Assessment of genetic diversity in cowpea (*Vigna unguiculata*) genotypes in Southern Ethiopia based on Morpho-Agronomic traits

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Abstract A field experiment was conducted at Gofa research station in the main crop season of 2016/17 to estimate the genetic diversity among cowpea genotypes based on morpho-agronomic traits. Thirty-six cowpea genotypes were tested using a simple lattice design. Shannon diversity Index value ranged from 0.633 to 0.953 with a mean of 0.84 confirmed that there was a high degree of deviation in the qualitative traits among cowpea genotypes. Analysis of variance for 14 quantitative traits showed significant differences (P < 0.05) among the cowpea genotypes. Yield and other agronomic traits showed high to moderate phenotypic (PCV) and genotypic coefficient of variation (GCV). On the basis of cluster analysis, thirty-six cowpea genotypes, based on the 14 quantitative traits, were grouped into 6 clusters. I, II, IV, V, III and VI, each with 9, 8,7,7,3 and 2 genotypes, respectively. The highest inter-cluster distance was noticed between cluster III and VI (4265.10) followed by cluster III and V (3569.30), cluster IV and VI (3365.38) suggesting wide diversity between them. Cluster III was found to be promising for yield and its major component traits, while the genotypes in Cluster VI had genotypes for earlier flowering and maturity. Therefore, clusters III, V and VI genotypes could be used as directly in multi-location trials for their suitability to be released for successful cowpea production or could be source materials for obtaining desirable new recombinants for early maturity and higher yield in South Ethiopia.

Keywords: Cowpea, Cluster analysis, Shannon Weaver diversity index

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] (2n=2x=22) is a dicotyledonous self-pollinated plant belonging to Fabaceae and native to Central Africa (Nameirakpam and Khanna, 2018). It is vital for the existence of many individuals in developing countries in the tropics, particularly in Africa and Asia (IITA, 2011). Cowpea seeds are high in protein (23-32%), carbohydrate (60%), fat (2%), and also a good source of essential compounds

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like vitamins B, C, iron, phosphorus, calcium, ß carotene and zinc (Chopra *et al.,* 2011; Adeyemi *et al.,* 2012; Srivastava *et al.,* 2016). This crop is important for human as food. It may also be used for green manure, animal feed, and attracts unprecedented attention in the sub-Sahara Africa for its medicinal value, and may have great economic importance to poor farmers as source of income from grain sales in the local market (Langyintuo *et al.,* 2003; Sprent *et al.,* 2010; Sprent *et al.*, 2009). Like other legumes, cowpea has nitrogen-fixing capacity from atmosphere, which supports to sustain soil fertility for future use and can therefore be used in intercrop systems with cereal crops such as maize and sorghum (Dakora and Keya, 1997).

Cowpea is widely grown in drier regions of the world where it is one of the drought tolerant legumes (Fabunmi *et al.*, 2012). Similarly, in Ethiopia, cowpea is grown in drier areas of the Rift Valley and the dry highlands of Hararghe (Oromiya region), central Tigray usually intercropped with sorghum/crop rotation and in the North eastern part of the country around Shewrobit, Kobo, South Wello, and Waghimira (Amahra region) areas (Negash *et al.*, 2013; Molla, 2015). In Southern Nations, Nationalities and Peoples' Region state (SNNPRS), Gambella and central Oromia Region sole-cropping and intercropping were practiced ,while farmers' in the Eastern Oromia and West Harerge zones experienced intercropping of cowpea with sorghum and maize to increase soil fertility, to produce diverse product and use it as a supporting mechanism for cowpea (Alemu, 2015; Beshir *et al.*, 2019). It is grown in low rainfall areas of SNNPRS especially in Segen people's area zone (Konso and Derashe), South Omo, Humbo, Hammer Bako, Loka Abaya, Goffa and Loma woredas (Tanto and Tefera, 2003).

In Ethiopia, cowpea yield under traditional farming is on the average 0.4 t /ha (Beshir *et al.*, 2019),while cowpea yield potential is high, averaging 1.5 to 6 t/ ha depending on genotype, but the actual yields are low (FAO, 2007). Despite its significance, the shortage of high-yielding varieties, poor agronomic practice, and insect pest attacks remain the most severe constraints on cowpea cultivation and storage (Tekle, 2014). In this case, there are expectations to increase productivity and crop acceptance by the use of appropriate measures that help overcome problems. To boost the potential for cowpea harvest, it is necessary to identify varieties with improved productivity and additional desirable traits to solve the problem of hunger or food insecurity, especially in the lowlands of Southern Ethiopia.

Genetic diversity is a raw material for evolution and is essential for populations to survive, succeed, and cope with environmental changes, new diseases and pest outbreaks (Hegde and Mishra, 2008). Genetic diversity researches on plants are very important in terms of developing superior

varieties and stabilizing the yields of these varieties in plant breeding plans. Genetic diversity is being studied using various methods such as morphological, biochemical and molecular markers. Research evidence on the categorisation of genotypes by means of morphological markers for their genetic difference helps researchers to use them to generate modern varieties. In order to achieve a higher yield quantitative assessment of the transmissible variability parameters accompanied by the understanding of genetic diversity is a pre requisite to the researcher to select genetically different parents with the prospective to produce high heterotic combinations. A better knowledge of the genetic diversity in cowpea will facilitate crop improvement. With regard to diversity studies, many researchers from various countries, namely Peksen and Peksen (2013); Vaibhav *et al.* (2015) and Gbaguidi *et al.* (2015) studied genetic variation on cowpea genotypes. However, the insignificant research has been done in assessing the agro-morphological diversity of cowpea genotypes in the southern regions. 36 cowpea genotypes were subjected to variability parameters and genetic diversity analysis to be used in forthcoming cowpea improvement program. Hence, this study was carried out to assess the genetic diversity among cowpea genotypes using morpho-agronomic traits.

Materials and methods

Description of the study area

The trial was carried out in 2016/2017 at the experimental farm of the Gofa research station, 7 km in the north of Sawula, the town of the Gofa Zone. Gofa is 520 km South of Addis Ababa at an altitude of 1317 meters above sea level and lies 6° 20'N latitude and 36° 55'E longitude. The soil is mainly made up of sandy loam. The rainfall during the crop period varies from 40.1mm to 246.5 mm with major precipitation in the month of September to October (Figure 1). The minimum and maximum temperature ranged between 16.4 °C and 28.2 °C, respectively.
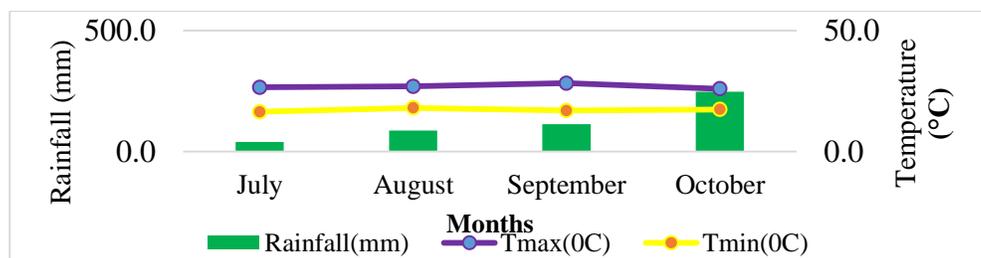
Figure 1. Total rainfall, mean maximum and minimum temperature of the experimental site during the experimental period

Source of experimental materials

Thirty-six cowpea genotypes including two local checks were used in the study. The seeds of the cowpea genotypes were obtained from Melkasa Agricultural Research Center of the Lowland Pulse Improvement Program. Seeds of the local materials were obtained from the farmers near the study area. The experimental materials for this study are presented in Table 1.

Table 1. List of Cowpea Genotypes tested

No	Genotype name	Type	Source	No	Genotype name	Source	Type
1	KB	Introduced	MARC	19	IT97K-449-38	MARC	elite
2	Bole	released	MARC	20	IT99K-316-2	MARC	elite
3	Kenketti	released	MARC	21	IT96D-719	MARC	elite
4	86D-378	elite	MARC	22	IT97K-356-1	MARC	elite
5	IT-89KD	elite	MARC	23	IT98K-506-1	MARC	elite
6	MEL-NURL-96-3	elite	MARC	24	IT00K-901-5	MARC	elite
7	IT96D-610	elite	MARC	25	IT97K-499-38	MARC	elite
8	IT93K-556-4	elite	MARC	26	IT95K-268-1-4	MARC	elite
9	IT97K-568-18	elite	MARC	27	BEB	HARC	released
10	95K-1095-4A	elite	MARC	28	Brazil-3	MARC	Introduced
11	IT87D-1137	elite	MARC	29	Brazil-1	MARC	Introduced
12	IT-960-604	elite	MARC	30	IT93k-293-2-2	MARC	elite
13	Tvu	released	MARC	31	W/W/T	MARC	released
14	OT-03L-2046-2	elite	MARC	32	IT-87D-721	MARC	elite
15	IT93K-2046-1	elite	MARC	33	93 K-619-1	MARC	elite
16	IT93K-452-1	elite	MARC	34	IT99K-1060	MARC	elite
17	IT98K-1111-1	elite	MARC	35	Gofa local (white)	Farmer	local
18	IT97K-569-9	elite	MARC	36	Gofa local(red)	Farmer	local

Note: MARC, Melkasa Agricultural Research center, W/W/T=white wonderer trailing

Experimental design and field management

The study was conducted on 36 cowpea genotypes of which 34 cowpea genotypes sourced from Melkasa Agricultural Research Center, Ethiopia and

two local checks from farmers. The experiment was carried out in a simple 6 X 6 lattice design where each experimental unit consisted of a rectangular plot (1.2 m x 3.0 m) of 3.6 m². Cowpea seeds were sown in two rows of 3 m long per plot providing 20 cm between seeds in the same row and 60 cm between rows. Di-ammonium phosphate (DAP) fertilizer was applied during planting at the rate of 100 kg/ha equally for all experimental units. All the cultural operations such as field preparation, weeding and crop protection were carried out equally for all experimental units according to the recommendations in order to raise a successful crop. Data on various agro-morphological traits were recorded during growth based on the descriptors available for cowpea (IBPGR, 1983). Qualitative and quantitative data were collected using the descriptors. Data on flower color and growth habit were assessed on plot basis while seed color, seed shape and seed size were scored visually from seed samples. Data on the plant height, number of pods per plant, number of seeds per plant, pod length, number of primary branches per plant, number of secondary branches per plant, and number of seeds per pod were recorded on five randomly selected plants from the each plot while other characters such as days to first flowering, days to 50% flowering, days to maturity, harvest index, above-ground biomass yield, 100 seed weight, and grain yield were recorded on the plot basis. Likewise, grain yield sample is taken from the net area of the plot adjusted to the storage moisture content (10%) based on the value of actual grain moisture read using Digital Grain Moisture Meter (DRAMINSKI, POLAND). Seed weight (g) was determined by randomly counting 100 seeds from each plot yield and weighed using an electronic sensitive balance (Mark: Cosmo digital scale).

Data analysis

Statistical parameters such as ANOVA, phenotypic and genotypic variances, genotypic and phenotypic coefficient of variation, cluster analysis and genetic distance between clusters were computed for 14 quantitative traits and Shannon-Weaver diversity index (H') for 5 qualitative traits were computed using the SAS computer program, version 9.0 (SAS, 2002) and Minitab 17 (Mintab, 2007). Descriptive value, frequency of traits, and frequency distribution for total genotypes were determined. The Shannon-Weaver diversity index (H') for qualitative traits that was estimated to characterize the phenotypic frequencies of the characters was estimated as follows:
The Shannon-Weaver index is calculated using the following formula:

$$H= -\sum_{i=1}^{n} PiLnPi$$

H = Shannon and Weaver diversity index Pi= Frequency of each phenotypic class *I* of a given character n = Number of phenotypic classes of each character.

The index (H) is converted towards the relative phenotypic diversity index (H ') by dividing it by its maximum value: H max (Ln (n)) to obtain 0 to 1 values.

$$H' = -\sum_{i=1}^{n} PiLnPi/Ln \text{ (n)}$$

The relative diversity index (H ') reaches its minimum value, which is zero for monomorphic characters. Moreover, the value of this index increases with the degree of polymorphism and reaches a maximum value (1) when all the phenotypic classes present in equal frequencies. Where *n* is the number of phenotypic classes for a trait and *Pi* is the proportion of the individuals in the *i*th classes. The estimated *H'* values of each qualitative trait were divided by *log* en for standardization if values of *H'* within 0 to 1 interval. The standardized Shannon and Weaver (1949) diversity index was classified as low (0-0.33), intermediate (0.34-0.66), and high (0.67-1).

Results

Qualitative characters and distribution of qualitative characters

Cowpea genotypes differed significantly in their qualitative morphological characters. In our study, various classes of these characters have been discussed and used. The frequency, percentage, and diversity index estimates for qualitative characters are given in Table 2.

The observed data shown in Table 2 specified that there was a significant qualitative trait deviation between the cowpea genotypes tested. Cowpea genotypes were mostly affected by prostrate growth habit (44.4%) compared to other traits, and this feature is considered to be the more dominant type. We also observed in this study, frequency of the genotypes with seed color showed a trend to decrease the order which were cream brown (72.2%), holstein white and black (13.89%), brown (5.56), and others (8.3%) respectively (Table 2). The variation in flower color attitude, with the percentage of violet, white, mauve-pink and other flower color cowpea genotypes were 47.22%, 19.44%, 2.78% and 30.56%, respectively.

The majority of the evaluated cowpea genotypes had possessed Rhomboid and kidney seed shape (61.11%) and bold seed size (63.91%) as seen in Table 2. It suggested that the cowpea genotypes assessed in the study exhibited a high variability in almost all of the qualitative traits observed.

Diversity analysis of qualitative characters

The diversity estimation for specific qualitative characters is given in Table 2. Polymorphism was prevalent in varying degrees for most characters, thus suggesting the existence of a wide range of variability in genotypes. For

the 5 qualitative traits investigated, large dissimilarities were formed among cowpea genotypes, and the estimated diversity (H′) for specific traits ranged from 0.633 for seed color to 0.953 for growth habit and overall mean of 0.84 for qualitative traits (Table 2).

In the present research, the diversity between cowpea genotypes was observed. The highest diversity was observed in growth habit with a diversity index H ′= 0.953, followed by seed shape (H' = 0.927). Most genotypes had a cream brown seed color in the form of a rhombic seed shape. On the average, the qualitative traits had high variability with a value of 0.84 diversity index. High diversity indices were calculated with growth habit (H'=0.953) being the most diverse as shown in Table 2. The standardized Shannon and Weaver (1949) diversity index is classified as low (0-0.33), intermediate (0.34-0.66) and high (0.67-1). All traits had high diversity indices except for seed color.

Table 2. Qualitative morphological traits, class partition frequencies of traits and estimation of diversity indices of the entire cowpea genotype

Trait	Classes	No of class	No of genotypes	Frequency(%)	H'
Growth habit	1: Acute erect		0	0.00	0.95
	2: Erect	3	13	36.1	
	3: Semi-erect		7	19.4	
	4: Intermediate		0	0.00	
	5: Semi-prostrate		0	0.00	
	6: Prostrate		16	44.4	
	7: Climbing		0	0.00	
Flower color	1: White	4	7	19.44	0.82
	2: Violet		17	47.22	
	3: Mauve-pink		1	2.78	
	4.other		11	30.56	
Seed shape	1: Kidney		10	27.8	0.93
	2: Ovoid	5	7	19.4	
	3: Crowder		3	8.3	
	4: Globose		4	11.1	
	5: Rhomboid		12	33.3	
Seed color	1: cream	4	0	0.00	0.63
	2: Cream brown		26	72.2	
	3: Brown		2	5.56	
	4: Brown ochre		0	0.00	
	5: brown olive		0	0.00	
	6: holstein white		5	13.9	
	and black		3	8.3	
	99:other				
Seed size	1:small	3	4	11.1	0.88
	2: Medium		9	25.0	
	3: Large		23	63.9	
Mean					**0.84**

Quantitative traits

Mean squares due to genotypes were highly significant ($P < 0.01$) for the first flowering days, maturity days, hundred seed weight, above-ground biomass yield, grain yield, seeds per plant and significant differences (P<0.05) for the eight traits studied *viz.*, number of primary branches per plant, number of secondary branches per plant, pod length, number of seeds per pod, number of pods per plant, plant height, days to 50% flowering and harvest index (Table 3). These findings suggested that the studied genotypes had sufficient genetic variability which can be exploited for selection/breeding. The mean values of the 36 genotypes for 14 quantitative characters are presented in Table 4. Statistically significant differences were found among the genotypes for all the analyzed traits. Maximum yield was recorded for G9 (3003 kg ha^{-1}), and followed by the genotypes G4, G10, and G11. In present study genotypes that exhibited a wide range for mean and coefficient of variance for almost all the characters studied.

Table 3. The analysis of variance for various traits of the cowpea genotypes

Characters	Replication (df=1)	Genotypes (df=35)	Error (df=25)	CV%
DFF	2.72	19.88**	4.22	4.29
DF	7.34	12.01*	3.6	3.53
DM	6.13	91.96**	2.23	1.64
HSW	1.10	19.11**	3.36	10.91
GY	146259.36	801575.31**	105554.4	19.16
BY	376477.68	2454771.20**	320478.71	13.32
HI	20.66	64.82*	26.86	13.47
PL	7.93	14.62*	5.32	15.17
PB	1.39	6.66*	2.36	14.22
SB	16.25	120.89*	36.89	26.59
PH	209.10	990.58*	307.60194	20.47
SD	45.44	7.69*	2.51	13.43
PT	164.11	208.10*	83.94	23.76
SDP	83995.34	56165.61**	10628.84	21.92

** and *significant at 1% and 5% probability levels, respectively. DFF= Days to first flowering, DF=Days to 50% flowering, PL=pod length, BY=Above ground biomass yield per ha (kg), DM= Days to maturity, PB=number of primary branch, SD= number of seeds per pod, GY =grain yield per ha (kg), SDP=Number of seeds per plant, HSW=Hundred seed weight, SB= number of secondary branch, PH=plant height, PT= number of pods per plant, and HI=Harvest index

Estimation of variability parameters

Range and means

Genotypes showed a wide range of variability for the quantitative traits of the studied cowpea genotypes (Table 5). The grain yield showed a wide range (746 - 3003 kg/ ha) followed by plant height (37 –132 cm) and biomass yield (2407-6334 kg/ha). Days to 50% flowering ranged from 48 (IT87D-721) to 59 days (IT97K-568-18), an interval of 11 days from the earliest to the late maturing genotypes. Harvest index from 24 to 48 %; pod length from 11 to 23 cm; primary branches per plant from 6 to 14; secondary branches per plant from 7 to 40; number of seeds per pod from 8 to 16 and number of pods per plant from 17 to 57. It could be concluded from Table 5 that most of the quantitative characters measured showed broad variability.

Phenotypic and genotypic variations

Assessments of different genetic parameters are presented in Table 5. The assessment of genetic variability revealed higher values (>20%) for phenotypic coefficient of variation (PCV) for grain yield per hectare (39.7%),number of seeds per plant (38.9%), number of secondary branches per plant (38.9%), number of pods per plant (31.3%), plant height (29.9%), above ground biomass yield per hectare (27.7%),pod length (20.8%), and moderate (between 10 to 20) for hundred seed weight (19.9%) ,number of primary branches per plant (19.7%), harvest index (17.5%), number of seeds per pod (19.1%) and low phenotypic coefficient of variation (less than 10) recorded for the first flowering days (7.4%), 50 % flowering days (5.3%) and maturity days (7.5%).

Similarly, the magnitude of genotypic coefficient of variation (GCV) was also high (>20%) for grain yield per hectare (34.8%) followed by number of seeds per plant (32.1%),number of secondary branches per plant (28.4%), ,above ground biomass yield (24.3%),plant height (21.7%), pods per plant (20.4%) and moderate (between 10 to 20) for hundred seed weight (16.7%) , pod length (14.2%), harvest index (11.3%), number of primary branches per plant (13.6%), number of seeds per pod (13.6 %) and low genotypic coefficient of variation (less than 10) recorded for the first flowering days (5.8 %), 50% flowering days (3.9 %) and maturity days (7.3 %). The magnitude of PCV ranged from 5.3 % (50% flowering days) to 39.7% (grain yield per hectare), while the magnitude of GCV ranged from 3.9 % to 50% flowering days to 34.8 % in grain yield per hectare (Table 5).

Table 4. Mean performance of 36 genotypes of cowpea for 14 quantitative characters

GC	DFF	DF	DM	HW	GY	BY	HI	PL	PB	SB	PH	SD	PT	SDP
G1	46	52	89	19	1134	3353	34	11	11	28	109	11	46	501
G2	44	54	85	18	1674	4452	38	13	10	28	64	9	49	458
G3	43	52	84	14	1333	3692	35	16	10	29	78	13	31	411
G4	51	57	89	13	2737	6334	43	16	12	23	107	14	39	548
G5	47	53	87	14	2351	5386	43	19	12	33	105	15	48	694
G6	49	54	106	14	2378	5435	44	12	13	40	111	14	38	539
G7	50	54	86	18	1461	3686	40	12	10	25	52	10	29	301
G8	46	52	89	20	2061	4974	41	15	14	27	87	10	39	393
G9	54	59	87	20	3003	6307	47	11	14	31	88	13	52	693
G10	48	54	88	18	2625	5393	47	13	12	33	92	12	50	631
G11	47	52	88	13	2576	5487	45	17	12	39	103	15	57	880
G12	46	52	87	14	2437	6051	39	23	12	16	95	13	54	730
G13	51	58	87	10	2429	5057	48	15	14	25	76	11	36	427
G14	49	54	101	15	891	3650	24	14	11	31	65	9	36	370
G15	45	50	100	18	1184	3508	33	14	12	21	75	13	35	439
G16	43	51	84	18	1239	3176	39	18	12	16	59	11	34	377
G17	49	55	89	19	1081	2737	39	18	9	15	65	10	32	316
G18	53	58	89	17	1715	4614	37	13	13	21	82	12	51	594
G19	54	58	97	21	1219	2865	42	18	9	14	90	8	43	358
G20	50	54	87	18	752	2541	32	15	9	11	68	11	25	267
G21	49	53	98	18	1087	3157	34	15	8	17	60	11	23	248
G22	47	54	98	19	1415	4042	35	18	11	16	67	10	38	386
G23	47	52	101	17	1806	4574	39	19	11	19	131	11	46	541
G24	49	53	101	17	1179	3668	31	15	12	30	75	12	42	545
G25	49	54	101	17	1325	3800	34	15	11	15	109	10	21	210
G26	50	55	89	17	2122	4892	43	17	9	28	90	11	41	426
G27	49	53	101	21	955	3022	31	19	10	13	99	12	24	298
G28	46	52	97	23	1862	5176	36	14	12	32	132	14	38	564
G29	48	54	103	22	1285	3378	39	15	12	18	96	16	35	581
G30	49	55	89	16	1957	4295	45	15	10	22	88	11	49	532
G31	53	58	87	11	2389	5168	46	15	12	24	117	12	51	671
G32	42	48	84	18	1009	3209	31	17	8	18	62	11	31	332
G33	43	51	85	20	746	2407	31	16	6	7	37	10	22	220
G34	52	58	86	13	2361	5541	42	17	12	19	97	15	45	704
G35	50	55	88	12	1942	4705	41	11	10	25	97	14	43	565
G36	44	52	86	15	1312	3242	38	12	8	16	57	10	17	186
GM	48	54	91	17	1695	4249	38	15	11	23	86	12	39	470
CV	4	4	2	11	19	13	13	15	14	27	20	13	24	22

GC=Genotype code, GM=Grand mean, CV=coefficient of variation, LSD(5%)=Least significant differences at 5% Note: G=genotypes, G1=KB,G2= Bole,G3= Kenketi,G4=86D-378,G5= IT-89KD,G6= MEL-NURL-96-3,G7= IT96D-610,G8= IT93K-556-4,G9= IT97K-568-18,G10=95K-1095-4A,G11= IT87D-1137,G12= IT96D-604,G13= Tvu,G14= OT-03L-2046-2,G15= IT93K-2046-1,G16= IT93K-452-1,G17= IT98K-1111-1,G18= IT97K-569-9,G19= IT97K-449-38,G20= IT99K-316-2,G21= IT96D-719,G22= IT97K-356-1,G23= IT98K-506-1,G24= IT00K-901-5,G25= IT97K-499-38,G26= IT95K-268-1-4,G27= BEB,G28= Brazil-3,G29= Brazil-1,G30= IT93k-293-2-2,G31= White wanderer trailing,G32= IT87D-721,G33=93 K-619.-1,G34= IT99K-1060,G35=Local 1(white seed color) & G36=Local 2(red/brown seed color)

Table 5. Estimates of mean, range, variance components, genotypic and phenotypic coefficient of variability for the 14 characters of cowpea genotypes

Traits	Mean	Range	σ2g	σ2e	σ2ph	PCV (%)	GCV (%)
DFF	48	42-54	7.6	4.7	12.4	7.4	5.8
DF	54	48-59	4.5	3.5	8.0	5.3	3.9
DM	91	84-106	44.9	2.2	47.1	7.5	7.3
HSW	17	10-23	7.9	3.4	11.2	19.9	16.7
GY	1695	746-3003	348010.5	105554.4	453564.9	39.7	34.8
BY	4249	2407-6334	1067146.3	320478.7	1387625.0	27.7	24.3
HI	38	24-48	19.0	26.9	45.8	17.6	11.3
PL	15	11-23	4.7	5.3	10.0	20.8	14.2
PB	11	6-14	2.2	2.4	4.5	19.7	13.6
SB	23	7-40	42.0	36.9	78.9	38.9	28.4
PH	86	37-132	341.5	307.6	649.1	29.9	21.7
SD	12	8-16	2.6	2.5	5.1	19.1	13.6
PT	39	17-57	62.1	83.9	146.0	31.3	20.4
SDP	470	186-880	22768.4	10628.8	33397.2	38.9	32.1

DFF=Days to first flower opening, DF= Days to 50 % flowering, DM=Days to maturity, HSW= Hundred seed weight, HI= Harvest index, PL=Pod length (cm), PB=number of primary branches per plant, SB= number of secondary branches per plant, PH=plant height (cm), PT= Number of pods per plant, SD= Number of seeds per pod, Number of seeds per plant, BY = Above ground biomass yield (kg/ha), GY= grain yield (kg/ha), σ2g, = Genotypic variance, σ2e= Environmental variance, σ2ph= Phenotypic variance, GCV= Genotypic coefficient of variability , PCV= Phenotypic coefficient of variability

Diversity studies of the quantitative traits

The genotypes were categorized into six distinct clusters (Table 6) using the Pseudo F and Pseudo t2 procedure of SAS (2002). Estimation of genetic diversity based on the D^2 value publicized that the 36 genotypes of cowpea can be clustered into six groups (Table 6). This designated the existence of diversity on the tested genotypes. Cluster I was the largest with 9 genotypes (25 %), Cluster II consisted of 8 genotypes (22.2 %), cluster IV and V had 7 genotypes (19.44%) each, cluster III had 3 genotypes (8.3%) and cluster VI had 2 genotypes (5.5 %). Cluster I had more number of genotypes (9 genotypes) followed by 8 genotypes in cluster II; cluster V and cluster IV had 7 genotypes each. The remaining two clusters namely cluster III and VI had 3 and 2 genotypes. While considering the inter-cluster distance, it ranged from 605.99 to 4265.1 as shown in Table 7. The highest inter-cluster distance was found between clusters III and cluster VI (4265.07), followed by cluster III and cluster V (3569.28), cluster VI and cluster IV (3365.37). Selection of parents for hybridization between the highest inter-cluster distances may give a high amount of heterosis effect and may generates useful recombinant in segregating populations. Therefore, the genotypes from these clusters can be selected for an

efficient breeding program for high yield and other desirable traits improvement.

Table 6. Clustering of cowpea genotypes based on D^{2}value

Cluster	Number of genotypes	Percentage	Name of genotypes
I	9	25	Kenketti, IT96D-610, KB ,Brazil-1, IT93K-2046-1, IT00K-901-5 ,IT97K-499-38 ,IT97K-356-1, OT-03L-2046-2
II	8	22.2	IT93K-556-4, IT95K-268-1-4, IT97K-569-9, IT98K-506-1, Bole, local check (white seed), IT93k-293-2-2, Brazil-3
III	3	8.33	86D-378, IT97K-568-18, IT96D-604
IV	7	19.44	IT-89KD, IT99K-1060, MEL-NURL-96-3, 95K-1095-4A, IT87D-1137, Tvu, White Wonder Trailing
V	7	19.44	IT96D-719, IT87D-721, IT98K-1111-1, IT97K-449-38, BEB, IT93K-452-1, Local check(brown seed)
VI	2	5.55	IT99K-316-2, 93 K-619.-1

Table 7. Distances between different cluster centroids of cowpea genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	0.00	1252.83	2991.95	2102.07	605.99	1280.85
Cluster II	1252.83	0.00	1739.92	858.15	1831.93	2526.02
Cluster III	2991.95	1739.92	0.00	922.17	3569.30	4265.10
Cluster IV	2102.07	858.15	922.17	0.00	2667.41	3365.38
Cluster V	605.99	1831.93	3569.30	2667.41	0.00	699.52
Cluster VI	1280.85	2526.02	4265.10	3365.38	699.52	0.00

Table 8. Cluster mean for fourteen quantitative characters in cowpea

Character	Cluster number					
	C-I	C- II	C-III	C-IV	C-V	C-VI
DFF	47.00	47.63	50.17	49.29	47.00	46.5
DF	52.89	53.38	55.50	55.00	53.21	52.5
DM	95.72	90.69	87.50	89.64	91.07	85.5
HSW	17.60	17.58	15.48	13.41	18.39	18.625
GY	1245.23	1892.45	2725.65	2444.03	1128.79	749.075
BY	3641.84	4710.30	6230.56	5352.52	3058.38	2474.17
HI	33.83	39.92	43.13	45.08	36.26	31.09
PL	14.35	14.60	16.33	15.16	16.54	15.175
PB	10.89	11.11	12.62	12.25	9.13	7.175
SB	23.54	25.17	23.17	30.29	15.63	9.075
PH	80.73	96.425	96.433	100.07	70.19	52.7
SD	11.64	11.42	13.33	13.59	10.36	10.375
PT	34.74	44.38	48.30	46.28	29.18	23.65
SDP	415.96	509.12	656.93	649.22	301.99	243.65

Considering the cluster average performance is shown in Table 8, cluster IV, which contains the genotypes IT-89KD, MEL-NURL-96-3, 95K-1095-4A and IT87D-1137 had a high mean value for the number of seeds per

pod, plant height, harvest index, number of secondary branches per plant . IT97K-568-18 and 86D-378 genotypes were found to be higher in obtaining top grain yield (3002.95 kg/ha; 2737 kg/ha) and biological yield (6307 kgha-1; 6334.03 kgha-1) from 36 genotypes studied (Table 4). Selection of parental material from these clusters can be used to develop superior varieties.

Discussion

Qualitative morphological traits and distribution of qualitative traits studied

Qualitative characters such as growth habit, seed color, seed size, seed shape and flower color make it easier to describe the morphological traits of a genotype and comfortable to assess diversity. Among the qualitative traits, there appeared to be great (five groups) in trait seed shape, followed by seed color and flower color, with four groups appearing in each trait while only three groups acting out in the two other traits. This research had demonstrated the diverse growth habits of different cowpea genotypes. Three plant growth habits were observed (44% prostrate, 36% erect and 19% semi-erect). Lazaridi *et al*. (2017) also classified 48 cowpea genotypes based on growth habits such as acute erect, semi-erect, intermediate, semi-prostrate, prostrate and climbing. Similar classification based on plant growth habit (erect, semi-erect and spreading) in cowpea was earlier reported by Madasu (2013).

A wide range of floral color variation of the cowpea genotypes have been reported, from white to other types. Four groups were formed based on the color of the flowers. Seven genotypes showed white flower, one genotypes expressed Mauve-pink, 11 genotypes had other flower color and remaining 17 genotypes showed violet flower color. The importance of flower color in genotypic classification was earlier reported by Madasu (2013) in cowpea. Lazaridi *et al.* (2017) also reported that three groups differentiate by their flower color: White (65.8%), Violet (24.3%) and Mauve-pink (9.9%).

In this study, cream brown seed color was dominantly followed by holstein white and black (13.89%), brown (5.56 %) and others (8.3%) correspondingly. Mishra (2013) and Madasu (2013) stated the genotype classification based on cowpea seed color. A marked difference in seed shape for different cowpea genotypes was observed in the current study. Based on seed shape, genotypes were classified as kidney, ovoid, Crowder, globose and rhomboid. Rhomboid seed shape was the dominant (33.33%) followed by kidney shape (27.78%), ovoid (19.44%), crowder (11.1%) and globlose (8.33%). Makanur *et al.* (2012) classified 35 cowpea genotypes based on seed shape as ovoid (three), kidney-shaped (seven) and remaining as rhomboid. The

proportions of genotypes in seed size boldness were 63.91 %, 25 % and 11.1 % for large, medium and small, respectively. Based on seed size, the genotypes were grouped large, medium and small with twenty-three, nine and four genotypes respectively in each group. Kumar (2016) classified which based on the 100-seed weight; the genotypes were classified as bold seeded, medium seeded and small seeded.

Diversity analysis of qualitative traits

Estimate of diversity indices

Many degrees of variation between cowpea genotypes were found for all investigated qualitative traits and the estimated Shannon and Weaver Diversity Index (H ') for traits. The individual ranges from 0.633 to 0.953 and the overall mean is 0.84 for quality traits. The highest diversity was observed in growth habits based on the Shannon-Weaver diversity index (H '), followed by seed shape, seed size, flower color and seed color. The result implies that there are variations among traits regarding qualitative characters considered in this study. Toscani *et al.* (2017) found low (0.00) to high (0.996) diversity in cowpea for qualitative traits.

Quantitative traits

In the present study, 36 cowpea genotypes were assessed for their yield and yield-related attributing traits. Analysis of variance indicated highly significant to significant differences presented for all traits studied specifying the presence of adequate genetic variability between the tested materials and the probability of enhancement in cowpeas. The findings of Bertini *et al.* (2009), is similar to that of the present results. Likewise, other researchers (Pandey and Singh, 2011; Manggoel *et al.,* 2012) had also indicated substantial genetic variations in their studies conducted on the assessment of different cowpea genotypes. Thus, it is implied that there was sufficient variability in material used for their study, which provides ample scope for selecting superior and desire genotypes by the researcher for further improvement.

Estimation of genetic variability parameters

The genotypic variances for all traits studied were lower than the phenotypic variances (Shanko *et al*., 2014). This may be due to the non-genetic factor that played a vital role in the expression of these traits. In the present study, high values of PCV and GCV were observed for grain yield per hectare, number of seeds per plant, number of secondary branches per plant, number of pods per plant, plant height, above-ground biomass yield per hectare, indicating

a greater scope for improvement of these traits through simple selection. These results are similar to those observed by Vavilapalli *et al.* (2014) and Varghese and Celine (2015). Moderate PCV and GCV were recorded for the weight of one hundred seeds, the harvest index, the number of primary branches per plant, the number of seeds per pod. Pod length recorded high PCV but moderate GCV. The study revealed that the high PCV and GCV trait contributed to noticeable variability. Enhancement of these traits through selection is desirable. Low GCV and PCV were recorded for days at 50% flowering, days until first flowering and days until maturity representing low variability which limits the possibilities of improvement of these traits by selection. Improvement of these traits through selection is desirable adjusted. Low GCV and PCV were recorded for the 50 per cent flowering days, the first flowering days, and maturity days to demonstrate the low variability which may limit the scope for improvement of these traits through selection. Low PCV and GCV values were recorded for days to maturity and plant height, while moderate PCV and GCV values which also had been reported for seeds per pod and test weight by Viswanatha and Yogeesh (2017).

Genetic diversity of quantitative traits

Attentiveness to genetic diversity provides a solid scientific basis for the choice of genotypes to be used in the hybridization program for further improvement. In the present study, 36 cowpea genotypes were grouped into six clusters. It indicated that the genotypes were very diversed. The maximum inter-cluster distance was observed between clusters III and VI followed by III and V. The inter-cluster average D2 values were maximum (4265.1) between cluster III with three genotypes, (86D-378, IT97K-568-18, IT96D-604) and cluster VI with two genotype (IT99K-316-2, 93 K-619.-1) followed by cluster III with three genotypes, (86D-378, IT97K-568-18, IT96D-604) and cluster V with seven genotypes (IT96D-719, IT87D-721, IT98K-1111-1, IT97K-449-38, BEB, IT93K-452-1, local check (brown seed color).The results were closely confirmed with the findings of Anamika and Tajane (2014) who clustered forty-four cowpea genotypes on the basis of six quantitative traits were grouped into six different clusters revealing sufficient amount of variability among the varieties. Meena *et al*. (2015) grouped 72 cowpea genotypes by using quantitative traits *viz*, days to 50% flowering, days to maturity, plant height, primary branches per plant, number of pods per plant, pod length, pod wall proportion, 100 seed weight and yield per plant. These observations were in agreement with Dalsaniya *et al.* (2009).

The estimate of genetic diversity and characterization of cowpea was based on 5 qualitative and 14 quantitative phenotypic descriptors. For the trait

seed shape, five different phenotypic classes were detected, followed by seed color and flower color each with four different phenotypic classes. Most genotypes had prostrate growth habit and violet flower color, based on the qualitative traits. Variation was observed in 5 qualitative traits among 36 cowpea genotypes evaluated. Diversity among cowpea genotypes were observed with growth habit (H'=0.953), seed shape (H'=0.927) being the most diverse and the seed color of seed being the intermediate diverse (H'=0.633). Analysis of variance showed highly significant to significant differences among the tested genotypes for all 14 quantitative traits, signifying the existence of genetic variability in the traits studied. A wide range of values had been observed in quantitative traits of the studied cowpea genotypes. Four genotypes out yielded (> 25qt/ha) the test genotypes and two local checks indicating the possibility of finding superior genotypes for release or the presence of broad difference among the cowpea genotypes evaluated that would provide ample opportunities for the genetic improvement of the crop through genetic recombination by hybridization of genotypes with desirable traits. Comparatively rapid progress can be achieved through selection. A perusal of genetic variability parameters revealed high phenotypic and genotypic coefficients of variation for number of seeds per plant, number of secondary branches per plant, plant height, number of pods per plant, above ground biomass yield and grain yield. PCV and GCV estimation showed that these characters with high variability and the prominence of the characters.

The 36 genotypes of cowpea were clustered into six distinct groups. The maximum inter-cluster distance (4265.10) was noticed between cluster III and VI followed by III and V (3569.30) and IV and VI (3365.38) , while it was low between cluster V and I (605.99), followed by cluster IV and II (858.15). Cluster III (86D-378, IT97K-568-18) and IV (95K-1095-4A , IT87D-1137) had genotypes with the highest above-ground biomass and grain yield, while the genotypes in Cluster I (kenketti), VI (93 K-619.-1) and V (IT87D-721, IT93K-452-1) matured much earlier. Crossing between genotypes within these groups could produce highly productive and early maturing cowpea genotypes. Based on the inter-cluster distances, the crosses between the genotypes of cluster III and cluster VI, cluster III and V, cluster IV and cluster VI can be attempted to generate desirable recombinants for yield improvement.

Cluster analysis further strengthened our findings in selecting the better performing genotypes by grouping them on the basis of the traits. A group of genotypes in cluster III and IV was identified as being different from other for number of traits including grain yield. Similarly, on the basis of mean performance, IT97K-568-18 (G9) and 87D-378 (G4) clustered together (cluster III) were the highest yielding genotypes (3,002.9 and 2,736.6 kg/ ha,

respectively), followed by the genotypes 95K-1095-4A (G10) and IT87D-1137 (G11) in Cluster IV appeared most promising and could be recommended for future cowpea improvement program or directly tested in multi-location trials for release to have successful cowpea production in South Ethiopia. Hence, these promising genotypes could be very useful in enriching the cowpea varieties that would be suited to the different types of farmers/consumers preferences and utilizing these valuable genotypes for varietal improvement under different cowpea improvement programs. Overall, the estimation of cowpea genotypes for genetic diversity is very useful to identify potential genotypes for improvement of grain yield as well as desirable traits in cowpea improvement programs in South Ethiopia.

Acknowledgements

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