant breeder for selecting superior genotypes on the basis of their phenotypic expression. In this regard, estimates of genotypic and phenotypic variance for various quantitative characters along with heritability and genetic advance expected by selection for yield and its components are useful in designing an effective breeding program (Sarath and Reshma, 2017).

The limited number of cowpea breeding programs in Egypt has contributed to the country's ineffectiveness in taking advantage of the continent's high genetic potential. A significant pool of cowpea landraces is thought to be available, but the limited detailed information available about their diversity and agronomic potential makes it difficult for breeding programs to thrive. Thus, the characterization of cowpea genetic resources available in Egypt is of extreme importance for conservation and breeding (Fadia *et al.,* 2019). Unlike commercial varieties, landraces maintained by farmers usually have high levels of genetic variability as they have evolved from years of uncontrolled cross-regional and infield genetic exchange, even between previously released and discontinued open-pollinated varieties, not being subjected to selection over a long period of time. However, knowledge about their variability is usually limited (Ana *et al.,* 2020).

Since the gene theory was put forward, genotypic selection has replaced phenotypic selection gradually. Since then, DNA molecular markers are becoming a research hot spot. The research on AFLP, SSR and RAPD is changing rapidly. Analysis of genetic diversity for cowpea breeding, the genetic diversity information is extremely important, which is the basis of breeding and genetic research. Accurate assessment of genetic variability is important for the preservation and utilization of germplasm resources, and the improvement of cultivars. For this reason, scholars all over the world have made extensive and in-depth research on the genetic diversity of cowpea (Coulibaly *et al.,* 2002; Nkongolo *et al.,* 2003; Malviya *et al.,* 2012)

This investigation was aimed to study the coefficient of variation and genetic differences within and between 6 different genotypes of cowpea as a first step including them in breeding programs to improve and/or establish new cultivars.

MATERIALS AND METHODS

The present investigation was carried out during two successive summer seasons of years 2019 and 2020 at the Faculty of Agriculture (Saba Basha), Alexandria University and the laboratory of vegetable seed of Sabahya Horticulture Research Station, Alexandria Government, Egypt to evaluate six local cultivars and landraces of cowpea for morphological characters, yield and its components as well as estimate some genetic parameters i.e. genotypic and phenotypic variation, genotypic and phenotypic coefficient of variation, heritability and correlation coefficient analysis.

Plant Materials:

Plant materials for this study consisted of six genotypes of cowpea (Four local cultivars and two landraces). The sources of these genotypes are illustrated in Table (1).

Table 1. The studied cowpea genotypes and their sources

Genotype	source
Giza 7 (Cv.) Karim 7 (Cv.) Kafr El-Shikh (Cv.) Kaha (Cv.)	Registered cultivars at Horticulture Research Institute
Behira Fowa	Landraces collected from Beheira Governorate Landraces collected from Kafr Al sheikh Governorate

Field Evaluation:

Seeds of the studied genotypes were sown on March 15th (during the years 2019 and 2020 summer seasons). The 6 genotypes were, randomly, distributed on a randomized complete blocks design with 3 replicates. Each replicate contained 12 rows, 2 rows for each genotype, rows were 5 m long and 70 cm wide approximately under drip irrigation conditions. The hills were thinned to one plant each 40 cm apart three weeks later. The other normal agricultural practices for cowpea production, i.e., irrigation, fertilization, weeds and pest control were practiced as recommended.

Recorded Measurements:

Morphological Measurements:

The following measurements were recorded on individual plants in each entry.

Vegetative Measurements; i.e., Plant length (cm) (Starting from the surface of the soil to the growing top) , Number of branches/plants

Flowering Measurements; i.e., Height of the first flower (cm) Starting from the surface of the soil to the first flower appears), Number of days from sowing to the first flower appears (days)

Yield and Its Components; i.e., Number of pods/plants, Total pods yield/plant (g), Total seeds yield/plant (g), 100 seeds weight (g).

Pod measurements: The following measurements were recorded on randomly 30 pods from each entry; Pod length (cm), Pod width (cm), Pod weight (cm), number of seeds/pods.

PCR based on RAPD and ISSR Analysis:

Genomic DNA Isolation: Genomic DNA was extracted from the young leaves of the six cow bean genotypes by using DNA extraction kits (Easy Pure Plant Genomic DNA Kit)

DNA samples were stored at -20◦C. DNA quality was checked by electrophoresis in a mini gel.

In the present study, two different markers RAPD and ISSR were employed to evaluate the efficiency of these markers in the diversity analysis of cow bean genotypes. The sequences of the used primers are shown in Table 2. PCR reactions were performed in 20µl total volume, using 1µl from diluted DNA, 1µl of each primer for the amplification reaction, 10µl master mix (Taq Ready Mix PCR Kit from the fast gene) and 8µl ddH2O (sterile water) for all reactions. The tubes were capped and placed in a thermocycler and the cycling was started immediately. Amplification protocol was carried out using PCR cycler 600 programmed for initial denaturation step at 94◦C for 5 min, followed by 40 cycles each at 94◦C for 30 sec, annealing at the recommended temperature for each primer as shown in Table2 and extension at 72◦C for 1min.

Table 2: sequences and annealing temperature of the RAPD and ISSR primers used in the study.

Molecular marker	Primers	Sequence (5´-3´)	Annealing temperature(◦C)
RAPD	OPA2	*GTG ATC GCAG*	37
	OPA07	*GAAAGGGGTG*	
	OP-B7	*CAG CAC CCA C*	
	Op-B1	*GTAGACCCGT*	
	OP-C9	*CTCACCGTCC*	
ISSR	14A	$(CT)_8TG$	57
	49A	$(CA)_6AG$	
	HB-9	$(CTC)_3(TCT)_2TGC$	
	HB-12	$(CAC)_3GC$	
	HB-15	$(GTG)_3GC$	
	HB-10	$(GAG)_2(AGA)_2 TGCCC$	

The products of both RAPD and ISSR- based PCR analyses were detected using agarose gel electrophoresis (1.5% in 1X TBE buffer) stained with ethidium bromide (0.3µl). PCR products were visualized on U.V. light; photographed and analyzed using Total Lab Quant soft wear program.

Statistical Procedures:

Data of the studied characters were, statistically, analyzed using a combined analysis of variance for the two evaluated seasons, according to Herbert *et al*. (1955) and as illustrated in Table (3). The differences among the various means were tested, using Duncan's multiple range tests. The program used in the analysis COSTAT version 3. 303, 2004.

Table 3. The combined analyses of variance

S.O.V	**DF**	**MS**	**EMS**
Blocks	(r-1)	MB	
Treatments	(gs-1)	MT	
Genotypes	(g-1	MG(M1)	$\delta^2e + r\delta^2gs + rs\delta^2g$
Seasons	(s-1)	MS(M2)	$\delta^2e + r\delta^2gs + rg\delta^2s$
Genotypes*Seasons	(g-1)(s-1)	M G*S(M3)	$\delta^2e + r\delta^2gs$
Error	(gs-1)(s-1)	ME(M4)	δ^2e
Total	rgs-1		

r = Number of replications, g = Number of genotypes, s = Number of seasons

Estimation of Genetic Parameters:

Components of Variance: Genotypic and phenotypic variances were computed from ANOVA table based on the expected mean sum of squares as follows:

- Genotypic variance (VG) = (M1-M3) / rs
- Seasons variance (VS) = (M2-M3) / rg
- Interaction variance (VGS) = (M3-M4) / r
- Phenotypic variance (VP) = VS + VG + V(GS) +VE

Heritability in broad sense was calculated as illustrated by Falconer (1989) using the following formula:

Heritability in broad sense $H_{bs}^2 = \frac{\sigma_g^2}{\sigma_{ph}^2} \times 100$

Where, $\sigma_g^2 =$ Genotypic variance and $\sigma_{ph}^2 = Phenotypic\ variance$

For molecular data and cluster analysis, data were scored for computer analysis on the basis of the presence of the amplified products for each primer. If a product was present in a genotype, it was designated as "1", if absent, it was designated as "0", after excluding the unreproducible bands. Pair-wise comparisons of genotype, based on the presence or absence of unique and shared polymorphic products, were used to determine similarity coefficients, according to Jaccard (1908). DNA fragment size was estimated by comparison with a 1-kbp DNA ladder Ready to use from Gene Direx. The similarity coefficients were then used to construct dendrograms, using the Unweighted Pair Group Method with Arithmetic Averages (UPGMA) employing the SAHN (Sequential, Agglomerative, Hierarchical, and Nested clustering) from Past program version 4.03.

RESULTS AND DISCUSSION

Pictures in Figure (1) and results in Table (4) reflected obvious differences among the six genotypes of cowpea for most of the studied characters. The longest plant was obtained by Giza 7 Cv. (73.14 cm), whereas the shortest plant was obtained by Kaha Cv. (43.4 cm). Kafr El-Shiekh Cv. gave the highest No. of branches/plant (25.1), meanwhile, Fowa landraces gave the lowest No. of branches/plant (19.6 branches). Concerning the height of the first flower (cm.), the highest mean value was obtained by Kafr El-Shikh Cv. (25.4 cm). Meanwhile, the lowest mean value was obtained by Kaha Cv. (11.1 cm). Regarding the number of days to which the first flower appears, Behira landraces were the latest flowering (39.2 days), whereas Giza 7 Cv. was the earliest flowering (26.3 days). Regarding pov. (0.79 cm) and Fowa landraces (0.80 cm). Concerning Pod weight, El-Behira landraces and Giza 7 Cv. scored the highest mean values for pod weight (3.08 and 2.98 g respectively). With respect to the number of seeds/ pods, El-Behira and Kafr El-Shikh Cv. gave the highest number of seeds/pod (8.1 seeds/pod for both). Kafr El-shikh cultivar surpassed the other genotypes of cowpea in all traits of yield and its components. This cultivar gave 75.3 pods/plant, 211.8 g pods yield/plant, 274.4 g seeds yield/plant and 42.6 g weight of 100 seeds, whereas, Fowa landraces gave the lowest mean values for all traits of yield and its components.

The coefficient of variation (C.V.) was less than 10 % for all the studied traits in all studied genotypes of cowpea. These results indicated that the six genotypes of cowpea are genetically identical concerning these traits.

Genotypes	Vegetative growth	Pods	Seeds
Fowa (landraces)			
Behira (landraces)			
Kaha (Cv.)			
Kafr El-Shikh (Cv.)			
Giza 7 (Cv.)			
Karim 7 (Cv.)			

Fig.1. Pictures of the vegetative growth, pods and seeds of the six genotypes of cowpea.

Analysis of variance in Table (5) showed that the mean square of genotypes was highly significant in all studied traits. These findings refer to that there were highly variations between genotypes under study. Generally, the data prove that all of the studied traits could be improved through the selection method, but with different degrees of the improving depending upon the amount of variation present in each population. Similar results were reported by Fana *et al.*, (2004), Gerrano *et al.*, (2015) and Inuwa *et al.*, (2018). They reported that significant and high significant differences between genotypes mean that these genotypes have high expected genetic advance and beginning breeding programs by self-pollination and selection may be very effective generation by generation.

Meanwhile, mean squares of years were significant only in height of the first flower, this can be interpreted as this property being affected by the different environmental conditions in both years of the study. In this regard, Khan *et al.* (2015) and Mafakheri *et al.* (2017) reported that the flowering measurements were affected by the change in environmental conditions. However, mean squares of interaction between genotypes ×years were not significant in all studied traits.

All variance components values presented in Table (6) revealed that the large portion of genotypic variance for the following characters: plant height, height of the first flower, number of pods/plants, total pods yield/plant, total seeds yield/plant and 100 seeds weight.

Moderate values were in remain traits understudied similar results were found by Omoigui 2006 and Patel *et al.*, 2016. They reported that the genotypic and phenotypic variability was a reference point for any breeding program to study the genotypic difference of the most important economic characters. It makes the breeding program by selection more effective

Genotypic and phenotypic coefficient of variance values (GCV and PCV) showed that there was a narrow range between the genotypic and phenotypic coefficient of variance in characters; Plant height, Height of the first flower, Number of days for the first flower, Number of branches/plants, Pod length, number of Seed/pods, Number of pods/plants, Total pods yield/plant, Total seeds yield/plant and weight of 100 seeds (Table 6). Meanwhile, the wider range was in traits Pod width and Pod weight. Similar results were found by (Pathak *et al*., 2016) and motioned that the traits which have a wider range between values of (GCV) and (PCV). These results indicating that these characters are more affected by environmental conditions.

Heritability estimates in the broad sense in Table (6) showed that differences between genotypic variance and phenotypic variance were narrow in the same traits which exhibited high heritability values the highest heritability values were in traits Plant height, Height of the first flower, Number of days for the first flower, Number of branches /plant, Pod length, Seeds number/pod, Number of pods/plant, Total pods yield/plant, Total seeds yield/plant and 100 seeds weight (estimates were 90.74, 82.81, 82.40, 84.54, 85.76, 89.12, 84.67, 90.10 and 90.42% for previous traits respectively). Moderate values were in Pod width and Pod weight (estimates were 73.70 and 66.81 for Pod width and Pod weight, respectively). Similar results were found by Shanko *et al.*, 2014. They found high heritability estimates in a broad sense for plant height, number of pods/plants, seeds yield/plant, 100-seed weight, number of days to flowering. Also (Udensi *et al.*, 2011) found that superior estimates were obtained for pod measurements, the average number of pods/plant and the average number of seeds/plants.

Table 4: Mean performance, range and coefficient of variation (C.V) of vegetative, flowering and pod measurements, yield and its components of the six genotypes from cowpea, calculated from the combined data over both 2019 and 2020 summer seasons.

Genotypes	Vegetative measurements						Flowering measurements					
	Plant length (cm.)			No. of branches /plant			No. of days from sowing to the first flower appears (days)			Height of the first flower (cm.)		
	Mean	Range	C.V	Mean	Range	C.V	Mean	Range	C.V	Mean	Range	C. V
Fowa (landraces)	62.55_{d}	59.21- 66.60	1.00	19.57_{d}	17.90-20.94	2.16	36.27_{b}	33.65-38.82	2.31	23.81_{b}	22.01-26.11	5.58
Behira (landraces)	54.50_{e}	50.76- 58.15	1.51	20.75_{c}	18.91-22.52	3.02	39.23_{a}	36.66-42.05	2.16	23.44_{b}	20.90-25.55	7.06
Kaha (Cv.)	43.37_{f}	40.77- 46.06	0.91	20.73_{c}	18.15-22.63	4.15	27.13_{d}	25.08-29.35	2.28	11.14_{e}	9.98-12.81	5.58
Kafr El-Shikh (Cv.)	66.83_{b}	63.01- 70.80	1.08	25.07_{a}	23.17-27.23	2.54	36.67_{b}	34.03-39.24	2.31	25.44_{a}	22.80-27.65	7.06
Giza 7 (Cv.)	73.14_{a}	68.85- 77.25	1.05	23.76_{b}	21.93-25.85	2.54	26.26_{e}	24.04-28.65	2.60	18.87_{d}	17.32-20.93	5.58
Karim 7 (Cv.)	65.93_{c}	61.78– 69.80	1.13	24.20_{b}	22.46-25.98	2.27	28.99_{c}	26.63-31.52	2.60	22.61_{c}	20.90-24.50	4.10
	Yield and its components											
	Number of pods / plants			Total pods yield / plant (g)			Total seeds yield / plant (g)			100 seeds weight (g)		
	Mean	Range	C.V	Mean	Range	C. V	Mean	Range	C. V	Mean	Range	C. V
Fowa (landraces)	56.08f	51.88-59.92	1.46	166.4e	157.3-175.5	1.69	132.9e	125.4-140.7	0.53	25.73e	23.80-27.92	1.86
Behira (landraces)	61.11d	57.14-65.25	1.17	166.6e	152.9-176.8	0.42	130.9f	123.5-138.6	0.53	29.80b	27.93-32.01	1.46
Kaha (Cv.)	60.06e	56.15-64.15	1.17	209.9b	198.5-221.5	0.38	172.9b	163.3-182.6	0.53	28.40c	26.17-30.56	2.21
Kafr El-Shikh (Cv.)	75.25a	70.79-80.45	1.29	208.8a	200.3-223.5	0.42	174.4a	256.7-291.6	2.16	42.63a	38.47-46.72	4.55
Giza 7 (Cv.)	64.65c	60.51-68.96	1.17	203.4c	192.3-214.7	0.42	168.4c	159.1-177.9	0.53	29.26bc	26.89-31.80	2.48
Karim 7 (Cv.)	71.98b	67.46-76.67	1.38	192.3d	181.7-202.9	0.42	163.3d	154.2-172.5	0.53	26.76d	24.51-29.18	2.48
	Pod measurements											
	Pod length (cm)			Pod width (cm)			Pod weight (g)			number of Seeds / pods		
	Mean	Range	C. V	Mean	Range	C. V	Mean	Range	C. V	Mean	Range	C. V
Fowa (landraces)	11.5d	10.07-12.76	4.83	0.79a	0.67-0.91	7.58	2.62b	2.38-2.88	4.53	6.2d	5.70-6.62	2.59
Behira(landraces)	15.1b	13.54-16.58	5.29	0.71b	0.66-0.78	2.35	3.08a	2.66-3.61	8.61	8.07a	7.60-8.61	1.72
Kaha (Cv.)	11.2d	10.45-12.13	2.21	0.80a	0.67-0.92	8.05	2.68b	2.41-2.94	3.65	4.73e	4.28-5.15	3.11
Kafr El-Shikh (Cv.)	16.4a	14.96-18.15	4.69	0.65b	0.60-0.70	1.85	2.69b	2.47-2.98	3.41	8.07a	7.51-8.61	2.28
Giza 7 (Cv.)	11.6d	10.40-13.11	4.69	0.67b	0.60-0.74	3.36	2.98a	2.66-3.36	5.83	7.1b	6.65-7.56	1.49
Karim 7 (Cv.)	13.7c	12.07-15.42	6.27	0.68b	0.64-0.74	1.36	2.59b	2.36-2.84	3.59	6.8c	6.37-7.25	1.49

Means with the same alphabetical letter in the column are not significantly different from each other using Duncan's Multiple Range Test at 5% probability.

Table 5. Mean squares of plant length and flowering and pod measurements, yield and its components for all genotypes under study, over two years of the study (2019 and 2020summer seasons).

S.O.V.	D. F.	Vegetative measurements		Flowering measurements	
		Plant length	Height of the first flower	The number of days to the first flower appears	Number of branches of flower holder
Blocks	2	0.05^{NS}	0.74^{NS}	0.52^{NS}	0.28^{NS}
Years(Y)	1	0.01^{NS}	1.64^{*}	0.27^{NS}	1.05^{NS}
Genotypes(G)	5	14.12^{**}	20.19^{**}	12.01^{**}	10.89^{**}
G x Y	5	0.17^{NS}	0.38^{NS}	0.38^{NS}	0.36^{NS}
Error	22	0.28	0.36	0.42	0.32
S.O.V.	**D. F.**	**Yield and its components**			
		Number of pods/plants	**Total pods yield/plant**	**Total seeds yield/plant**	**100 seeds weight**
Blocks	2	0.69^{NS}	2.06^{NS}	0.15^{NS}	1.04^{NS}
Years(Y)	1	0.0005^{NS}	0.66^{NS}	0.41^{NS}	0.27^{NS}
Genotypes(G)	5	27.37^{**}	58.66^{**}	94.14^{**}	28.33^{**}
G x Y	5	0.43^{NS}	2.07^{NS}	0.69^{NS}	0.18^{NS}
Error	22	0.64	1.64	2.24	0.65
S.O.V.	**D. F.**	**Pod measurements**			
		Pod length (cm)	**Pod width (cm)**	**Pod weight (g)**	**No. of seeds / pod**
Blocks	2	0.70^{NS}	0.0008^{NS}	0.04^{NS}	0.0003^{NS}
Years(Y)	1	0.27^{NS}	0.0000003^{NS}	0.00009^{NS}	0.004^{NS}
Genotypes(G)	5	8.16^{**}	0.022578^{**}	0.25^{**}	0.51^{**}
G x Y	5	0.11^{NS}	0.000616^{NS}	0.02^{NS}	0.03^{NS}
Error	22	0.30	0.002	0.019	0.008

** Highly significant differences at 1% level of probability.
Ns: not significant differences.

Table 6. Variance components values (σ^2_G, σ^2_E and σ^2_{PH}) genotypic and phenotypic coefficient of variability (GCV, PCV) and heritability (over mean of 12 traits understudied).

Traits	Variance					Coefficient of variability		Heritability in broad sense %
	σ^2_Y	σ^2_G	σ^2_{YG}	σ^2_E	σ^2_{PH}	GCV	PCV	
Plant height	-0.00907	2.32559	-0.03653	0.282929	2.562913	3.808003	4.196604	90.7401
Height of the first flower	0.069916	3.301249	0.004307	0.364856	3.740328	15.80438	17.90642	88.26093
Number of days for first flower	-0.00577	1.937903	-0.01503	0.422873	2.339971	5.976569	7.216566	82.81736
Number of branches of flower holder	0.038117	1.755433	0.012241	0.324388	2.130178	7.855456	9.53242	82.40778
Pod length	0.009043	1.342556	-0.06267	0.299135	1.588059	10.12655	11.97832	84.54067
Pod width	-1.5E-35	0.003763	-0.00067	0.002014	0.005106	0.524252	0.711306	73.70269
Pod weight	-0.00121	0.037816	0.00093	0.019059	0.056597	1.363517	2.040683	66.81667
Seeds number / pod	-0.00126	0.080556	0.006242	0.008384	0.093923	1.179821	1.375595	85.76806
Number of pods / plants	-0.02374	4.491116	-0.07207	0.643984	5.039296	6.92456	7.769763	89.12189
Total pods yield / plant	-0.07836	9.432541	0.140861	1.644085	11.13912	4.919554	5.809624	84.6794
Total seeds yield / plant	-0.01559	15.57492	-0.51621	2.243075	17.2862	8.961104	9.945695	90.10032
100 seeds weight	0.005339	4.691259	-0.15685	0.648327	5.188076	15.41656	17.04921	90.42388

σ^2_Y: Years variance, σ^2_G: Genotypic variance, σ^2_{YG}: Years ×Genotypes interaction, σ^2_E: Error variance, σ^2_{PH}: Phenotypic variance, PCV: Phenotypic coefficient of variance and GCV: Genotypic coefficient of variance.

Cluster analysis based on morphological traits provides two major groups the first one includes Kaha Cv. and the second includes the rest of the genotypes. Meanwhile, the second cluster is divided into 3 sup groups the first include Kafr Elshikh Cv., the second includes Geza7 and Karem7 Cvs. and the third contains Fowa and Behira Lrs (Fig. 2).

Five primers for RAPD and six for ISSR techniques were screened for their ability to amplify the genomic DNA of the six studied cowpea genotypes. Data were analyzed based on the comparison of the amplified fragments using gel documentation for each primer. If a fragment was present in a sample, it was designated as "1", if absent, it was designated as "0". If a fragment was present or absent in the genotype then absent or present in the others, it was called a unique species-specific marker, but if a fragment was absent and present in more than one genotype, it was called polymorphic finally if the fragments were present in all genotypes, it was called monomorphic.

A total of 98 RAPD fragments were amplified with the five used primers ranged from 16 (primer 3) to 27 (primer 4), zero of them were common fragments (monomorphic), 24 of them showed to be polymorphic and other 74 showed to be unique fragments (Tables 7 - 11 and Plate 1).

Table7: Amplified DNA fragments (AF) obtained for the six genotypes using first RAPD primers.

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.198	810.532	0	0	0	0	0	1	Unique
2	0.225	698.290	0	0	1	0	0	0	Unique
3	0.236	657.147	0	0	0	1	0	0	Unique
4	0.247	618.428	0	1	0	0	0	0	Unique
5	0.264	563.029	1	0	0	0	0	0	Unique
6	0.269	547.700	0	0	1	1	0	0	Polymorphic
7	0.286	498.637	0	1	0	0	0	0	Unique
8	0.297	469.257	0	0	0	0	0	1	Unique
9	0.313	429.586	1	0	0	0	0	0	Unique
10	0.335	380.455	0	0	0	0	1	0	Unique
11	0.341	368.059	1	0	0	0	0	0	Unique
12	0.352	346.374	0	0	0	0	0	1	Unique
13	0.357	336.943	0	0	0	1	0	0	Unique
14	0.385	288.685	1	1	0	0	0	0	Polymorphic
15	0.390	280.826	0	0	0	1	1	1	Polymorphic
16	0.407	255.669	1	1	0	0	0	0	Polymorphic
17	0.409	252.862	0	0	0	1	0	1	Polymorphic
18	0.429	226.429	0	0	0	0	1	0	Unique
19	0.434	220.264	1	0	1	1	0	0	Polymorphic
20	0.445	207.286	0	1	0	0	0	0	Unique
21	0.462	188.718	1	0	0	0	0	0	Unique
Detectable fragments			7	5	3	6	3	5	

Cluster analysis, according to DNA- RAPD analysis, divided the 6 studied genotypes into 3 main clusters. The first cluster includes Kafr Elshikh Cv., the second cluster includes Behira Lr., meanwhile, the third cluster includes Geza7, Kareem7, Kaha Cvs. and Fowa Lr.; which contain two sup order the first one contain Geza7 and Kareem7 Cvs. with similarity (15%), The second contains Fowa Lr. and Kaha Cv.with similarity (30%) (Fig.2).

Table 8: Amplified DNA fragments (AF) obtained for the six genotypes using second RAPD primers.

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.156	1045.858	0	1	0	0	0	0	Unique
2	0.171	950.716	1	0	0	0	1	0	Polymorphic
3	0.180	897.838	0	1	0	0	0	0	Unique
4	0.190	842.526	1	0	0	0	0	0	Unique
5	0.220	696.210	0	1	0	0	0	0	Unique
6	0.229	657.487	0	0	0	0	0	1	Unique
7	0.249	578.973	0	0	0	0	0	1	Unique
8	0.254	560.855	0	0	0	0	1	0	Unique
9	0.263	529.661	0	1	0	0	0	0	Unique
10	0.283	466.411	0	0	1	0	0	0	Unique
11	0.288	451.816	0	0	0	0	1	0	Unique
12	0.322	363.976	1	1	0	0	0	0	Polymorphic
13	0.327	352.586	0	0	0	0	1	0	Unique
14	0.341	322.556	0	0	0	1	0	0	Unique
15	0.361	284.038	0	1	0	0	0	0	Unique
16	0.366	275.150	0	0	0	1	0	0	Unique
17	0.390	236.208	0	0	0	1	0	0	Unique
Detectable fragments			3	6	1	3	4	2	

Table 9: Amplified DNA fragments (AF) obtained for the six genotypes using third RAPD primers.

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.222	811.211	0	0	0	0	0	1	Unique
2	0.236	742.264	0	0	1	0	0	0	Unique
3	0.253	666.373	0	0	0	0	0	1	Unique
4	0.258	645.565	0	0	1	0	0	0	Unique
5	0.264	621.452	1	0	0	0	0	0	Unique
6	0.283	550.878	0	1	0	0	0	0	Unique
7	0.286	540.492	1	0	0	0	0	0	Unique
8	0.306	476.082	0	0	0	0	1	0	Unique
9	0.308	470.079	0	0	0	0	0	1	Unique
10	0.350	360.118	0	0	1	0	0	0	Unique
11	0.353	353.329	1	0	0	0	0	0	Unique
12	0.372	313.203	0	0	0	0	0	1	Unique
13	0.386	286.583	0	0	0	1	0	0	Unique
14	0.411	244.549	0	0	0	1	0	0	Unique
15	0.433	212.690	0	0	1	0	0	1	Polymorphic
16	0.453	187.344	0	0	0	1	0	0	Unique
Detectable fragments			3	1	4	3	1	5	

Table10: Amplified DNA fragments (AF) obtained for the six genotypes using forth RAPD primers.

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.161	1240.209	0	0	1	0	0	0	Unique
2	0.185	1070.896	0	0	1	0	0	0	Unique
3	0.211	913.456	0	0	1	0	0	0	Unique
4	0.252	710.862	0	0	1	1	0	0	Polymorphic
5	0.276	613.816	0	0	0	1	0	0	Unique
6	0.293	553.202	0	0	0	1	0	0	Unique
7	0.299	533.269	0	0	0	0	0	1	Unique
8	0.323	460.468	0	0	0	1	0	1	Polymorphic
9	0.328	446.600	1	0	0	0	0	0	Unique
10	0.355	378.619	0	1	0	1	0	0	Polymorphic
11	0.358	371.736	0	0	1	0	0	0	Unique
12	0.361	364.977	0	0	0	0	1	0	Unique
13	0.372	341.231	1	0	0	0	0	0	Unique
14	0.378	328.936	0	0	0	0	1	0	Unique
15	0.381	322.956	0	0	0	1	0	0	Unique
16	0.393	300.102	0	0	0	0	0	1	Unique
17	0.399	289.289	0	0	0	0	1	0	Unique
18	0.405	278.866	0	1	0	1	0	0	Polymorphic
19	0.416	260.722	0	0	0	0	1	0	Unique
20	0.419	255.982	1	0	0	1	0	0	Polymorphic
21	0.434	233.543	0	1	0	0	1	0	Polymorphic
22	0.437	229.297	0	0	0	0	0	1	Unique
23	0.449	213.071	0	0	0	1	1	0	Polymorphic
24	0.455	205.394	0	1	0	0	0	0	Unique
25	0.472	185.112	1	0	0	0	0	0	Unique
26	0.525	133.862	1	0	0	0	0	0	Unique
27	0.554	112.106	1	0	0	0	0	0	Unique
Detectable fragments			6	4	5	9	6	4	

Table11: Amplified DNA fragments (AF) obtained for the six genotypes using fifth RAPD primers.

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.163	1334.914	0	0	1	1	0	1	Polymorphic
2	0.191	1169.424	0	0	1	1	0	1	Polymorphic
3	0.224	1000.522	0	0	0	1	0	0	Unique
4	0.227	986.434	0	0	1	0	0	0	Unique
5	0.247	897.449	0	0	1	1	0	0	Polymorphic
6	0.305	682.247	1	0	0	0	0	0	Unique
7	0.320	635.548	0	0	0	1	0	0	Unique
8	0.343	570.075	1	1	0	0	0	0	Polymorphic
9	0.355	538.638	0	0	1	0	0	0	Unique
10	0.383	471.863	1	0	1	1	0	0	Polymorphic
11	0.432	374.303	0	0	1	1	0	1	Polymorphic
12	0.461	326.355	1	0	1	1	0	1	Polymorphic
13	0.489	285.896	1	0	1	1	1	0	Polymorphic
14	0.526	240.022	0	0	0	0	1	0	Unique
15	0.547	217.340	1	0	0	0	0	0	Unique
16	0.555	209.275	0	0	0	0	0	1	Unique
17	0.610	161.365	1	0	0	0	0	0	Unique
Detectable fragments			7	1	9	9	2	5	

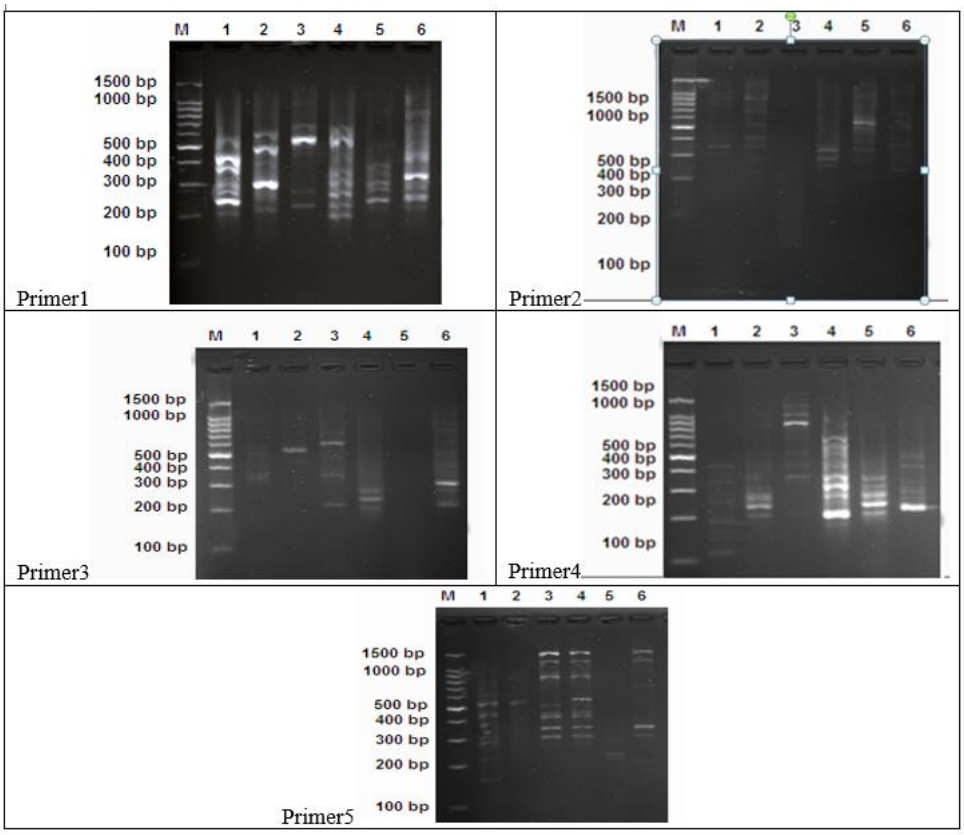

Plate 1: RAPD banding patterns in the six genotypes accessions generated using 5 primers. (1, 2,3,4,5 and 6 for Geza7, Kareem7, Fowa, Kaha, Behira and Kafr El-Shikh, respectively).

A total of 99 ISSR fragments were amplified with the six used primers ranged from 10 to 22, 8 of them were common fragments (monomorphic), 33 of them showed to be polymorphic and 58 showed to be unique fragments (Tables 12 - 17 and Plate 2).

Cluster analysis, according to DNA- ISSR analysis, divided the 6 studied genotypes into 2 major groups. The first main group contained Kafr Elshikh. The second main group

contains the rest genotypes, which contain two sups order the first one contains Geza7 Cv. Meanwhile, the includes Kareem7and Kaha Cvs. and Behira and Fowa Lrs. (Fig. 2).

Of the total 347 reproducible amplicons generated by the 11 RAPD and ISSR primers in sum, showing 66 fragments for Geza7, 50 for Kareem7, 58 for Fowa, 71 for Kaha, 46 for Behira and 56 for Kafr El-Shikh. 132 fragments were unique fragments 29 of them detected in Geza7, 17 in Kareem7 and Behira,18 in Fowa,24 in Kaha and 27 for Kafr El-Shikh genotypes (Tables 18 to 20).

Cluster analysis, based on RAPD plus ISSR analysis, divided the 6 studied genotypes into 3 major groups. The first contained Geza and Kareem7 Cvs. with similarity of (30%), the second consisted of Fowa Lr. and Kaha Cv., and the third one contained Behira Lr. and Kafr Elshikh Cv. (Fig. 3).

Studies on genetic diversity and relatedness at its molecular level have been surprisingly scarce. Hossain *et al*. (2003) characterized cold-tolerant and cold-sensitive Jew's mallow germplasms. Qi *et al.* (2003a, b) classified wild Jew's mallow species using Inter Simple Sequence Repeat (ISSR) marker. Recently Akter *et al.* (2008) and Mir *et al.* (2008) reported the utility of studying genetic variability for different traits in Jew's mallow genotypes using Jew's mallow-specific SSR markers. ISSRs will have an important role in securing plant variety rights by virtue of its unique efficiency in distinguishing even closely related germplasm. To date, more polymorphism has been detected with the use of ISSRs than that with any other assay procedure (Gupta *et al.*, 1994).

Table 12: Amplified DNA fragments (AF) obtained for the six genotypes using first ISSR primers.

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.253	791.535	0	0	0	1	0	0	Unique
2	0.259	769.035	0	0	0	0	0	1	Unique
3	0.290	662.580	1	0	0	0	0	0	Unique
4	0.293	653.094	0	0	0	0	0	1	Unique
5	0.338	526.072	0	1	0	0	0	0	Unique
6	0.343	513.581	0	0	0	1	0	0	Unique
7	0.355	484.798	0	0	0	1	1	0	Polymorphic
8	0.377	436.153	0	1	0	0	0	0	Unique
9	0.389	411.709	1	0	0	0	0	0	Unique
10	0.421	353.017	0	1	0	1	1	1	Polymorphic
11	0.426	344.634	1	0	0	0	0	0	Unique
12	0.438	325.320	0	0	0	1	0	0	Unique
13	0.449	308.567	1	1	0	0	1	0	Polymorphic
14	0.466	284.357	1	0	1	0	0	0	Polymorphic
15	0.491	252.163	1	0	1	0	0	0	Polymorphic
16	0.503	238.031	0	0	0	1	0	0	Unique
17	0.512	227.954	0	0	0	0	1	0	Unique
18	0.515	224.690	0	0	1	0	0	0	Unique
19	0.522	217.257	1	0	0	0	0	0	Unique
20	0.531	208.059	0	0	0	0	0	1	Unique
21	0.546	193.587	0	0	0	0	1	0	Unique
Detectable fragments			7	4	3	6	5	4	

Table13: Amplified DNA fragments (AF) obtained for the six genotypes using second ISSR primers.

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.206	962.158	0	0	1	0	0	0	Unique
2	0.228	848.128	1	0	0	0	0	0	Unique
3	0.233	824.158	0	0	0	0	0	1	Unique
4	0.236	810.102	0	0	1	0	0	0	Unique
5	0.253	734.862	1	0	1	0	0	1	Polymorphic
6	0.267	678.176	0	0	0	0	1	0	Unique
7	0.268	674.299	0	1	1	1	0	0	Polymorphic
8	0.286	608.175	1	0	0	0	0	0	Unique
9	0.311	526.954	0	0	1	0	0	0	Unique
10	0.314	517.967	0	0	0	1	0	0	Unique
11	0.325	486.306	1	0	0	0	0	0	Unique
12	0.364	388.858	0	0	1	0	0	0	Unique
13	0.372	371.423	1	0	0	0	0	0	Unique
14	0.410	298.703	0	0	1	1	1	1	Polymorphic
15	0.433	261.797	0	1	1	0	0	0	Polymorphic
16	0.439	252.944	0	0	0	0	0	1	Unique
17	0.481	198.808	1	0	0	0	0	0	Unique
Detectable fragments			6	2	8	3	2	3	

Table14: Amplified DNA fragments (AF) obtained for the six genotypes using third ISSR primers.

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.216	874.623	0	0	0	0	0	1	Unique
2	0.236	781.263	1	1	0	1	0	0	Polymorphic
3	0.241	759.524	0	0	0	0	0	1	Unique
4	0.268	652.168	0	1	0	1	0	1	Polymorphic
5	0.282	602.619	0	0	0	0	1	0	Unique
6	0.301	541.340	0	0	0	1	0	0	Unique
7	0.307	523.315	1	1	0	0	0	1	Polymorphic
8	0.323	478.128	0	0	0	1	0	1	Polymorphic
9	0.329	462.208	0	1	0	0	0	0	Unique
10	0.349	412.870	0	1	1	1	0	0	Polymorphic
11	0.359	390.213	0	0	0	0	1	0	Unique
12	0.403	304.404	0	0	0	0	0	1	Unique
13	0.416	282.868	0	0	0	0	0	1	Unique
14	0.433	256.989	0	0	0	1	0	0	Unique
15	0.441	245.643	0	0	1	0	0	0	Unique
16	0.477	200.476	0	0	0	0	1	0	Unique
17	0.485	191.625	0	0	1	0	0	0	Unique
Detectable fragments			2	5	3	6	3	7	

Table15: Amplified DNA fragments (AF) obtained for the six genotypes using fourth ISSR primers:

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.258	1111.675	1	1	1	1	1	1	Monomorphic
2	0.357	406.023	1	0	1	1	1	1	Polymorphic
3	0.333	518.315	0	0	1	1	1	1	Polymorphic
4	0.299	732.523	1	1	1	1	1	1	Monomorphic
5	0.278	907.003	0	0	1	1	1	1	Polymorphic
6	0.238	1362.533	1	1	1	1	1	1	Monomorphic
7	0.209	1830.131	0	0	0	0	0	1	Unique
8	0.148	3404.144	0	1	0	1	1	1	Polymorphic
9	0.205	1906.145	1	1	1	1	1	0	Polymorphic
Detectable fragments			6	6	8	9	9	9	

Table16: Amplified DNA fragments (AF) obtained for the six genotypes using fifth ISSR primers

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.092	5432.261	0	0	0	0	0	1	Unique
2	0.111	3822.460	1	0	1	1	1	1	Polymorphic
3	0.134	2497.878	1	1	1	1	1	1	Monomorphic
4	0.150	1857.951	1	1	1	1	1	1	Monomorphic
5	0.164	1434.051	1	1	1	1	1	1	Monomorphic
6	0.175	1170.026	0	0	0	0	0	1	Unique
7	0.196	793.397	1	1	0	1	0	1	Polymorphic
8	0.220	508.962	0	1	1	0	1	0	Polymorphic
9	0.234	392.840	1	1	1	0	0	0	Polymorphic
10	0.253	276.425	1	0	0	0	0	0	Unique
11	0.297	122.490	1	1	1	1	1	0	Polymorphic
12	0.329	67.768	1	1	1	1	1	0	Polymorphic
Detectable fragments			9	8	8	7	7	7	

Table17: Amplified DNA fragments (AF) obtained for the six genotypes using sixth ISSR primers.

Fragments	RF	Sizebp	Genotypes						Polymorphism
			Geza7	Kareem7	Fowa	Kaha	Behira	Kafr Elshek	
1	0.123	5538.394	1	0	0	0	1	0	Polymorphic
2	0.153	3924.725	1	0	0	0	1	1	Polymorphic
3	0.167	3342.010	0	1	0	0	0	0	Unique
4	0.170	3228.868	0	0	1	1	1	1	Polymorphic
5	0.187	2656.386	0	0	0	0	0	1	Unique
6	0.192	2508.200	1	0	1	1	0	0	Polymorphic
7	0.208	2087.320	1	1	1	1	1	1	Monomorphic
8	0.222	1777.410	0	0	0	0	0	1	Unique
9	0.224	1737.064	1	1	1	1	0	0	Polymorphic
10	0.240	1445.582	0	0	0	1	0	0	Unique
11	0.243	1396.643	1	0	0	0	0	0	Unique
12	0.251	1274.086	0	1	0	0	0	0	Unique
13	0.254	1230.952	0	0	0	1	0	0	Unique
14	0.269	1036.225	1	0	0	0	0	0	Unique
15	0.287	842.770	1	1	1	1	0	0	Polymorphic
16	0.308	662.227	1	0	0	1	0	0	Polymorphic
17	0.310	647.195	0	1	0	0	0	0	Unique
18	0.325	544.814	0	0	0	1	0	0	Unique
19	0.333	497.006	1	0	0	0	0	0	Unique
20	0.351	404.219	0	1	0	0	0	0	Unique
21	0.365	344.203	0	1	1	0	0	0	Polymorphic
22	0.386	270.466	0	0	0	1	0	0	Unique
Detectable fragments			10	8	6	10	4	5	

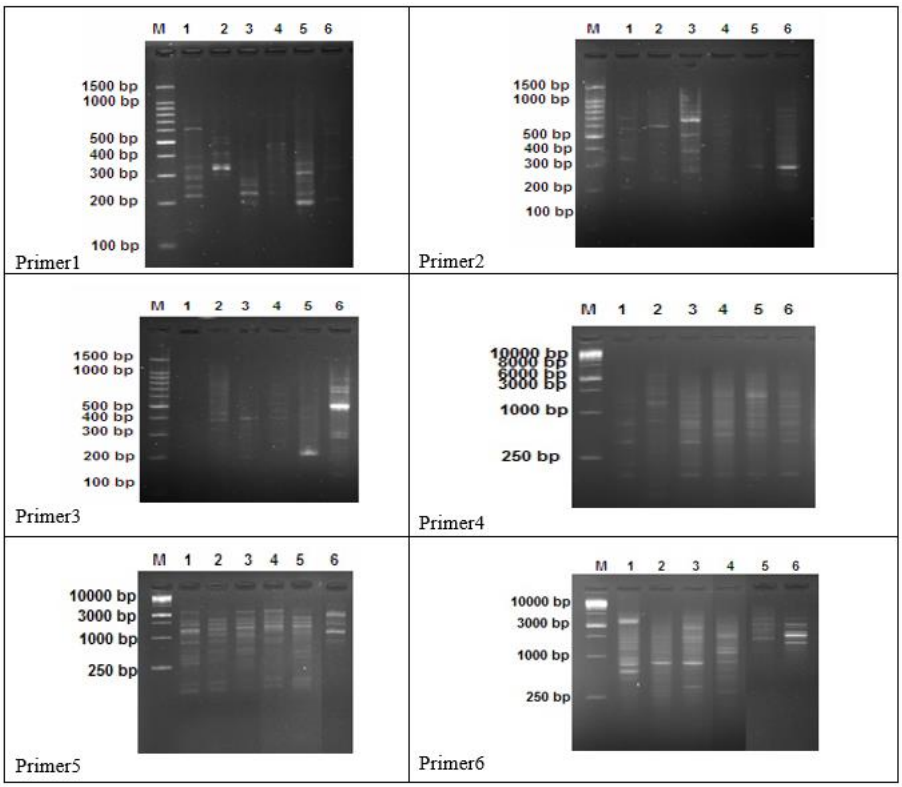

Plate 2: ISSR banding patterns in the six genotypes accessions generated using 6 primers. (1, 2,3,4,5 and 6 for Geza7, Kareem7, Fowa, Kaha, Behira and Kafr El-Shikh, respectively).

Cluster analysis based on morphological traits provides two major groups the first one includes Kaha Cv. and the second includes the rest of the genotypes. Meanwhile, the second cluster divided into 3 sup group the first includes Kafr Elshikh Cv., the second includes Geza7 and Karem7 Cvs. and the third contain Fowa and Behira Lrs (Fig. 2 and Tables 18- 20).

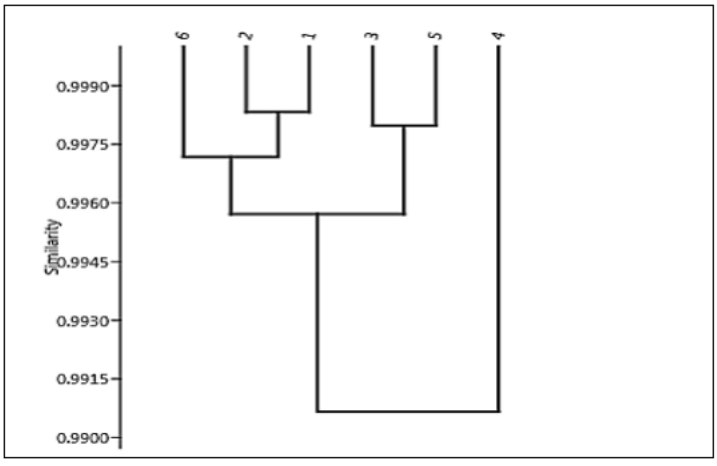

Fig.2: Cluster analysis using UPGMA method depicting genetic similarity (correlation) between six genotypes of cowpea derived from sharing data of morphological. (1, 2,3,4,5 and 6 for Geza7, Kareem7, Fowa, Kaha, Behira and Kafr El-Shikh, respectively).

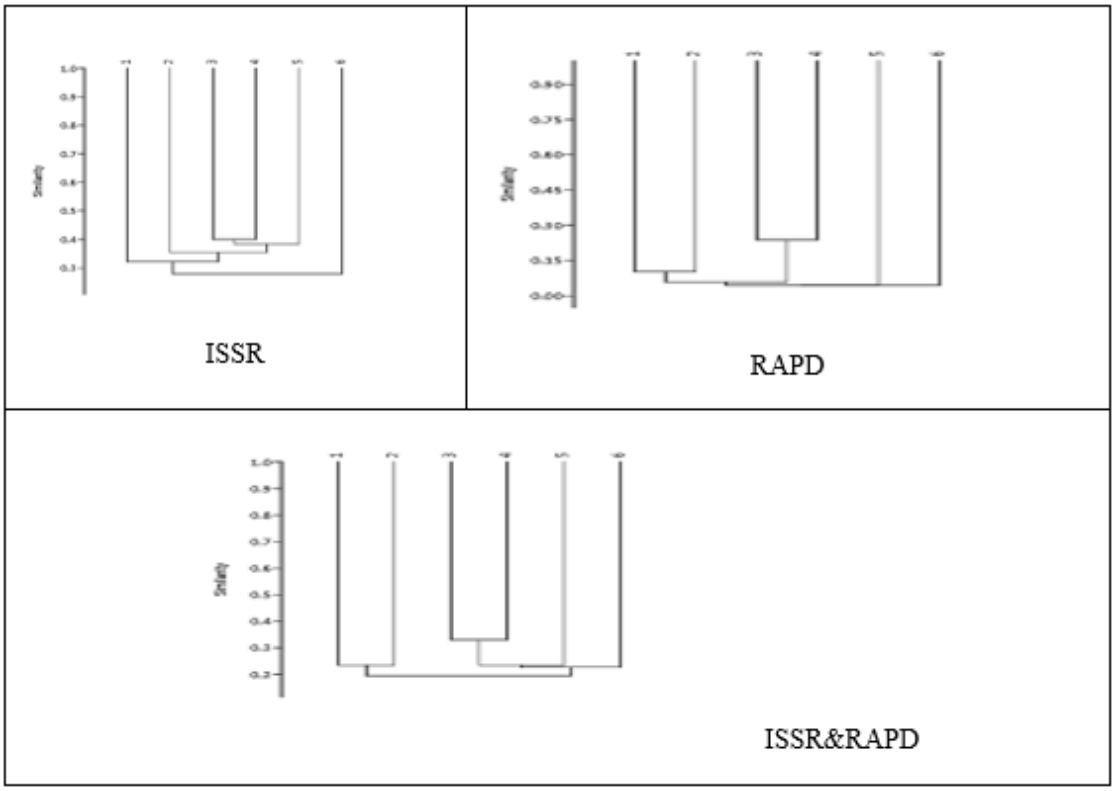

Fig.3: Cluster analysis using UPGMA method depicting genetic similarity (Jaccards coefficient) between three genotypes of cowpea derived from band sharing data of RAPD, ISSR and pooled RAPD + ISSR data. (1, 2,3,4,5 and 6 for Geza7, Kareem7, Fowa, Kaha, Behira and Kafr El-Shikh, respectively).

Table 18: Amplified DNA fragments (AF) obtained for the six genotypes using RAPD and ISSR primers:

Markers	Primer	MB	PB	UB	TAF	P%
RAPD	1	0	6	15	21	28.6
	2	0	2	15	17	11.8
	3	0	1	15	16	6.3
	4	0	7	20	27	25.9
	5	0	8	9	17	47.1
Total AF		0	24	74	98	24.5
%		0	4.8	14.8	19.6	4.9
ISSR	1	0	5	16	21	23.8
	2	0	4	13	17	23.5
	3	0	5	12	17	29.4
	4	4	5	1	10	50.0
	5	3	6	3	12	50.0
	6	1	8	13	22	36.4
Total AF		8	33	58	99	33.3
%		1.3	5.5	9.7	16.5	33.3
Total(RAPD+ISSR) AF		8	57	132	197	28.9

Table 19: Amplified specific DNA fragments (AF) obtained for six genotypes using RAPD and ISSR primers.

Primers	Genotypes						Total
RAPD	**Geza7 (Cv.)**	**Kareem7(Cv.)**	**Fowa (Lr.)**	**Kaha (Cv.)**	**Behira (Lr.)**	**Kafr Elshek (Cv.)**	
1	4	3	1	2	2	3	15
2	1	5	1	3	3	2	15
3	3	1	3	3	1	4	15
4	5	1	4	3	4	3	20
5	3	0	2	2	1	1	9
Total	16	10	11	13	11	13	74
ISSR							
1	4	2	1	4	2	3	16
2	5	0	4	1	1	2	13
3	0	1	2	2	3	4	12
4	0	0	0	0	0	1	1
5	1	0	0	0	0	2	3
6	3	4	0	4	0	2	13
Total	13	7	7	11	6	14	58
Total (RAPD+ISSR)	29	17	18	24	17	27	132

Table 20: Amplified DNA fragments (AF) obtained for the six genotypes using RAPD and ISSR primers.

Primers	Genotypes						Total
RAPD	**Geza7 (Cv.)**	**Kareem7(Cv.)**	**Fowa (Lr.)**	**Kaha (Cv.)**	**Behira (Lr.)**	**Kafr Elshek (Cv.)**	
1	7	5	3	6	3	5	29
2	3	6	1	3	4	2	19
3	3	1	4	3	1	5	17
4	6	4	5	9	6	4	34
5	7	1	9	9	2	5	33
Total	26	17	22	30	16	21	132
ISSR							
1	7	4	3	6	5	4	29
2	6	2	8	3	2	3	24
3	2	5	3	6	3	7	26
4	6	6	8	9	9	9	47
5	9	8	8	7	7	7	46
6	10	8	6	10	4	5	43
Total	40	33	36	41	30	35	215
Total(RAPD+ISSR)	66	50	58	71	46	56	347

All three methods assessed a high level of genetic variations. Based on combined results for morphological and molecular genetic diversity estimates, genotype Kafr el-sheikh and fowa were distinct from other genotypes and can be exploited to harness their unique features in breeding programs. Genotypes swapped among different clusters in different methods of clustering (Table 21). Rahman *et al.* (2011) reported that genotypes also swapped from one cluster to another cluster among different methods and this pattern is somewhat irregular. These differences are not an indicator of the failure or limitation or weakness of the methods (Roldán-Ruiz, *et. al.*, 2001). These results may be due to the diversity at the molecular level, which may not reflect the diversity at the morphological or physiological level, as described by Karhu *et al*. (1996). Another possible reason for this variation in clustering might be the environmental influence and genotype-environment interaction. Compared to morphological and physiological characteristics, the DNA genome provides a direct comparison of genetic diversity at the DNA level, is phenotypically neutral and is not modified by environment and management practices (Messmer *et. al.*, 1993). Morphological and physiological characters are the ultimate expression of the molecular constitution of a variety where a number of biochemical processes are involved. So where a number of biochemical processes are involved. So different types of clustering in different methods are not unusual (Han-yong *et. al.*, 2004).

Table 21: Grouping of genotypes on the basis of morphological and molecular data by using PAST4.03programe:

Morphological groups	genotypes	RAPD groups	genotypes	ISSR groups	genotypes	Common genotypes
A	Kaha	A	kafrelshik	A	kafrelshik	kafrelshik
B	Geza7,Kareem 7,Fowa ,Behira and kafrelshik	B	Behira	B	Geza7,Kareem 7,Fow,Behira and kaha	Geza7,Kareem 7,Fow,Behira
B1	kafrelshik	C	Geza7,Kareem7 ,Fow and kaha	B1	Kareem7 and kaha	Kareem7 and kaha
B2	Geza7 and Kareem7	C1	Geza7 and Kareem7	B2	Fow and behira	Geza7 and Kareem7
B3	Fow and Behira	C2	Fow and kaha			Fowa

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ARABIC SUMMARY

تقدير معامل الاختلاف وبعض المقاييس الوراثية لبعض الأصناف البلدية من اللوبيا

على ابراهيم على عبيدو [1] - سامح عبد المنعم محمد عبد الله [2] - محمد عبد الجواد نصار [1] - هبة الله محمد علي راضي[2] - أسامة فؤاد خليل ابو العينين [2].

1- قسم الإنتاج البناتي - كلية الزراعة (سابا باشا)- جامعة الأسكندرية – مصر.

2- معهد بحوث البساتين - مركز البحوث الزراعية بالصباحية - اسكندرية – مصر.

تم إجراء هذا البحث خلال موسمين صيفيين متتاليين لعامي 2019 و 2020 في كلية الزراعة (سابا باشا) ، جامعة الإسكندرية ومختبر بذور الخضروات بمحطة بحوث البساتين بالصبحية ، الإسكندرية ، مصر؛ لتقييم ستة أصناف وسلالات محلية من اللوبيا من ناحية بعض الصفات المورفولوجية والمحصول ومكوناته وتقدير بعض المتغيرات الوراثية.

وقد أظهرت النتائج اختلافات واضحة بين التراكيب الوراثية الستة للوبيا في معظم الصفات المدروسة. كما كان معامل الاختلاف (C.V.) أقل من 10٪ لجميع الصفات المدروسة في جميع التراكيب الوراثية المدروسة للوبيا. وتشير هذه النتائج إلى أن الستة التراكيب الوراثية من اللوبيا متطابقة وراثيا فيما يتعلق بهذه الصفات. أظهر تحليل التباين أن تباين التراكيب الوراثية كان ذا دلالة عالية في جميع الصفات المدروسة. تشير هذه النتائج إلى وجود اختلافات كبيرة بين التراكيب الوراثية قيد الدراسة بشكل عام ، تفيد النتائج أن جميع الصفات المدروسة يمكن تحسينها من خلال طريقة الانتخاب ، ولكن بدرجات مختلفة من التحسن اعتمادًا على مقدار التباين الموجود في كل مجموعة. وفي الوقت نفسه، كان متوسط مربعات السنوات معنويًا فقط في ارتفاع الزهرة الأولى ، ويمكن تفسير ذلك على أن هذه الخاصية تتأثر بالظروف البيئية المختلفة في كلا عامي الدراسة. قسم التحليل العنقودي، بناءً على تحليل RAPD بالإضافة إلى ISSR ، الأنماط الجينية الستة المدروسة إلى 3 مجموعات رئيسية. الأول احتوى على صنفي جيزا وكريم 7 بنسبة تشابه (30٪) والثانية تتكون من السلالة فوه وصنف قها ، والثالثة تضم السلالة من بحيرة وصنف وكفر الشيخ .

و ابرزت النتائج عن ان صنفى كفر الشيخ و فوة قد يتم الاستفادة بصفاتهما و تنميتها بطرق التربية المناسبة