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Agronomic Performance, Genetic Variability and Interrelationships of Traits in some Cowpea (*Vignaunguiculata* L.Walp) Genotypes under the Semi-Arid Tropics of Sudan[1]

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Abstract: The effectiveness of selection in any cropdepends on the magnitude of the available genetic variability in the gene pool of the species. In this study, 12 cowpea genotypes (ten accessions and two check cultivars) were assessed for agronomic performance, extent of genetic variability and the association between different traits. The genotypes were sown in two consecutive seasons (October 2015/2016 and 2016/2017) at Shambat using a randomized complete block design with three replicates. Agronomic performance, variance components, genetic coefficient of variation, heritability, genetic advance and genotypic and phenotypic correlation coefficients were estimated. The genotypes exhibited wide variation in all of the studied traits. Seed yield ranged from 477.71 (genotypeHSD-5674) to 2204 kg/ha (genotypeHSD-5131).Highest estimates of genetic coefficient of variation (48.98) and genetic advance as percentage of the mean (81.21) were obtained for number of pods/plant and seed yield/plant, whereas days to maturity showed the lowest estimates. However, days to maturity had the highest heritability estimate (86%) and seed yield/plant had the lowest (40%) value. Seed yield (Kg/ha)had significant positive genotypic and phenotypic association with each of seed yield/plant, number of pods/peduncle and

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number of pods/plant indicating that selection for these traits may be effective in yield improvement of the present cowpea genotypes. Genotypes HSD-5131, HSD-5130 and HSD-5672 appeared promising for future seed yield improvement breeding programs under the semi-tropics of Sudan.

Key words: cowpea genotypes; yield, genetic variability; heritability; genetic advance; association

INTRODUCTION

Cowpea (*Vigna unguiculata* L.Walp) is an annual herbaceous legume cultivated throughout the tropics and subtropics as it has the ability to grow under hot, dry and poor soils conditions(Boukar *et al.*2004). The crop is used as food and feed due to its high protein content (22-30 %) in the seed. In addition, the crop is also used as vegetable, fodder (green or dry) and as anincome-generating commodity for farmers (Timko *et al.* 2007). Moreover, cowpea fixes atmospheric nitrogen in its root nodules, which improves soil fertility and increases the yield of succeeding cereal crops than those under continuous cereal production (Khan *et al.* 2015).

In Sudan, cowpea is mainly grown under rain-fed conditions (350 – 500 mm) in Kordofan and Darfour states; it is also grown under irrigation in very small scattered patches in northern Sudan along the River Nile. As food, cowpea seeds can be eaten as what is called “Ballila” (water-boiled seeds) or it can be cooked with okra and onion into a thick soup and eaten with porridge. Also, the paste from soaked seeds can be fried with oil as small doughnuts (falafel) which can be eaten alone or with bread. It is also considered as excellent roughage for all kinds of livestock. In addition, the crop is used as a trap crop in areas where striga is a problem (El Naim and Jabereldar 2010).

Although cowpea has an important role in tropical agriculture, it received little attention in Sudan. The productivity and yield of seeds and fodder are low because of the low yield potential of the existing cultivars, the limited use of certified seeds and the failure to convince the farmers about the advantages of planting certified seeds versus their own seeds as well as to the effect of many biotic and abiotic factors (Elawad 2000). For improvement of a crop species, a thorough knowledge of genetic variation in the traits of interest among the existing germplasm is important to identify the potential parents and traits of interest to be used in the improvement programs (Santos *et al*. 2014; Elteib and Gasim 2020). Although some studies have been conducted on the proper cultural practices of the crop for high seed yield and as potential forage crop in Sudan, limited work on assessment of genetic variability and interrelationships between yield traits are available, especially under irrigation conditions. The objective of this study was to assess the genetic variability and the association between different traits in some cowpea genotypes.

MATERIALS AND METHODS

Ten cowpea genotypes designated: HSD-2976, HSD-29130, HSD-5130, HSD-5131, HSD-5132, HSD-5670 and HSD-5671, HSD-5672, HSD-5674 and HSD-5864 (provided by the Plant Genetic Resources Unit of Agricultural Research Corporation (ARC), Wad Medani) as well as two check cultivars (Aiengzal a late maturing cultivar and Hydoob an early maturing cultivar), were used in this study. They differ in growth habit, seed color, seed texture, seed eye color, flower and pod color. The genotypes and check cultivars were grown in the Demonstration Farm, Faculty of Agriculture, University of Khartoum (lat. 15°40` N, long. 32°32` E, 380m above sea level) in a randomized complete block design with three replicates. Each genotype was sown in 4×4 meter in plots of five ridges. Spacing was 70 between ridges and 40 cm between the holes along the ridge. Three seeds were sown per hole on the shoulder of the ridge; sowing was in Oct. 2015/2016 and 2016/2017 seasons. Three weeks later, the plants were thinned to two per hole. The experimental plots were irrigated at an interval of 14 days. Weeding was carried out by hand hoeing whenever required.

Ten plants from each genotype in each replicate were randomly selected from the middle ridge for collecting the following agronomic parameters: days to 50 % flowering, days to 50 % maturity, number of main branches/plant, number of nodes on the main stem, number of pods/peduncle, number of pods/plant, 100-seed weight (g) and seed yield g/plant and kg/ha.

Statistical analysis

Combined analysis of variance, for the two seasons, was carried out on the collected data using software PLABSTAT (Utz 1997) as described by Gomez and Gomez (1984) for randomized complete block design. Phenotypic (σ^2_p) and genotypic (σ^2_g) variances, genotypic coefficient of variation(GCV),broad-sense heritability(h^2_B) and genetic advance (GA) and genetic advance as a percentage of the mean, assuming selection of superior 5% of the genotypes, were estimated as suggested by Burton and De Vane (1953) and Johnson *et al.* (1955), as follows:

Genotypic coefficient of variation (GCV)=$[\sqrt{\sigma^2_g}$ /grand mean)] X100
Broad sense heritability (h^2_B) = (σ^2_g/σ^2_p) X 100
Where:
σ^2_g = genotypic variance; σ^2_p = phenotypic variance

Genetic advance (GA) = $(k\times \sigma^2_g)/\sigma_p$

GA as perecentage of the mean (GA % of mean) $= \frac{\text{GA}}{\text{grand mean}} \times 100$

Where: k= Standardized selection differential at 5% selection intensity (k = 2.063).

Covariance analysis was carried out between the different traits means and used to estimate phenotypic (r_p) and genotypic (r_g) correlation coefficients as suggested by Miller *et al.* (1958) as follows:

Genotypic correlation coefficient (r_g) = $\sigma_{gxy}/\sqrt{(\sigma^2_{gx} X\ \sigma^2_{gy})}$
Phenotypic correlation coefficient (r_p) =$\sigma_{pxy}/\sqrt{(\sigma^2_{px} X\ \sigma^2_{py})}$

Where: σ_{gxy} = genotypic covariance between two traits, x and y; σ_{pxy}= phenotypic covariance between two traits, x and y.

RESULTS

Agronomic performance

Analysis of variance revealed highly significant differences ($P \leq 0.01$) among the studied genotypes and checks for all of the studied traits. Table 1 shows the variation in mean performance among the studied genotypes and checks. With respect to phenological parameters (days to 50 %flowering and maturity),Hydoob (early maturing check), reached days to 50 % flowering in 73 days and the earliest genotypes(HSD-5674, HSD-5132, HSD-2976 and HSD-5672) reached days to 50 % flowering in a period from 71 to 77days. On the other hand, the latest genotypes (HSD-5130and HSD-5131) reached 50 % flowering in a period from 96 to 102 days, compared to AIENGAZAL cultivar (late maturing check), which reached days to 50 % flowering in 93 days. The earliest and latest flowering genotypes followed similar trend in reaching the earliest and latest days to maturity. The overall average days were 85 and111days for 50 % flowering and maturity, respectively.

Regarding vegetative parameters, number of main branches/plan ranged from 2.45 in (HSD-5132)to7.13, recorded for HSD-5131. HSD-5131produced the highest number of nodes on the main stem (20.20) and HSD-5671 as well as HSD-5674 recorded the lowest number of nodes on the main stem (10). The number of pods/peduncle ranged from 1.5 in (HSD-29130 andHSD-5132) to 2.90 in (HSD-5131). HSD-5131also produced the highest number of pods/plant (49 pods), whereas HSD-29130 and HSD-5132 recorded the lowest number (11) of pods/plant. Hydoob gave the highest 100 -seed weight(17.83g) and HSD-5674 recorded the lowest 100-seed weight (7.47 g). Seed yield/plant ranged from 131g in (HSD-29130)2601g in (HSD-5131). Seed yield kg/ha ranged from 477.71 kg/ha (given by HSD-5674) to 2204 kg/ha (scored by HSD-5131).The average yield was 1005.94kg/ha. compared to Aiengzal yield (923.64 kg/ha) and Hydoob yield (1031.72).The yield of four accessions, namely HSD-5131, HSD-5130, HSD-5672 and HSD-2976 surpassed the yield of the two check cultivars by an amount of 123.66to 172.59 kg/ha. The yield of the four genotypes was 2204.31, 1376.80, 1297.61

and1047.30 kg/ha, respectively. The yield of the other genotypes was less than that of Aiengzal cultivar (the late maturing check).

Genetic variability

Table 2 shows the variance components [phenotypic (σ^2_p), genotypic (σ^2_g) and environmental variances (σ^2_e)], genotypic coefficient of variation (GCV), heritability estimate (h^2_B), genetic advance (GA) and genetic advance as percentage of the mean. The estimated phenotypic variances were greater than genotypic ones for all traits. Each trait exhibited greater genotypic variance than environmental one, except for seed yield (kg/ha), which showed lower genotypic variance than environmental variance. Highest estimate of GCV (48.98) and highest GA % (81.21 %) were obtained for number of pods/plant and seed yield/plant, whereas days to flowering and days to maturity showed the lowest estimate of GCV and lowest estimate of GA %. However, days to maturity exhibited the highest heritability estimate (86 %) and seed yield/plant gave the lowest (40 %). Heritability estimate greater than 70 % were obtained for number of nodes on the main stem, days to 50 % flowering and number of main branches/plant.

Genotypic and phenotypic association

Seed yield (kg/ha) had a highly significant ($P \leq 0.01$) positive genotypic correlation with each of yield/plant, number of pods/peduncle and number of pods/plant. The same traits exhibited significant ($P \leq 0.05$) positive phenotypic correlation with yield (kg/ha), except for the number of pods/peduncle, which showed no significant association. Also, seed yield (kg/ha) had positive significant genotypic correlation ($P \leq 0.05$) with number of main branches. Yield/plant had highly significant ($P \leq 0.01$) positive genotypic and phenotypic association with number of pods/peduncle and number of pods/plant, but a significant ($P \leq 0.05$) positive phenotypic association with number of main branches/plant. Number of pods/plant had a highly significant ($P \leq 0.01$) positive genotypic and positive ($P \leq 0.05$) phenotypic correlation with number of pods/peduncle. Moreover, Number of pods/plant exhibited significant ($P \leq 0.05$) positive genotypic and phenotypic correlation with number of main branches/plant. However, number of pods/peduncle had a highly significant ($P \leq 0.01$) negative association with 100-seed weight. Number of nodes on the main stem was significantly ($P \leq 0.01$) and positively associated with days to 50 % flowering and days to 50 % maturity at both genotypic and phenotypic levels, But significantly ($P \leq 0.05$) associated with number of main branches/plant at the phenotypic level. Although days to 50 % flowering and days to 50 % maturity had significant ($P \leq 0.01$) positive phenotypic and genotypic association with each other and with the number of nodes on the main branch, their association with seed yield/plant and total yield kg/ha and the rest of the traits was not significant at both genotypic and phenotypic levels.

Table 1.Means of nine traits of cowpea genotypes evaluated for two consecutive seasons (2015/16-2016/17)

Accession/ trait	Days to50% flowering	Days to50% maturity	No. ofmain branches/ plant	No.of nodes on main stem	No. of pods/ peduncle	No.of pods/ plant	100-seed weight (g)	Seed yield/plant (g)	Seed yield (kg/ha)
HSD-2976	77.20	106.13	6.33	13.47	1.61	22.95	14.34	236.52	1047.30
HSD-29130	91.03	116.06	5.12	14.60	1.50	11.12	16.65	130.81	694.32
HSD-5131	96.07	123.13	7.13	20.20	2.91	49.21	11.64	600.63	2204.31
HSD-5132	71.13	104.24	2.45	10.13	1.50	12.13	15.90	142.33	740.90
HSD-5670	94.23	111.02	4.20	12.40	2.21	17.01	11.13	232.92	815.11
HSD-5671	81.18	104.11	3.47	10.00	2.22	26.14	8.42	315.91	849.52
HSD-5672	77.24	99.04	4.47	11.20	2.62	39.32	9.02	476.13	1297.61
HSD-5674	71.13	93.15	5.27	10.00	2.40	19.05	7.52	203.51	477.71
HSD-5130	102.22	132.24	5.53	15.82	1.92	22.43	17.05	248.22	1376.80
HSD-5864	84.46	104.11	2.87	10.87	1.91	11.13	13.04	148.70	611.13
Aiengzal	93.23	112.14	4.05	14.73	1.71	15.24	13.61	224.52	923.64
Hydoob	73.25	99.09	4.00	10.47	2.13	16.21	17.83	182.05	1031.72
Grand mean	84.36	108.71	4.57	12.82	2.05	21.82	13.01	261.85	1005.94
LSD ($P \leq 0.05$)	10.10	7.70	1.38	2.91	0.60	13.20	5.04	183.30	797.21
CV%	7.10	4.10	18.06	12.90	17.50	39.40	23.61	44.23	51.42

Table 2.Variance components [(σ^2_p), (σ^2_g) and(σ^2_e)], (GCV), (h^2_B), (GA) and (GA%) for nine traits in cowpea genotypes evaluated in 2015/16 and2016/17 seasons

Traits	σ^2p	σ^2g	σ^2e	GCV	h2 B	GA	GA % mean
Days to 50 % Flowering	136.38	100.17	36.21	11.86	0.73	17.67	20.95
Days to 50 % Maturity	153.76	132.74	21.01	10.60	0.86	22.05	20.28
No. main branches/plant	2.31	1.64	0.67	28.02	0.71	2.22	48.58
No. nodes on main stem	13.60	10.60	3.00	25.40	0.78	5.92	47.18
No. of pods/peduncle	0.26	0.14	0.12	18.25	0.54	0.56	27.31
No. of pods/plant	176.33	114.23	62.10	48.98	0.65	17.72	81.21
100-seed weight (g)	18.51	9.67	8.84	23.90	0.68	4.63	35.59
Seed yield/plant (g)	26859.81	14942.60	11916.21	46.68	0.40	187.82	71.73
Seed yield (kg/ha)	373754.36	148298.42	225456.94	38.28	0.56	499.7	49.67

Table 3.Genotypic and phenotypic correlation coefficients between pair-wise traits in cowpea genotypes evaluated in two consecutive seasons (2015/16-2016/17)

Trait	X2	X3	X4	X5	X6	X7	X8	X9
X1	0.96** 0.85**	0.47 0.26	0.85** 0.71**	0.04 0.08	0.13 0.11	0.02 -0.01	0.23 0.13	0.34 0.31
X2		0.50 0.34	0.92** 0.79**	-0.07 -0.11	0.09 0.08	0.20 0.05	0.16 0.07	0.40 0.34
X3			0.73** 0.59*	0.45 0.34	0.62* 0.59*	-0.18 -0.08	0.58* 0.51	0.66* 0.41
X4				0.17 0.05	0.32 0.30	-0.07 0.00	0.39 0.32	0.45 0.31
X5					0.97** 0.63*	-0.74** -0.32	0.97** 0.68**	0.76** 0.28
X6						-0.42 -0.13	0.99** 0.94**	0.91** 0.67*
X7							-0.48 -0.24	0.01 0.31
X8								0.88** 0.57*

*, **Significant at (P≤0.05) and (P≤0.01) probability levels, respectively

X1= days to 50 %flowering; X2=days to 50 % maturity; X3= number of main branches; X4=number of nodes on the main stem; X5= number of pods/peduncle; X6=number of pods/plant; **X7=**100-seed weight (g); X8= seed yield/plant (g); X9= seed yield (kg/ha).

Notes: First figure in the upper part of each cell represents genotypic correlation (r_g) and the second figure in the lower part of each cell represents phenotypic correlation (r_p)

DISCUSSION

Agronomic performance

In the present study, the high significant differences among the genotypes for the studied traits indicates the existence of a wide range of variation regarding these traits. Therefore, the potential for selection and development of new cowpea genotypes with better agronomic and yield performance is possible. Similar conclusion was reached by Viswanatha and Yogeesh (2017) in other cowpea genotypes.

The cowpea genotypes showed significant variation in days to flowering and maturity. As a result of the consequences of the current climate change, early maturing genotypes are becoming the most important and attractive aspect for breeders and framers as they are always looking for early maturing genotypes to fit the crop to the short rainy seasons and to escape certain pests and diseases to guarantee their expected economic yield. Based on the study of Dugje *et al.* (2009) who classified cowpea maturity into extra-early (60 days), early (61-80 days) and late (>80 days)groups, the genotypes HSD-5132, HSD-5674, HSD-5672, HSD-2976 (including Hydoob cultivar) were the most early maturing. The rest of the genotypes, including Aiengzal cultivar, were late maturing. Also this study revealed differences among the genotypes for number of main branches/plant. The number of main branches on the plant determines its pod bearing capacity, which contributes to seed yield (Hall *et al.* 1997).Hence, identification and selection of genotypes with high branching capacity is of great importance in yield improvement. According to the study of Makanur *et al.* (2013), who classified the branching ability of cowpea into less (<4), medium (4-6) and high (>6) branching ability, in the present study, three genotypes (HSD-5132, HSD-5864, HSD-5671) could be classified as of less branching ability, six genotypes(HSD-5670, HSD-5672, HSD-29130, HSD-5674, HSD-5130, HSD-2967) as well as HAYDOOB and AIENGZAL cultivars as of medium branching ability and two genotypes (HSD-2976 and HSD-5131) as of high branching ability. From the study, it was observed that genotypes with more branches produced high seed yield per plant and per hectare. Hall *et al.*

(1997) and Elnaim and Jabereldar (2010)reported that the genotypes with more branches, high number of leaves which was reflected in their high photo-assimilate production, hence they produced high seed yield/plant and per hectare. Also, the variation in number of pods/plant and 100-seed weight among the genotypes resulted in differences in their seed yield per plant and per hectare. Olge *et al*. (1987) classified cowpea into four categories [small seed (10-15 g), medium seed (15.1-20 g), large seed (20.1-25 g) and very large seed (more than 25g)]. Thus the present genotypes could be classified into small seed size (HSD-2976, HSD-5131, HSD-5670 and HSD-5864) and medium seed size (HSD-5132 and HSD-5130). Aiengzal cultivar could be categorized as small seed size cultivar and Hydoob as medium seed size. The rest of the genotypes (HSD-29130, HSD-5671, HSD-5672and HSD-5674) could be classified as very small seed as their 100-seed weight were less than 10g.Therefore, these genotypes could be used for fodder production as small-seeded cowpea genotypes are not preferred as food. Also the variation among the genotypes in yield could be attributed to the genetic characteristic of the genotypes (growth habit) as well as the effect of environment. The prostrate and semi-prostrate genotypes (HSD-5674, HSD-29130, HSD-5132 and HSD-5864) produced the lowest seed yield kg/ha. as they had the lowest number of pods/plant. On the other hand, the semi-erect genotypes (HSD-5131, HSD-5672, HSD-2976 and HSD-5130) gave the highest yield kg/ha. These have the advantage to intercept more solar radiation, associated with more assimilate production that is reflected in high number of pods/plant, the most important yield component as reported by Elnaim and Jabereldar (2010)in other Sudanese cowpea genotypes and Doumbia *et al*. (2013) in West African cowpea genotypes.

Genetic variability

In the present study, the greater genotypic variances than the environmental ones in the studied traits revealed the major contribution of the genotypic component to the total phenotypic variation in these attributes. A similar conclusion was reported by Ajayi *et al*. (2014).Also the study showed that the trait ofhigh GCV among the evaluated genotypes*i e*number of pods/plant, gave high GA % of the mean and the trait which exhibited low GCV (days to maturity) gave low GA as parentage of the mean. However, the association of heritability and GA as percentage of the mean in this study did not follow the same pattern as that between GCV and GA as high heritability was not always accompanied by high genetic advance; hence, the amount of genetic advance should not be estimated with heritability alone but with the help of genetic coefficient of variation. Similar results were also reached in Cowpea by Viswanatha and Yogeesh (2017).On the other hand, the high heritability estimate (86 %)for days to maturity indicate the low influence of environment on this trait. Hence, selection based on phenotypic performance could be practiced to improve early maturing cowpea genotypes.

Association between the traits

Genetic improvement in a crop requires in-depth knowledge of variability along with information on the association among various traits to formulate efficient selection strategy especially when highly heritable traits are associated with the most important yield traits (Shanko *et al.* 2014).Moreover, phenotypic and genetic association are valuable for breeding programs as they reveal the existence of pairs of traits that can be related by common genes (pleiotropy) or tightly linked genes (Lachyan and Dalvi 2015).

In the present study, the higher genotypic correlation coefficients than the phenotypic association in all of the studied traits, indicate the important role of the genetic structure in determining these traits. Similar findings have been reported by Udensi *et al*. (2012).

The highly significant positive genotypic and phenotypic association of seed yield/plant with each of number of pods/peduncle, number of pods/plant and number of main branches/plant, indicate that selection for these traits may be effective in the improvement of cowpea seed yield (Santos *et al*. 2014). Pleiotropic or linked gene could cause such association (Lachyan and Dalvi 2015). Nevertheless, the developmentally induced relationship between these traits as a consequence of indirect gene action might cause this positive associations (Rashawn and Helaly 2015).Therefore, selection based on phenotypic performance of these traits could be effective in improving yield of the present enotypes.

The significant negative association of 100-seed weight with number of pods/peduncle might be due to competition for assimilates, indicating that selection for plants with many pods/peduncle will be accompanied by plants with low 100-seed weight.

The positive genotypic and phenotypic association of number of days to 50 % flowering and days to 50 % maturity with the number of main branches/plant indicate that early maturity might be achieved in plants with high number of branches on the main stem. On the other hand, the positive non-significant association of days to 50 % flowering and days to 50 % maturity with number of pods/plant, 100-seed weight, seed yield per plant and yield per hectare, indicate that seed yield parameters could be improved without adverse effect on earliness.

CONCULSIONS

Based on the result of this study, and from the wide variation in agronomic and genetic parameters among the evaluated genotypes, it can be concluded that:

- Selection within the present genotypes can be effective in developing improved cowpea cultivars in the semi- arid tropics.
- For efficient selection, the amount of genetic advance should be estimated with the help of both heritability and genetic coefficient of variation.
- Selection of genotypes with high number of pods/peduncle, number of pods/plant and number of main branches/plant will give high cowpea seed yield.
- Accessions like HSD-5131, HSD-5130 and HSD-5672 appear promising for seed yield production in the semi-arid environment.

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الآداء الحقلى و التباين الوراثى و الارتباط لبعض الصفاة فى الطرز الوراثية اللوبيا الحلوتحت ظروف المناطق المدارية شبة الجافة فى السودان

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المستخلص: يعتمد كفاءة الانتخاب في أي محصول على حجم التباين الوراثي المتاح في المستودع الجينى للنوع. هدفت هذه الدراسة لتقييم 12طرزاوراثيًا (عشرة مداخيل وصنفان) من اللوبيا الحلو للاداء المحصولى ومدى التباين الوراثي والارتباط بين الصفات المختلفة. زرعت الطرز الوراثية لموسين متتالين (إكتوبر2015/2016 و 2016/2017) بشمبات بإستخدام تصميم القطاعات الكاملة بثلاثة مكررات.تم تقدير الاداء المحصولى ومكونات التباين ومعامل الاختلاف الوراثى و درجة التوريث والتقدم الوراثي ومعامل الارتباط الوراثي والظاهري. أظهرت الطرز الوراثية تباينًا كبيرًا في جميع الصفات المدروسة. تراوحت الانتاجية فى المدى من 447.71 كجم/هكتار(الطرز HSD-5674)إلى 2204 كجم/هكتار((الطرز HSD-5131). أعلى تقدير لمعامل التباين الوراثي (48.98) والتقدم الوراثي كنسبة مئوية من المتوسط (81.21٪) سجلت لعدد القرون/النبات وإنتاجية البذور/النبات ، بينما سجلت عدد الأيام للنضج أقل التقديرات. من جهة أخرى، أعطى عدد الأيام للنضج أعلى درجة تورث (86 ٪) و إنتاجية البذور/النبات أقل درجة توريث (40 ٪). أظهر إنتاجية البذور (كجم/هكتار) ارتباطًا وراثيًا وظاهريًا موجباً و معنويًا مع إنتاجية البذور/ النبات وعدد القرون/ حامل الزهرة وعدد القرون / النبات، مما يدل على أن الانتخاب لهذه الصفات قد يكون فعالًا في تحسين إنتاجية الطرزالوراثيةللوبيا قيد الدراسة. من الدراسة،الطرز الوراثية مثل HSD-5131و HSD-5130 و HSD-5672 تَظْهَر بأنها واعدة لبرامج تربية وتحسين إنتاجية البذورالمستقبلية في المناطق شبه الاستوائية في السودان.