



Research Article

Genetic variability, heritability, genetic advance and divergence in Ethiopian cowpea [*Vigna unguiculata* (L) Walp] landraces

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Abstract

Information on genetic variability in cowpea germplasm is important for crop improvement and for efficient utilization of the existing genetic resources. Hence, the objectives of the present investigation were to estimate genetic variability, heritability, genetic advance and to identify divergent parents from distantly related clusters among Ethiopian cowpea accessions. The field experiment was carried out using 42 accessions at Abergelle Agricultural Research Center on station during the 2019 cropping season. Data were collected for 8 agronomic traits and analysis of variance revealed significant differences ($p < 0.01$) among the accessions for the traits studied. Seed yield had higher Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) coupled with the highest genetic advance as percent of mean (100%). All the traits had moderate (68.01) to very high (99.98%) broad sense heritability. Further, high heritability coupled with high genetic advance as percent of mean was attained for days to flowering, grain filling period, plant height, pod length, seed yield and thousand seed weight reflecting the presence of additive gene action for the expression of these traits and improvement of these traits could be done through selection. The cluster analysis based on agronomic traits revealed four distinct groups at 90% similarity level. The highest inter cluster D^2 was recorded between cluster III and cluster IV ($D^2=133.69$ units). The range of inter cluster distance was 15.25 to 133.69 units, respectively. In conclusion, the high genetic distance revealed among clusters has to be exploited via crossing and selection of the most divergent parents for future cowpea improvement program.

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp., Fabaceae ($2n = 2x = 22$)] is an important dual purpose (food and forage) legume crop widely grown under low input production systems and in arid and semi-arid agro-ecologies of the world [1,2]. It is predominantly a self-pollinated crop, with natural cross-pollination up to one percent. Cowpea could play significant role in mitigating malnutrition such as micronutrient deficiencies for poor farmers of Sub-Saharan countries [3]. It has distinct features such as its earliness in maturity, tolerance to drought, heat, acidity and low fertility, and seed types with high protein content and low cooking time [4]. It is well adapted to the drier regions of the tropics, where other food legumes do not perform well. Cowpea is eaten in the form of dry seeds, green

Pods, green seeds and tender green leaves. As a pulse crop, cowpea provides more than half the plant protein for human diets in some areas of semi-arid tropics is being referred to as “poor-man’s meat” [5].

Cowpea grain typically contains 230–250 g/kg Crude Protein (CP) and 500–670 g/kg starch on a Dry Matter (DM) basis and cowpea forage, i.e. the crop residue after harvesting grain, 210g CP and 600g digestible dry matter per kg DM. These excellent nutritional qualities of cowpea make as one of the potential crop as a component of the cropping system and livelihood for the smallholder farmers living in drier regions of Ethiopia [6]. Thus, this crop can contribute greatly towards meeting the food requirement of people in areas where food security and malnutrition are major challenges. Regardless of the various merits of cowpea in Ethiopia, the national production and

productivity is far below the potential due to several abiotic and biotic constraints among which drought, insect pests, parasitic weeds and virus facing cowpea production to have resulted in a very low yield [7].

Though, Ethiopia is one of the centers of origin and/or diversity of cowpea [8] and more than 66.5% of arable land is very suitable for cowpea production [9], the country has not been in a position to be benefited from international and continental cowpea improvement program or from the national pulse crops research. This is because low attention in research for cowpea is given as compared to other pulse crops. To harness the potential of cowpea landraces grown in Ethiopia baseline information regarding cowpea production status in the country /baseline information has been generated. Greater the variability in a population, there is the greater chance for effective selection for anticipated varieties. However, very few studies have been conducted on cowpea genetic variability using quantitative traits employed in the country. Hence, the objectives of the present study were to assess variability, heritability, genetic advance and to identify divergent parents from distantly related clusters for the future cowpea improvement program.

Materials and methods

Description of the experimental site

The field trial was conducted at Abergelle district central zone of Tigray, northern Ethiopia during the 2019 main cropping season. The site (Mearey) is located at about 903 km

north of Addis Ababa and 120 km south west of Mekelle city. It has an approximate geographical coordinates of 13°14'06" N latitude and 38°58'50" E longitudes having an altitude 1560 meter above sea level (Figure 1). The area is characterized by an erratic rainfall pattern with "kola" agro climatic zone. The rainy season is mono modal pattern concentrated in one season during the summer (July to August) and receives from 350- 600 mm, annual precipitation. The mean minimum and maximum temperature of the area ranges from 18- 42°C, respectively [10]. The soil texture of the specific site of the study area is sandy clay textural class with high available P (13.82 mg kg⁻¹), very low in total N (0.08%) and low organic matter (0.72%) with a neutral pH of 7.18.

Description of the planting materials

The experimental plant materials comprised a total of 42 cowpea accessions/local landraces along with one released variety Bekur as a check was used in this study. The landraces were Ethiopian origin kindly provided by the Ethiopian Institute of Biodiversity (EIB) collected from different agro-ecological regions of the country, varying in altitude, rainfall, temperature, and soil type. The accession numbers and source of the genotypes are presented in Table 1.

Experimental design and crop management

The experiment was laid out using (6, 7) α - lattice design with three replications. The plot size was 7.2 m² (4m x 1.8m) with three rows of inter-row (60 cm) and intra-row (20 cm)

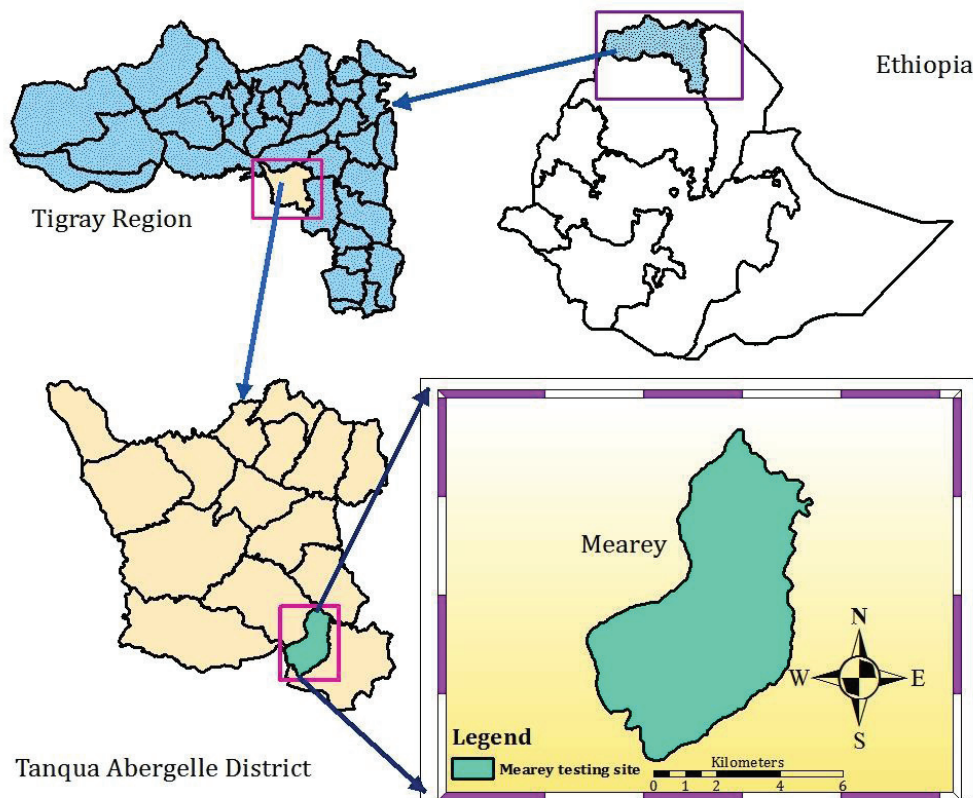


Figure 1: Map of the study site.

**Table 1:** Description of the cowpea accessions used in the study.

S. No	Accessions	Seed size description	Seed coat color	Growth habit	Collection region	Source
1	Adongor/ local	Small	White	Decumbent	Tigray	Abergelle ARC
2	Acc#216747	Small	White	Climbing	Gambela	EIB
3	Acc#208643	Small	Brown	Decumbent	Oromia	EIB
4	Acc#211441	Small	Brown	Decumbent	Oromia	EIB
5	Acc#26058	Medium	White	Decumbent	Tigray	EIB
6	Acc#211443	Small*	Light white	Decumbent	Oromia	EIB
7	Acc#211440	Small	Dark white	Climbing	Oromia	EIB
8	Acc#216749	Small	Silver	Climbing	Gambela	EIB
9	Acc#235122	Small	White	Decumbent	Tigray	EIB
10	Acc#210856	Small	light gold	Climbing	Oromia	EIB
11	Acc#223402	Small	White	Climbing	Oromia	EIB
12	Acc#211429	Small	Black	Climbing	SNNP	EIB
13	Acc#223403	Small	Light ranger	Climbing	Oromia	EIB
14	Acc#221727	Small	White	Climbing	Tigray	EIB
15	Acc#210857	Small	Gray	Climbing	Oromia	EIB
16	Acc#211446	Small	White	Decumbent	Oromia	EIB
17	Acc#211557	Large***	White	Decumbent	Amhara	EIB
18	Acc#211436	Small	White	Climbing	Amhara	EIB
19	Acc#211491	Small	Light white	Decumbent	SNNP	EIB
20	Acc#215821	Small	Red cherry	Decumbent	Gambela	EIB
21	Acc#227104	Small	White	Decumbent	SNNP	EIB
22	Acc#26060	Small	Light white	Decumbent	Tigray	EIB
23	Acc#230575	Small	Black	Decumbent	Amhara	EIB
24	Acc#211433	Small	Red cherry	Climbing	B/Gumuz	EIB
25	Acc#222890	Small	White	Climbing	Gambela	EIB
26	Acc#211490	Medium**	Red cherry	Decumbent	SNNP	EIB
27	Acc#208776	Small	Black	Climbing	Oromia	EIB
28	Acc#211430	Small	Black	Decumbent	SNNP	EIB
29	Acc#222891	Small	White	Climbing	Gambela	EIB
30	Acc#211444	Small	Red cherry	Decumbent	Oromia	EIB
31	Acc#26059	Small	Light white	Climbing	Tigray	EIB
32	Acc#216748	Small	White	Decumbent	Gambela	EIB
33	Acc#211447	Small	Light white	Decumbent	B/Gumuz	EIB
34	Acc#211384	Small	White	Decumbent	Amhara	EIB
35	Acc#216746	Large	White	Decumbent	Gambela	EIB
36	Acc#228624	Small	Light ranger	Climbing	Amhara	EIB
37	Acc#29597	Small	White	Climbing	B/Gumuz	EIB
38	Acc#215762	Small	White	Decumbent	Amhara	EIB
39	Acc#215760	Small	Brown	Climbing	Amhara	EIB
40	Acc#211383	Small	Brown	Climbing	Amhara	EIB
41	Acc#215761	Small	Reddish	Climbing	Amhara	EIB
42	Bekur/ released variety	Small	Brown	Decumbent	Amhara	Sirinka ARC

Where: EIB: Ethiopian Institute of Biodiversity; ARC: Agricultural Research Center

*Small= <15g/100-seed weight, **Medium= 15-19g/100-seed weight, ***Large= >20g/100 seed weight [11]

spacing's. The distance between plots, intra-blocks, and replications was 0.5m, 1m and 1.5m, respectively. Blended NPSZnB fertilizer was applied at the rate of 100 kg ha⁻¹ during planting. Weeds were controlled periodically by hand weeding and other field management and crop protection activities were done as required.

Data collection

Some phenological (days to flowering, days to maturity, grain filling period), morphological (plant height, pod length) and yield and related traits (seed yield, thousand seed weight, number of seeds per pod) of each genotype was collected following the descriptor for cowpea developed by the International Board for Plant Genetic Resources [12]. The data collected on plot basis were days to flowering, days to maturity, grain filling period (days), thousand seed weight (g) and seed yield (g). In addition, the data collected on individual plant basis were plant height (cm), pod length (cm) and number of seeds per pod. For single plant based traits, the average of data from the five random samples of plants per plot were used and seed yield per plot in grams was converted to kg ha⁻¹ for analyses.

Data analysis

Data for agronomic traits were subjected to analysis of variances (ANOVA) for lattice design procedures of SAS Version 9.2 [13] to test the presence of significant differences among genotypes. Variability among accessions was estimated using genotypic variances and coefficients of variations as suggested by Burton and De vane [14] and these components of variance (δ^2p , δ^2e , δ^2g) were used for the estimation of coefficients of variation (PCV, GCV) as described by Singh and Chaudhary [15].

1. **Genotypic Variance** $GV = \frac{(MSg - MSe)}{r}$, where MSg = Mean Square of genotypes, MSe = Mean Square of error (environmental variance or δ^2e), and r = number of replications;
2. **Phenotypic Variance**, $PV = GV + MSe$, where GV = Genotypic Variance and MSe = Mean Square of error;
3. **Genotypic Coefficient of Variation**, $GCV = (\sqrt{GV})/x \times 100$, where GV = Genotypic Variance and x = grand mean of the character;
4. **Phenotypic Coefficient of Variation**, $PCV = (\sqrt{PV})/x \times 100$, where PV = Phenotypic Variance and x = mean of the character.
5. **Broad sense heritability** (H^2) of all traits was calculated according to the formula as described by Allard [16] as follows: $H^2 = [(\sigma^2g) / (\sigma^2p)] \times 100$, where σ^2g and σ^2p are genotypic and phenotypic variances respectively.
6. **Genetic Advance** (GA) for selection intensity (K) at 5% was computed according to Allard [16] as given here: $GA = K\sigma^2pH^2$, where, GA = expected genetic advance, K = the standardized selection differential at 5% selection intensity ($K=2.063$), σ^2p = is phenotypic standard

deviation on mean basis and H^2 = heritability in broad sense.

7. **Genetic advance as percentage of population means** (GAM) was also estimated with the methods described by Johnson, et al. [17] to compare the extent of the predicted advance of different traits under selection using the following formula: $GAM = \frac{GAx100}{x}$, where GA = genetic advance under selection and x = mean of the population.
8. Hierarchical [18] cluster analysis was performed to group accessions and construct a dendrogram by Ward's method by using SAS software. The measure of dissimilarity was Euclidean distance. The average inter-cluster distance was calculated using the generalized Mahalanobis's D^2 statistics [19]. The R^2 (RSQ), Cubic Clustering Criteria (CCC), Pseudo-F Statistics (PSF) and pseudo- T^2 statistics were considered for defining optimum cluster numbers [20]. The contributions of each of the traits to divergence were estimated as described as Sharma [21] with the formula [$CTIC = \frac{SD}{x}$], where SD and x are the standard deviation and mean performance of each trait, respectively.

Results and discussion

Genetic variability

The mean squares and estimates of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variances, Phenotypic Coefficients of Variation (PCV) and Genotypic Coefficients of Variation (GCV) along with the mean of traits investigated are presented in Table 2. The analysis of variance showed that the mean squares for the genotypes were highly significant ($p < 0.01$) for all agronomic traits indicating presence of adequate variability among Ethiopian cowpea accessions. Genetic variance ranged from 1.68 for number of seeds per pod to 590157.45 for seed yield (kg ha⁻¹) while phenotypic variance values ranged from 2.47 to 590283.96 for seed yield (kg ha⁻¹). The GCV ranged from 6.90% for days to maturity to 48.80% for seed yield. Similarly, PCV ranges from 7.45% for days to maturity to 48.81% for seed yield. The GCV and PCV values are normally categorized as low (<10%), moderate (10–20%) and high (>20%) as indicated by Deshmukh, et al. [22].

The highest Phenotypic Coefficient of Variation (PVC) and Genotypic Coefficient of Variation (GCV) were recorded for seed yield (48.81, 48.80) followed by 1000-seed weight (33.36, 33.37) and grain filling period (23.25, 21.15) while low PVCs and GVCs were recorded for days to maturity (7.45, 6.90), number of seeds pod⁻¹ (13.53, 11.16), plant height (13.96, 13.88), days to flowering (15.01, 14.80) and pod length (17.82, 16.44), respectively. The present study suggests that the phenotypic coefficient of variation (PCV) was relatively higher than the corresponding Genotypic Coefficient of Variation (GCV). However, the difference between PCV and GCV were narrow



Table 2: Estimates of phenotypic and genotypic variances and coefficient of variations, heritability in broad sense, genetic advance and genetic advance as percent of mean.

Traits	MSg	MSe (σ^2_e)	Mean	σ^2_g	σ^2_p	GCV%	PCV%	H ² %	GA	GAM%
DF	247.04**	2.37	61.04	81.55	83.93	14.80	15.01	97.17	18.34	30.05
GFP	93.29**	6.04	25.50	29.08	35.13	21.15	23.25	82.79	10.11	39.65
DM	112.8**	6	86.53	35.60	41.60	6.90	7.45	85.57	11.37	13.14
PH	567.3**	2.32	98.87	188.33	190.65	13.88	13.96	98.78	28.10	28.42
PL	15.91**	0.88	13.61	5.01	5.89	16.44	17.82	85.11	4.25	31.25
NSP	5.82**	0.79	11.61	1.68	2.47	11.16	13.53	68.01	2.20	18.96
SY	1770599**	126.51	1574.15	590157.45	590283.96	48.80	48.81	99.98	1582	100
TSW	4256.39**	24.48	112.55	1410.63	1435.12	33.37	33.66	98.29	76.71	68.16

*, ** = significant at $P \leq 0.05$ and $P \leq 0.01$, respectively.

Where: DF = Days to Flowering, GFP = Grain Filling Period, DM = Days to Maturity, PH = Plant Height, PL = Pod Length, NSP = Number of Seeds Per Pod, SY = Seed Yield, TSW = Thousand Seed Weight; MSg = Mean Square of Genotypes, Mse = Mean Square of Error (Environmental Variance, Δ^2_e), Σ^2_g = Genotypic Variance, Σ^2_p = Phenotypic Variance, PCV = Phenotypic Coefficient of Variance (%), GCV = Genotypic Coefficient of Variance (%), H² = Broad Sense Heritability (%), GA = Genetic Advance and GAM = Genetic Advance As Percent of Mean (%)

indicating little influence of environment on the expression of these traits and considerable amount of variation was observed for the traits studied.

The results of the study was in conformity with the findings of Reshma, et al. [23] who reported high value of PCV and GCV for seed yield per plant, 100-seed weight and number of pods per plant. Additionally, Manggoel, et al. [24] and Mofokeng, et al. [25] also reported high PCV and GCV for days to flowering, number of branches, pod number per plant, pod weight per plant, seed number per pod, hundred seed weight and seed yield in cowpea.

Broad sense heritability

The estimate of broad sense heritability for all the traits under study is presented in Table 2. All agronomic traits recorded high heritability ranged from 68.01(number of seeds per pod) to 99.98% (seed yield) indicating additive gene effects control the expression of the traits. Heritability is classified as low (<40%), medium (40–59%), moderately high (60–79%) and very high ($\geq 80\%$), according to Singh [26]. In the current study, the highest estimates of broad sense heritability were recorded for seed yield (99.98) followed by plant height (98.78), thousand seed weight (98.29), days to 50% flowering (97.17), days to maturity (85.57), pod length (85.11), grain filling period (82.79) and number of seeds per pod (68.01). Similarly, Manggoel, et al. [24], Thorat and Gadewar [27], Khan, et al. [28], Khanpara, et al. [29], Reshma, et al. [23] and Mofokeng, et al. [25] reported high heritability values in cowpea.

Expected genetic advance for selection

Genetic advance is a measure of predetermined progress under artificial selection program. According to Jonhson, et al. [17] the value of GAM is categorized as low (< 10%), moderate (10–20%) and high (> 20%). In this study, the highest GAM was recorded for seed yield (100%) followed by 100-seed weight (68.16%), grain filling period (39.65%), pod length (31.25%), days to flowering (30.05%) and plant height (28.42%), indicating that these traits are governed by additive genes and selection will be rewarding for improvement of cowpea for these traits. In agreement with the current study, high GAM for

days to flowering, number of branches, pod number per plant, pod weight per plant, seed number per pod, hundred seed weight, seed number per plant and seed yield [25]; number of pods per plant and 100 seed weight [30]; pod weight, number of pods per plant, days to 50% flowering, and number of seeds per pod [29,30]; number of branches per plant, plant height, pod yield per plot, total number of pods per plant and number of seeds per pod [31] were reported in cowpea.

Furthermore, high heritability coupled with genetic advance were recorded for days to flowering, grain filling period, plant height, pod length, seed yield and thousand seed weight, indicates additive gene action control the expression inheritance of these traits in cowpea [32]. A similar result was reported by Thorat and Gadewar [27], Sharma, et al. [33] and Das, et al. [34] for seed yield and Khan, et al. [28] for the number of pods per plant and Reshma, et al. [23] for plant height, seed yield per plant, number of pods per plant, pod length and hundred seed weight in cowpea. Overall, the estimates of heritability (H²), genetic advance as percent of mean (GAM); genotypic coefficients of variation (GCV) and phenotypic coefficient of variation (PCV) were high for seed yield and thousand seed weight which are critical to identify potential for development of superior cowpea genotypes and/or improvement of population through selection.

Clustering of accessions

The tested accessions were grouped in four different clusters with the number of accessions per cluster varying from 6 to 16 (Table 3). The covariance matrix gave hierarchical clustering (Figure 2) using average linkage method and the appropriate number of clusters was determined from the values of Pseudo F and Pseudo T² statistics among 42 cowpea accessions (Table 4). Cluster I was the largest cluster comprising 16 accessions, followed by clusters II and IV that contained 10 and 10 accessions, respectively, where cluster III contained the smallest accession (6) number. Of the 16 accessions grouped in cluster I, 43.75%, 25%, 12.5%, 12.5% and 6.25% of accessions originated from Oromia, Tigray, Amhara, SNNP and Gambella regions, respectively.

Similarly, in cluster II 50%, 20%, 20% and 10%; cluster



IV 40%, 30%, 20% and 10% of the total accessions grouped in the second largest clusters (Cluster II and IV) had in that order origins that are Gambella, B/Gumuz, SNNP and Oromia; Amhara, Oromia, Tigray and SNNP while the least of accessions (6) grouped in cluster III, 66.66%, 16.67% and 16.67% were originated from Amhara, Gambella and B/Gumuz regions of Ethiopia, respectively (Table 4). The cowpea accessions originating from the same regions entered into different clusters indicating the absence of relationships between genetic diversity and geographic origin. For instance, the accessions

from Oromia, Amhara, SNNP, Tigray Gambella and B/Gumuz regions of origin grouped into the four distinct clusters (Tables 3,4).

The main reasons for the grouping of accessions of the same origin into different clusters could be the exchanges of germplasm by farmers among neighboring regions, natural and artificial selection, genetic enrichment, genetic drift and environmental variation. Furthermore, Tesfaye, et al. [35] reported no relationship between genetic origin and /or diversity and geographic distribution.

Mean performance of clusters

The mean value of 8 agronomic traits per cluster is presented on Table 5. In this study, the mean values varied among clusters for the traits studied. Accessions those took longer days to flowering, maturity, plant height and extended grain filling period were found in cluster III. Cluster IV exhibited maximum mean values for pod length, seed yield and thousand seed weight. On the contrary, no significant variation was recorded among clusters for number of seeds per pod.

On the basis of overall mean performance, cluster IV showed the best performance for most important traits including seed yield. Therefore, cluster IV would be preferable for selection

Table 3: Distribution of 42 cowpea accessions in 4 different clusters.

Region	N° of accessions per cluster with respective percentage				Total N° of accessions
	I	II	III	IV	
Oromia	7 (43.75%)	1 (10%)	0	3 (30%)	11
Amhara	2 (12.50%)	0	4 (66.66%)	4 (40%)	10
Gambella	1(6.25%)	5 (50%)	1 (16.67%)	0	7
Tigray	4 (25%)	0	0	2 (20%)	6
SNNP	2(12.50%)	2 (20%)	0	1 (10%)	5
B/Gumuz	-	2 (20%)	1 (16.67%)	0	3
Total	16	10	6	10	42
% of clusters	38.10	23.80	14.30	23.80	100
Origin of accessions	1-5	1,3,5,6	2,3,6	1,2,4,5	

1= Oromia, 2= Amhara, 3= Gambella, 4= Tigray, 5= SNNP, 6= B/Gumuz

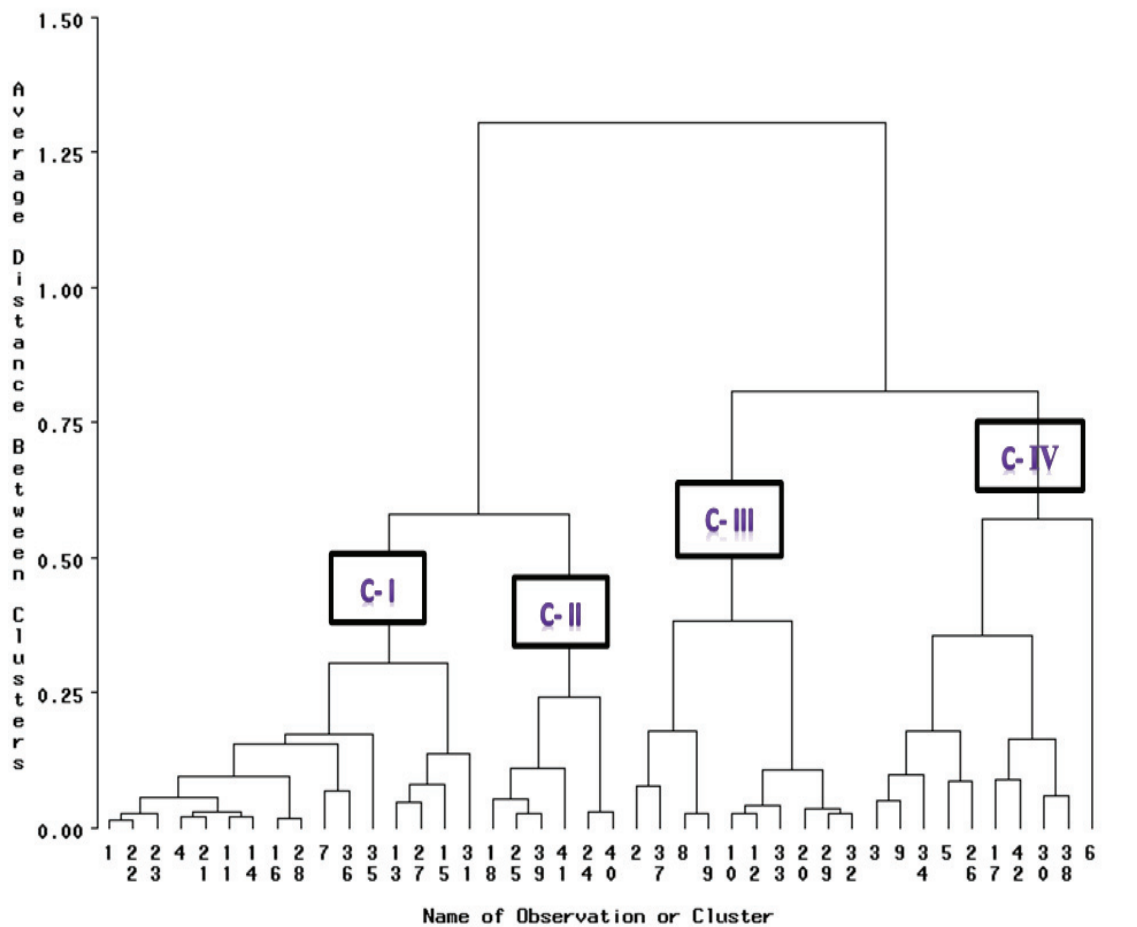


Figure 2: Dendrogram showing clusters 1 - 4 using the 8 traits of 42 cowpea accessions.



of parents with high mean values for the improvement of accessions. Conversely, cluster III had minimum values for yield and yield related traits. It showed the poorest performance of traits while the highest plant height was recorded in this cluster. Therefore, this cluster is preferable for increasing number of pods per peduncle. In general, there was highly significant variation in mean performance among the clusters for most of the traits, and this offers a huge opportunity to select potential parents across the clusters for specific traits for future cowpea improvement program. Overall, the variation observed among the 42 cowpea accessions suggests that agronomic traits can reveal diversity existing among cowpea genotypes. Molosiwa, et al. [36], Moolendra, et al. [37] and Tesfaye, et al. [35] had also reported similar results.

Seed yield and thousand seed weight were the major contributors for genetic divergence to the entire accessions (Table 5) while days to flowering, grain filling period, and days to maturity, plant height, pod length and number of seeds per pod had small contribution towards genetic divergence. In agreement with the study; Tesfaye, et al. [35] classified the levels of trait contribution for inter cluster divergence for cowpea $\geq 15\%$ as high contributor, $\geq 8\% < 15\%$ as medium contributor and $< 8\%$ as little contributor for inter cluster divergence in Ethiopia [38–41].

Genetic divergence analysis

The standardized Mahalanobis D^2 (square distances) statistics showed that there is high genetic distance and highly significant variation at $P \leq 0.01$ and $P \leq 0.05$ among the

Table 6: Inter cluster distance (D^2) values among 42 cowpea accessions by the 8 agronomic traits.

Cluster	I	II	III	IV
I				
II	15.25*			
III	16.89**	49.86**		
IV	66.39**	21.55**	133.69**	

*** Indicates significance at 0.05 and 0.01 level of significance; Chi-square (χ^2)= 14.07 and 18.48 at 0.05 and 0.01, probability level, respectively

four clusters (Table 6), indicating wide diversity among cowpea accessions. The highest average inter-cluster distance was recorded between the cluster III and IV ($D^2=133.69$ units) followed by the cluster I and IV ($D^2=69.39$ units), cluster II and III ($D^2=49.86$ units) while the lowest was between cluster I and II ($D^2=15.25$ units). Overall, the present study indicates that the accessions in cluster III and V were more diverged than any one of the other clusters while the nearest inter-cluster distance between cluster I and II were not genetically diverse. Thus, the accessions belonging to the distant clusters could be used for cowpea breeding program to get a wider range of variability in the segregating F2 population.

Conclusion

The result of the study revealed the existence of significant ($p < 0.01$) genetic variability among Ethiopian cowpea landraces. Seed yield had higher Genotypic Coefficient of Variation (GCV) and phenotypic coefficient of variation (PCV) coupled with the highest genetic advance as percent of mean (100%). Further, high heritability coupled with high genetic advance as percent of mean was recorded for days to flowering, grain filling period, plant height, pod length, seed yield and thousand seed weight reflecting the presence of additive gene action for the expression of these traits and improvement of these traits could be done through selection. The cluster analysis based on agronomic traits revealed four distinct groups at 90% similarity level. The highest inter cluster D^2 was recorded between cluster III and cluster IV ($D^2=133.69$ units). The range of inter cluster distance was 15.25 to 133.69 units, respectively. Therefore, based on the present findings, it can be conclude that the high genetic distance revealed among clusters has to be exploited via crossing and selection of the most divergent parents for future cowpea improvement program.

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Table 4: List of cowpea accessions in each of the four different clusters.

Cluster	Accessions			
I	Adongor	Acc#223402	Acc#230575	Acc#228624
	Acc#26060	Acc#221727	Acc#223403	Acc#210857
	Acc#211446	Acc#211441	Acc#208776	Acc#26059
	Acc#211430	Acc#227104	Acc#211440	Acc#216746
II	Acc#216749	Acc#216748	Acc#215821	Acc#216747
	Acc#211491	Acc#210856	Acc#211447	Acc#29597
	Acc#222891	Acc#211429		
III	Acc#222890	Acc#211433	Acc#211436	Acc#215761
	Acc#215760	Acc#211383		
IV	Acc#20864	Acc#215762	Acc#211557	Acc#211384
	Acc#235122	Acc#26058	Bekur	Acc#211443
	Acc#211444	Acc#211490		

Table 5: Mean performance of cowpea accessions grouped into four clusters based on 8 agronomic traits.

Traits	Cluster				Mean	SD	CTIC (%)
	I	II	III	IV			
Days to flowering	58.72	60.75	72.17	58.35	62.500	1.572	2.515
Grain filling period	27.09	25.82	19.22	26.38	24.630	1.530	6.212
Days to maturity	85.81	86.57	91.39	84.73	87.130	5.589	6.415
Plant height	95.34	104.13	111.57	91.67	100.680	1.177	1.169
Pod length	12.07	14.75	12.49	15.62	13.730	0.661	4.814
Number of seeds per pod	11.61	11.63	11.95	11.38	11.640	0.663	5.696
Thousand seed weight	99	113	100	141.2	113.300	17.02	15.02
Seed yield	1116.67	1850.30	520.20	2662.3	153.737	99.45	64.69

CTIC = Contribution to Inter-Cluster Divergence



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