

Agro-Morphological and Genetic Parameters of some Cowpea Genotypes

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ABSTRACT

Success of most crop improvement programs depends mainly upon the existence of the genetic variability and the heritability of desirable traits in the material under selection. Magnitude and type of genetic variability are important for determining the selection criteria and breeding schemes to be used for improvement purposes. Three related experiments were conducted at Sakha Agricultural Research Station, Agricultural Research Center during three successive summer seasons; 2013-2015 to evaluate 24 cowpea genotypes including the check variety (Balady) and to select the best ones considering the yield and yield components under the study. Data revealed that highly significant differences exist among the genotypes for most of the studied traits. The result, however, revealed The genotype (G12) had the highest values for total fresh (25.8 kg/plot) and dry yield (2.639 kg/plot). On the other hand, G5 showed the lowest value (10.6 k/plot) for total fresh yield. The genotype (G4) surpassed the other genotypes in both evaluated seasons; 2014 and 2015 for all the studied traits. This may indicate the possibility to carry out a selection program to improve and develop new cultivar. In addition, results showed considerable variation among the genotypes in broad sense heritability estimate (h^2) in 2013 and was 60.9% and 99% for the stem diameter and fresh yield for second cut, respectively. On the other hand, the heritability estimates were 82.7% and 98.9% for number of branches and dry yield for the first cut; respectively, in 2014 and 83.1% and 99.3% for number of branches for first cut, and fresh yield for second cut; respectively, in 2015.

The genetic relationship among genotypes based on agro-morphological analysis showed significant variation among the genotypes over all the traits under the study. High similarity between (G20) and (G21) in 2013 and a close relation between (G3) and (G4) in 2014 and 2015 had achieved. Similarity level ranged from 43.98% to 96.02% in the first season (2013) and from 19.55% to 83.39% in the second season (2014) and from 21.91% to 84.17% in the third season (2015).

Keywords: Forage cowpea, Cluster analysis, Heritability in broad sense, Phenotypic and Genotypic coefficients of variation Genetic advance as a percent of mean.

INTRODUCTION

There is a very wide gap between the productions of green forage and the demanded which affect meat or milk production in Egypt. Moreover, the acute shortage of feed is during summer season (Hathout, 1987).

Cowpea (*Vigna unguiculata* sp. L. Walp) forms an integral part of a sustainable agriculture and land use system (Ogbonnaya *et al.*, 2003). Cowpea plays considerable role in the nutritional balance and economy of the rural population in West Africa sub-region (Krasova-Wade *et al.*, 2006). It is a food legume crop that plays an important role in the lives of millions of people in Africa, which serves to improve the nutrient level. Cowpea is grown for both grain and fodder exhibiting wide scale of variability. The crude protein content is 5% and 23% on fresh and dry leaves; respectively, (Aravindham *et al.*, 1995). Cowpea forms excellent forage and gives heavy vegetative growth which covers the ground well and helps tolerate the soil erosion. As a leguminous crop, it fixes about 240 Kg/ha of atmospheric nitrogen and make available 60-70 kg/ha nitrogen for succeeding crop grown in rotation with it (Dumet *et al.*, 2008, Musvosci, 2009). Moreover, it is a very good crop to be used in feeding animal during summer for its high quality and quantity and nutritive value.

The success of good breeding and selection program usually depends on the genetic variability present in the breeding materials and the variation in the population. Heritability and genetic advance are important selection parameters of different traits in the genetic stock, which facilitate evaluation and identification of suitable genotypes. It helps to select genotypes from different genetic population by choosing good genotypes for its improvement.

Phenotypic and genotypic coefficients of variation and heritability are very important indicators in improving traits (Denton & Nwangburuk, 2011). Johanson *et al.*, (1995) illustrated the importance of selection and evaluating varieties for quantitative and yield ability in any breeding program, therefore the varieties can be introduced to a given local environment.

The genetic diversity in cowpea genotypes would facilitate development of cultivars for adaptation to specific production constraints. The genetic similarities and differences of breeding materials could help sustain long term selection. Many workers (Damarany, 1994; Uguru, 1995; Pathmanathan *et al.*, 1997; Ubi *et al.*, 2001; Omoigui *et al.*; 2006) have calculated different components of variance, heritability and genetic advance

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Received February 08, 2018, Accepted March 04, 2018

for different characteristics in cowpea and have mentioned that selection was effective.

The objectives of the present study are evaluating 24 cowpea genotypes and selecting the best genotypes by focusing on genetic variability, heritability and genetic advance for yield and related traits. In addition, determine genetic relationships among evaluated and selected genotypes using similarity through number of quantitative traits which, mean that the differences between traits of tested genotypes attributed to the genetic divergence of it (Iqbal *et al.*, 2008).

MATERIALS AND METHODS

The present study was carried out at Sakha Agricultural Research Station Farm during three successive summer seasons; 2013- 2015. Twenty-four cowpea genotypes were evaluated in a Randomized Complete Block Design with three replicates. Each replicate consisted of one row with 4m long and 0.6m wide with hills spaced at 30cm between plants. After two weeks of sowing on 17th of May 2013, stand was thinned to one plant per hill. Recommended agricultural practices were applied. Two cuts were taken during the growing season. The first and second cuts were taken on 17th of July and 8th of Sept. 2013, respectively. Data were recorded on fresh and dry forage yield (kg/plot), plant height (cm) and stem diameter (cm). Analyses of variance (ANOVA) using Discovery Statistic Soft Ware were issued. Estimation of genetic parameters according to the formula given by Robinson and Comstock (1955) was carried out.

Heritability (h^2) in broad sense was computed as a ratio of genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956).

Genetic advance calculated according to the formula given by Johnson (1955). Selection at 20% intensity using yield and yield components was performed selected the best five genotypes in addition to the local variety as a check, and evaluated in two seasons; 2014 and 2015. The materials were sown in a randomized complete block design with four replicates. Plot size was 12m² (3 × 4m) which consists of five rows, 1.8m wide and 3m long and 30cm between hills. After two weeks, hills were thinned to one plant per hill. Recommended agricultural practices were applied. The

Table 1. Analysis of variance for traits under study of 24 cowpea genotypes at two cuts and total yield in 2013 season

S.O.V.	d.f	Fresh yield (kg/plot)			Dry yield (kg/plot)			Plant height (cm)		Stem diameter	
		Cut1	Cut2	Total	Cut1	Cut2	Total	Cut1	Cut2	Cut1	Cut2
Rep.	2	2.592	1.246	2.441	0.027	0.018	0.025	8.181	73.745	0.054	0.028
		**	**	**	**	**	**	**	**	**	**
Geno.	23	2.828	37.759	44.747	0.047	0.484	0.495	90.454	223.643	0.031	0.044
error	46	0.826	0.376	1.122	0.008	0.005	0.013	7.978	7.707	0.012	0.017

trials were fertilized with 30 kg P₂O₅ /fad which were added during land preparation and 33 kg N/fad which were divided into two equal parts, part added before the first irrigation and the other after the first cut. Two cuts were taken in each season. The sowing dates were done on 10th and 6th of May in the two seasons, respectively. The 1st and 2nd cuts were taken on 10th of July and 13th of August in 2014, respectively. While, in 2015 the 1st and 2nd cuts were taken on 7th of July and 11th August, respectively. Data under study were recorded for the following traits; fresh and dry forage yield (kg/plot), plant height (cm), stem diameter (cm) and number of branches/plant. The statistical analyses mentioned for the 1st season earlier were carried out for the data of both the 2nd and the 3rd seasons.

Cluster analysis:

Genotypes were clustered using un-weighted pair group method using arithmetic average as outlined by Korach (1995). It was based on similarity matrix obtained with un-weighted pair group method using arithmetic average (UPGMA), and the relationships among genotypes were displayed as dendrogram calculated based on Jukes-Cantor Coefficient using PAST program.

RESULTS AND DISCUSSION

1-Genetic Variability:

Analysis of variance showed that the mean squares for all studied traits; fresh and dry yield in the two cuts and total yield, plant height and stem diameter were highly significant among the genotypes at the first season 2013 (Table 1).

Table (2) shows means of four morphological traits under the study. Wide range of variations was observed among the 24-cowpea genotypes under comparison. The maximum value for the total fresh yield (25.8 kg/plot) was detected for (G12), while the lowest value (10.6 kg/plot) was recorded for (G5). The results are in agreement with those reported by Davis *et al.* (1986).

It is worth mentioning that the (G.12) and (G.22) had the highest values for the total dry yield (2.639 and 2.676 Kg/plot), respectively. On the other hand, (G5) had the lowest value (1.218 Kg/plot) for total dry yield.

Table 2. Mean performance of the 24-cowpea genotypes for the four traits under study in 2013 season

No	Fresh yield (kg/plot)			Dry yield (kg/plot)			Plant height (cm)		Stem diameter(cm)	
	Cut1	Cut2	Total	Cut1	Cut2	Total	Cut1	Cut2	Cut1	Cut2
1	7.3	13.3	20.7	0.741	1.467	2.207	53.3	70.6	0.567	1.1
2	8.0	8.9	16.9	0.904	1.068	1.972	49.0	71.0	0.500	1.2
3	6.3	6.5	12.8	0.741	0.780	1.521	51.7	46.1	0.667	1.1
4	8.0	14.0	21.9	0.874	1.694	2.599	60.3	67.7	0.833	1.2
5	6.5	4.1	10.6	0.735	0.484	1.218	48.3	53.3	0.533	1.2
6	9.6	12.0	21.6	0.915	1.500	2.415	57.3	68.0	0.567	0.9
7	7.9	11.0	18.9	0.739	1.210	1.949	52.3	68.3	0.633	1.1
8	8.8	10.1	19.0	0.880	1.230	2.110	67.3	77.0	0.433	1.1
9	6.5	15.3	21.8	0.764	1.763	2.528	61.0	55.6	0.767	1.3
10	9.5	3.0	12.5	1.026	0.300	1.326	48.0	56.0	0.400	0.9
11	9.2	12.3	21.5	0.963	1.233	2.196	55.3	67.3	0.533	1.2
12	9.8	16.0	25.8	1.039	1.600	2.639	49.0	84.0	0.600	1.3
13	9.2	11.3	20.5	0.868	1.232	2.100	57.0	68.3	0.600	1.1
14	8.4	17.0	25.4	0.759	1.819	2.578	48.7	70.3	0.600	1.2
15	8.6	11.7	20.3	0.777	1.283	2.060	61.7	72.3	0.733	1.3
16	8.1	8.6	16.7	0.807	0.929	1.735	54.7	54.3	0.667	0.8
17	8.4	11.7	20.1	0.907	1.248	2.156	55.0	68.3	0.533	1.2
18	8.0	16.0	24.0	0.728	1.840	2.568	50.3	68.3	0.600	1.2
19	8.4	13.3	21.7	0.672	1.613	2.285	47.3	62.3	0.500	1.0
20	7.4	11.8	19.2	0.656	1.396	2.052	55.0	58.3	0.700	1.2
21	8.0	10.8	18.8	0.560	1.127	1.687	55.3	58.3	0.567	1.2
22	9.5	15.2	24.6	0.871	1.805	2.676	55.6	71.6	0.600	1.2
23	8.0	10.2	18.1	0.653	1.118	1.772	61.3	64.3	0.700	1.1
24	7.8	13.7	21.5	0.642	1.503	2.146	63.7	74.3	0.633	1.1
F.test	**	**	**	**	**	**	**	**	**	**
L.S.D 0.01	1.994	1.345	2.324	0.196	0.155	0.250	6.197	6.091	0.240	0.286
L.S.D 0.05	1.494	1.008	1.741	0.147	0.116	0.187	4.642	4.642	0.180	0.214

The genotype (G 8) surpassed the rest of the genotypes for plant height trait at the first cut with value of 67.3cm, but at the second cut (G12) had the highest value of 84 cm. Moreover, (G4) was the best genotype regarding the stem diameter in the first cut. Genotype (G12) had values of 0.833 cm and 1.3cm for the first and second cuts, respectively. These data might indicate a very wide variation among genotypes under study for considered traits. Therefore, it might be used to identify different cowpea genotypes (Sharawy and El-Fiky, 2003).

The analysis of variance of the selected five cowpea genotypes and local variety (Balady) as a check variety is shown in Table 3. Data revealed that the existence of highly significant differences among the genotypes for all the studied traits in the two seasons; (2014 and 2015).

2-Response to Selections:

Table (5) shows means of traits under study at the second season (2014). The results show that, G4 surpassed the rest of the genotypes for all the studied traits with value of 64.7 and 8.06 Kg/plot for the total fresh and dry forage yield, 77 and 83 cm for plant

height, 0.88 and 0.80 for stem diameter, and 8 and 10 for the number of branches per plant for the first and second cuts, respectively. On the other hand, the lowest value was detected for (G6) for all traits in all cuts. In addition, G4 and G6 behaved the same in 3rd season.

Table (5) shows means of the five studied traits where (G4) had value of 65.3 Kg/plot for the total fresh forage yield while (G6) had 48.5 Kg/plot. Regarding the total dry yield (G4) had the highest value of 7.768 and (G5) had the lowest value of 5.309 (Kg/plot). Concerning plant height trait (G4) had 76 and 85cm for the first and second cut and (G4) had the lowest values; 69 and 71cm for (G6). Regarding the stem diameter (G4) had 0.90 and 0.84 and (G6) had the lowest values of 0.80 and 0.70 for first and second cuts, respectively.

The numbers of branches were 8 and 10 for (G4) while (G6) had the lowest values of 7 and 8 branches/plant found to be for first and second cuts, respectively.

The numbers of branches were 8 and 10 for (G4) while (G6) had the lowest values of 7 and 8 branches/plant found to be for first and second cuts, respectively.

Table (6) shows the genotypic (σ^2_g), phenotypic variation (σ^2_p), genotypic coefficient of variation (GCV), phenotypic coefficient of variance (PCV), broad sense heritability (h^2) and genetic advance as percent of mean, (GAM).

Estimates in 2013 season generally had higher PCV values than that of GCV which indicate of some environmental implication alongside genotypic reasons of variation observed between varieties used in this study. Phenotypic variance was higher than the genetic variance of all morphological traits. This observed

variation may due to environmental factor rather than genetic. Similar results have been reported by Nwosu *et al.* (2013). The heritability in broad sense was significantly high for all the traits under investigation.

It ranged from 60% to 99.2% and considered important in selection of different cowpea genotypes from a population (Manggoel *et al.*, 2012 & Rashwan, 2010). The high heritability values indicate that the predominance of additive gene action in the expression of the traits which can be improved through single cycle of selection.

Table 3. Genetic parameters of some morphological traits for cowpea genotypes during 2013 season

	Traits	'X	$^2\delta_g$	$^2\delta_p$	G.C.V	P.C.V	(H^2)%	Δg	G%
1	Fresh yield cut1	8.22	1.001	1.414	12.18	14.47	70.8	117.8	14.3
2	Fresh yieldcut2	11.57	18.69	18.89	37.3	37.5	99.0	595.98	51.5
3	Total Fresh yield	19.80	21.81	22.37	23.6	23.9	97.4	643.6	32.51
4	Dry yield cut1	0.801	0.020	0.024	17.4	19.1	82.9	17.8	22.2
5	Dry yield cut2	1.302	0.239	0.241	37.5	37.7	99.2	68.2	52.38
6	Total Dry yield	2.103	0.241	0.248	23.7	23.3	97.2	67.6	32.14
7	Plant height cut1	54.9	275	31.5	9.5	10.2	87.3	685.9	12.49
8	Plant height cut2	65.68	108.3	112.2	15.8	16.1	96.5	1431.0	21.39
9	Stem diameter cut1	0.603	0.027	0.033	27.2	30.1	81.8	20.8	34.49
10	Stem diameter cut2	1.129	0.014	0.023	10.5	13.4	60.9	12.9	11.42

Table4. Genetic parameters of some morphological traits for cowpea genotypes during 2014 and 2015 season

No.	Traits 2014	'X	$^2\delta_g$	$^2\delta_p$	G.C.V%	P.C.V%	(H^2)%	Δg	G%
1	Fresh yield cut1	32.3	8.6	9.0	9.1	9.3	95.3	400.3	12.39
2	Fresh yield cut2	27.6	15.1	15.6	14.1	14.3	96.8	535.3	19.39
3	Total Fresh yield	56	44.8	45.7	12.0	12.1	98.0	927.5	16.56
4	Dry yield cut1	3.750	0.761	0.769	23.3	23.4	98.9	121.4	32.37
5	Dry yield cut2	3.250	0.157	0.324	12.2	17.5	48.5	38.6	11.87
6	Total Dry yield	7.0	1.08	1.1	14.84	14.98	98.2	144.2	20.6
7	Plant height cut1	72.5	15.2	15.9	5.5	5.3	95.5	533.1	7.35
8	Plant height cut2	79	16.3	17.1	5.11	5.2	95.3	551.7	6.98
9	Stem diameter cut1	0.798	0.013	0.014	14.3	14.8	92.8	15.4	19.29
10	Stem diameter cut2	0.697	0.015	0.016	17.6	18.14	93.8	16.6	23.8
11	No.of branches cut1	7.1	0.211	0.225	6.5	7.1	82.7	58.5	8.2
12	No.of branches cut2	8.5	0.384	0.421	7.2	7.6	91.2	82.8	9.74
No.	Traits2015	'X	$^2\delta_g$	$^2\delta_p$	G.C.V%	P.C.V%	(H^2)%	Δg	G%
1	Fresh yield cut1	30.7	9.6	9.8	10.1	10.2	97.9	429.3	13.98
2	Fresh yield cut2	29.1	13.3	13.4	12.5	12.6	99.3	508.8	17.48
3	Total Fresh yield	59.8	45.8	46.2	11.3	11.4	99.1	943.3	15.77
4	Dry yield cut1	3.608	0.274	0.279	14.5	14.6	98.2	72.6	20.12
5	Dry yield cut2	3.295	0.196	0.201	13.4	13.6	97.5	61.2	18.57
6	Total Dry yield	6.903	0.940	0.950	14.04	14.12	98.9	134.9	19.54
7	Plant height cut1	72.5	15.2	15.9	5.4	5.5	95.5	533.6	7.36
8	Plant height cut2	79	16.3	17.1	5.1	5.2	95.3	551.8	6.98
9	Stem diameter cut1	0.798	0.013	0.014	14.3	14.8	92.9	15.4	19.29
10	Stem diameter cut2	0.697	0.015	0.016	17.6	18.1	93.7	16.6	23.8
11	No.of branches cut1	7.0	0.211	0.254	6.5	7.1	83.1	58.6	8.37
12	No.of branches cut2	9.0	0.384	0.421	7.3	7.6	91.2	82.8	9.2

Table 5. Analysis of variance of six selected cowpea genotypes for the two cuts and the total yield in 2014 and 2015 seasons

S.O.V	d.f	Fresh yield (kg/plot) 2014			Dry yield (kg/plot) 2014			Plant height (cm) 2014		Stem diameter 2014		No. of branches 2014	
		Cut1	Cut2	Total	Cut1	Cut1	Total	Cut1	Cut2	Cut1	Cut2	Cut 1	Cut2
		Rep.	3	0.778	2.523	4.334	0.027	0.100	0.153	3.444	1.444	0.001	0.001
Geno.	5	26.867	47.022	137.355	0.770	0.971	3.240	47.600	51.200	0.014	0.016	0.764	1.262
error	15	1.111	1.649	2.861	0.026	0.033	0.060	2.111	2.378	0.002	0.001	0.130	0.109

S.O.V	d.f	Fresh yield (kg/plot) 2015			Dry yield (kg/plot) 2015			Plant height (cm) 2015		Stem diameter 2015		No. of branches 2015	
		Cut1	Cut2	Total	Cut1	Cut1	Total	Cut1	Cut2	Cut1	Cut2	Cut 1	Cut2
		Rep.	3	1.403	0.419	2.449	0.020	0.013	0.041	1.042	1.667	0.001	0.000
Geno.	5	29.642	40.167	138.662	0.839	0.602	2.899	24.842	47.600	0.007	0.011	1.296	1.787
error	15	0.889	0.372	1.343	0.016	0.012	0.028	2.242	5.400	0.001	0.001	0.068	0.135

Table 6. Mean performance of the six cowpea genotypes for the four traits in 2014 season

Genotypes	Fresh yield(kg/plot)			Dry yield (kg/plot)			Plant height (cm)		Stem diameter (cm)		No. of branches/plant	
	Cut1	Cut2	Total	Cut1	Cut1	Total	Cut1	Cut2	Cut1	Cut2	Cut1	Cut2
	1	32.3	29.3	61.5	3.710	3.394	7.104	73	80	0.800	0.700	7.0
2	31.7	26.7	58.5	3.619	3.056	6.674	71	78	0.760	0.650	7.0	8.0
3	33.2	30.5	63.7	3.881	3.722	7.602	75	82	0.850	0.740	7.0	9.0
4	35.5	29.2	64.7	4.441	3.628	8.064	77	83	0.880	0.800	8.0	10.0
5	33.5	29.0	62.5	3.767	3.336	7.103	72	78	0.780	0.660	7.0	8.0
6	27.7	21.1	48.9	3.080	2.365	5.445	67	73	0.720	0.630	6.0	8.0
F.test	**	**	**	**	**	**	**	**	**	**	**	**
L.S.D 0.01	2.196	2.676	3.524	0.243	0.379	0.510	3.027	3.213	0.093	0.066	0.751	0.688
L.S.D 0.05	1.589	1.935	2.549	0.336	0.274	0.364	2.190	2.324	0.067	0.048	0.543	0.498

Table 7. Mean performance of the six cowpea genotypes for the four traits in 2015 season

Genotypes	Fresh yield (kg/plot)			Dry yield (kg/plot)			Plant height (cm)		Stem diameter (cm)		No. of branches/plant	
	Cut1	Cut2	Total	Cut1	Cut1	Total	Cut1	Cut2	Cut1	Cut2	Cut1	Cut2
	1	30.0	29.0	59.0	3.652	3.304	6.897	74	80	0.830	0.780	8.0
2	31.0	29.7	60.7	3.543	3.332	6.805	72	77	0.850	0.740	7.0	8.0
3	32.0	30.7	62.7	3.841	3.505	7.345	75	83	0.860	0.820	8.0	9.0
4	33.3	32.0	65.3	4.089	3.679	7.768	76	85	0.900	0.840	8.0	10.0
5	32.0	30.3	62.3	3.776	3.395	7.170	74	78	0.800	0.780	8.0	9.0
6	25.0	23.0	48.5	2.755	2.554	5.309	69	71	0.800	0.700	7.0	8.0
F.test	**	**	**	**	**	**	**	**	**	**	**	**
L.S.D 0.01	1.942	1.271	2.415	0.191	0.228	0.349	3.120	4.842	0.066	0.066	0.543	0.766
L.S.D 0.05	1.405	0.919	1.747	0.264	0.105	0.252	2.257	3.502	0.048	0.048	0.393	0.554

Genetic advance is more reliable index for selection of traits. It is rebuttable to highly additive gene effect (Ubi *et al.*2001). Ashkok *et al.* (2000) reached similar results and suggested mass selection breeding method as a mean of improvement of traits controlled by additive gene action.

3-Variability after one cycle of Selection:

Table (7) showed that the phenotypic variation and the value of PCV is higher than the values of the GCV

for all traits except for plant height and the values of heritability which were highly significant for all traits under the study except for dry yield in 2nd cut which had low percent with value of 48.5%.

Also the genetic advance had high values for all the traits except dry yield 2nd cut with value 38.6. Also low value observed for the stem diameter in 1st cut and 2nd cut with values of 15.4 and 16.6, respectively.

Cluster analysis :-

Results of cluster analysis are graphically illustrated in a dendrogram (Fig 1). Data revealed that the studied traits showed diversity among cowpea genotypes. At the first year, the data showed the lowest similarity level (43.98%) between G1 and G3. On the other hand, the highest level of similarity was 96.62% between G20 and G21. The following level of similarity was 92.57% for (G22) which recorded between two nodes (G11 and G13).

The dendrogram showed the relationships among the 24-cowpea genotypes according to the forage yield and its components (Fig 1). The genotypes were divided into two main groups and to sub group. The genotypes (3, 5, 10 and 9) were in one group, while genotypes (1, 7, 2, 4, 6 and 8) were in different group and (11, 13, 17, 15, 14, 18, 22, 19, 16, 20, 21, 23, 24 and 12) in another group.

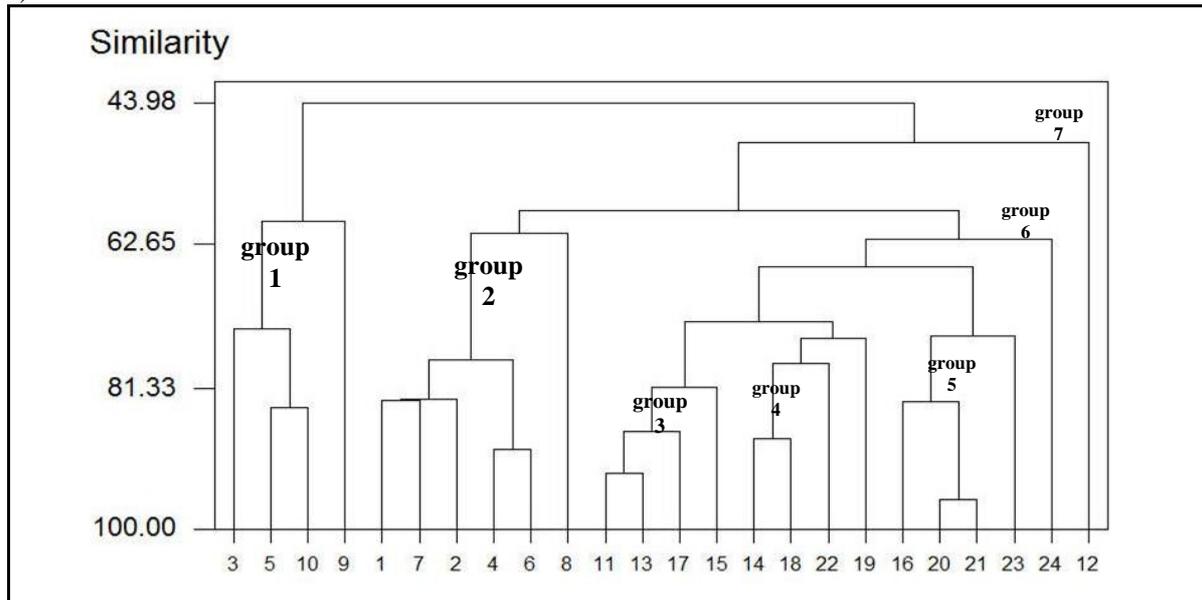


Fig. 1. Similarity levels of 24-cowpea genotypes calculated by cluster analysis using Euclidean Distance, Average Linkage based on agro– morphological traits

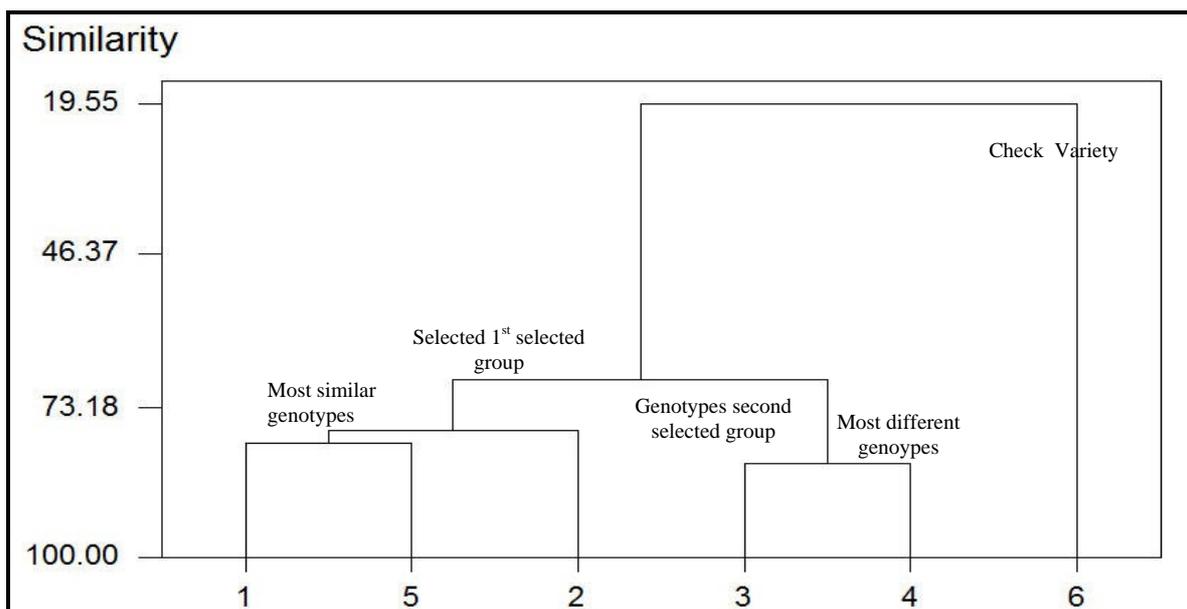


Fig. 2. Similarity levels for six-cowpea genotypes calculated by cluster analysis using Euclidean Distance, Average Linkage based on agro– morphological traits

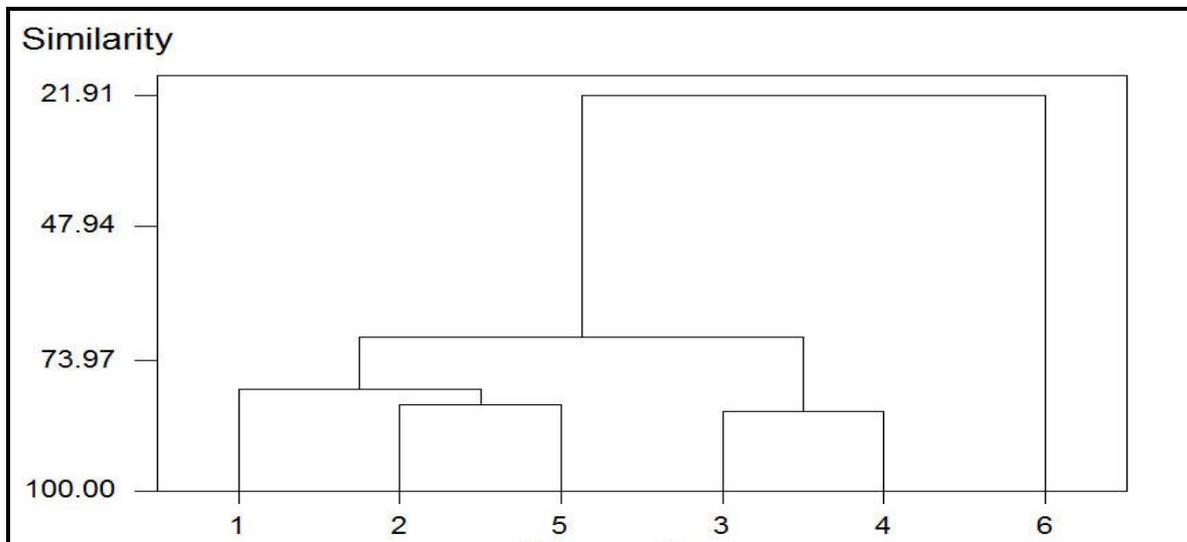


Fig. 3. Similarity levels of six cowpea genotypes calculated by cluster analysis using Euclidean Distance, Average Linkage based on agro-morphological traits in 2015

G20 and G21 were more closely related to each other where the similarity levels among them were more than 96.02. On the other hand, less similarity founded between G3 and G12. Therefore, there is diversity between the genotypes. Cluster analysis is considered a valuable tool for subdividing number of genotypes in groups including similarity and dissimilarity genotypes which it genotype might be classified in seven distinguished groups. Those are; group one includes genotypes 3, 5, 10, 9, group two includes genotypes 1, 7, 2, 4, 6, 8, , group three includes genotypes 11, 13, 17, 15, group four includes genotypes 14, 18, 22, 19, group five includes genotypes 16, 20, 21, 23, group six includes genotypes 24 and group seven includes genotypes 12, may help in breeding program. These results are in agreement with Gad El-Hak, *et al.*, (1988), Sultan *et al.*(2016) and Khatab *et al.* ,(2016).

(Fig. 2) and (Fig. 3) show the six genotypes at the second and third season. The results indicated that similarity level were 19.55 between two nodes G1 and G6 while, the highest similarity level were between G3 and G4 with similarity level 83.39 at the second season. Similar results were detected in the third year between the same genotypes with similarity level (21.91) for the lowest similarity value and (84.17) for the highest similarity value.

The dendrogram result showed that G6 was one main group and the G3 and G4 in subgroup and G1, G2 and g5 in second subgroup in both seasons. G3 and G4 are closely related to each other while G1 and G6 had dissimilarity with each other.

CONCLUSIONS

Evaluation and characterization as well as identification the suitable parents of cowpea germplasm are very crucial for improving the desired characters. The study showed that there is sufficient genetic variation among the 24 genotypes that can be employed for cowpea improvement program for the phenotypic characters. Genotype G4 could be used in intercrossing as parent to improve the dry yield as well as fresh yield. Regarding the similarity and dissimilarity genotypes G1 and G6 could be used for exploiting the hybrid vigor. Since the PCV seems from the results greater than the GCV we recommend evaluation the lines across different environments in Egypt.

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الملخص العربي

الصفات الزراعية المورفولوجية والثوابت الوراثية لبعض التراكيب الوراثية في لوبيا العلف

شيرين النحراوى

حيث أظهرت النتائج في موسم ٢٠١٣م ان درجة التوريث تراوحت ما بين ٦٠,٩% الى ٩٩% لصفة سمك الساق في الحشة الأولى ومحصول العلف الأخضر في الحشة الثانية في موسمي ٢٠١٤ و ٢٠١٥ على التوالي. كما تراوحت نسبة درجة التوريث ما بين ٨٢,٧%, ٩٨,٩% لعدد الأفرع بالنبات والمحصول الجاف بالحشة الأولى على التوالي وتراوحت ما بين ٨٣,١ و ٩٩,٣% لصفة عدد الأفرع على النبات بالحشة الأولى والمحصول الأخضر بالحشة الثانية على التوالي في موسم ٢٠١٥م.

كما أظهرت نتائج تحليل المجاميع او تجربة النسب إستنادا الى الصفات المورفولوجية فروق معنوية بين التراكيب خلال كل الصفات المدروسة ونسبة تشابه عالية ما بين التركيبين ٢٠ ، ٢١ في موسم ٢٠١٣ ووجود علاقة وراثية قريبة ما بين التراكيب الوراثية ٣ و ٤ في كلا الموسمين ٢٠١٤ ٢٠١٥.

يعتبر تحليل التباين بين التراكيب الوراثية المختلفة للصفات المختلفة وتقدير درجات الارتباط بالمحصول ودرجة التوريث ودرجة القرابة من الأهمية بما كان لنجاح برامج التربية المختلفة. تمت إقامة التجارب الخاصة بهذه الدراسة في محطة بحوث سحا الزراعية - مركز البحوث الزراعية خلال ثلاث مواسم متتالية ٢٠١٣ و ٢٠١٤ و ٢٠١٥م لتقييم ٢٤ تركيب وراثي من لوبيا العلف متضمنة الصنف التجاري (لوبيا بلدي) وانتخاب أفضلها. حيث أظهرت النتائج أن التركيب الوراثي (٤) تفوق علي باقي التراكيب الوراثية في موسمي ٢٠١٤ و ٢٠١٥م لكل الصفات المدروسة. واطهرت النتائج وجود فروق معنوية بين التراكيب المختبرة خلال كل الصفات المدروسة. وهذا يوضح امكانية الانتخاب واستخدام برامج التربية اعتمادا على هذه الصفات مستخدماً تلك التراكيب الوراثية كما كانت هناك فروق كبيرة بين التراكيب الوراثية لمعظم الصفات المدروسة وراثياً من خلال درجة التوريث بمفهومها الواسع