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## Genetic divergence in forage cowpea: A review

**Ajay Tiwari and Mayuri Sahu**

### Abstract

Cowpea is a very useful versatile legume crop grown in India for its delicious pods, grain, fodder and green manuring purpose in various regions of India. It has a wide range of genetic diversity which provides a tremendous scope for genetic improvement of economic traits. An improvement in yield and quality in self pollinated crop like cowpea is normally achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridization. Hence, the information in a collection of some indigenous genotypes of cowpea in order to formulate a sound breeding plan for its improvement has been reviewed here. Cowpea [*Vigna unguiculata* (L.) Walp.] is the most important grain legume and fodder crop of the semi-arid warm tropics and subtropics. There is a great scope for improvement of genotypes with versatile crop duration, high green pod yield, low fiber and high yield along with protein content in grain as well as fodder. Diversity analysis has been a fundamental protocol for crop improvement; it unravels the genetic potentials of genotypes. Successful conservation of germplasm largely depends on the understanding of the diversity within the species Karuri *et al.* (2010). Germplasm with wider genetic base provides buffer and resilience against climatic and other environmental changes and ensures sustainable food security. The presence of genetic variability among crop genotypes depicts the richness of the gene pool and assures plant breeders of the possibilities of combating subsequent food security crisis for the crop. Moreover, understanding the nearness and diverseness of genotypes within the same species is an important primary knowledge to guide selection and improvement in a breeding programme. In essence, diversity leads to the identification of superior genotypes which may be recommended as cultivar and identification of genotypes with desirable phenotypic traits for selection as parents for eventual breeding and improvement programmes.

**Keywords:** Cowpea, D<sup>2</sup> statistics, cluster, genetic divergence

### Introduction

Cowpea is one of the most widely grown vegetable crop throughout India. Success of any breeding programme depends much on genetic diversity available to the breeders and the judicious selection of parents. The success of breeding programme is achieved by the efficient utilization of heritability and variability available in the population. The importance of genetic diverse genotypes as a source of obtaining transgressive segregants with desirable combinations have been realized by several workers (Cruz *et al.*, 1994) [8]. Mahalanobis (1936) [25] gernelized distance has been used as an efficient tool in quantitative estimation of genetic diversity and a rational choice of potential parents for a breeding programme. Knowledge of interrelationship between yield and its components is obvious for efficient selection of desirable plant type.

Cowpea chromosome number 2n=22, a member of the family leguminosae/ fabaceae, is a crop grown throughout the tropics and the subtropics covering Africa, Asia, South America, parts of Southern Europe and the United State (Steele, 1976) [41]. The cowpea is a very old crop, probably native to Central Africa, although it has been grown in South-Eastern Asia for more than 2000 years. Based on the distribution of diverse wild cowpea, East and Southern Africa are considered as the primary region of diversity. Vavilov (1939) [47] considered India as the main Centre of Origin. In India, it has been known since the Vedic times. The cowpea is one of several species of the widely cultivated genus Vignahas been subdivided in five sub species; three cultivated, *unguiculata*, *sesquipedalis* and *cylindrical* and two wild, *dekintiana* and *mensenensis* Verdcourt (1970) [49].

Cowpea is extensively grown in southern India particularly in the state of Andhra Pradesh, Karnataka, Tamil Nadu and Maharashtra Bhadru and Navale (2012) [4]. While the fodder cowpea occupies 0.3 million hectare out of 0.65 million hectare area under different pulse and vegetable cowpea types Sanjeev *et al.* (2015) [39].

**Table 1:** Trend in area, production and productivity of Cowpea in Chhattisgarh, India and World.

Place	Area in ha	Production mt.	Productivity kg/ ha
Chhattisgarh	43.13	13.55	314
India	5312	5510	-
World	10980000	5635000	513

Source: <http://agridept.cg.gov.in/agriculture/kharif-12.htm>, FAO Stat 2017

Cowpea is one of the most important legume crops. It is now gaining importance in the recent years due to its high food

value, good fodder and used as an excellent green manure crop. Cowpea is a drought tolerant crop with a better growth in warm climate. It can be grown in very poor soil (pH range 4.5-9), organic matter < 0.2, and sand content of the soil > 85%) and where rainfall is scanty. The cowpea is valued for its nutritive quality especially because of its high crude protein content in addition to its green fodder yield. All the plant parts of cowpea that are used for food are nutritious providing protein, vitamins and minerals. Its grain contains on average 23-25% protein and 50-70% starch Vir and Singh (2014) [50].

**Table 2:** Utilization of Cowpea (*Vigna unguiculata* (L.) Walp. In different purpose

Particular	Unit	Aerial part, fresh	Hay	Aerial part, dehydrated	Pod husks	Haulms	Grain
Dry matter	% as fed	20.9	91.2	92.5	51.6	95	89.9
Crude protein	% DM	18.1	14.8	17.1	12.7	13.7	25.2
Crude fiber	% DM	24.1	32.6	-	31.8	29.9	5.6
Gross energy	MJ/kg DM	18.1	17.5	12.6	18.2	17.9	18.7
Minerals- Macro							
Calcium	g/kg DM	12.5	13.1	-	-	11.4	1.1
Phosphorus	g/kg DM	2.4	3.9	-	-	2.6	4.2
Potassium	g/kg DM	19.1	33.2	-	-	15.1	15
Magnesium	g/kg DM	3.1	6.6	-	-	5.6	2.2
Sodium	g/kg DM	..	2.6	-	-	0.7	0.1
Minerals- Micro							
Manganese	mg/kg DM	..	97	-	-	129	20
Zinc	mg/kg DM	46	56	-	-	33	38
Copper	mg/kg DM	30	6	-	-	8	9
Iron	mg/kg DM	1690	-	-	-	1	422

Source: [www.feedipedia.org](http://www.feedipedia.org)

The genetic variability for quantitative characters are at most importance in selecting the desired genotypes for future breeding programme. Information on genetic variability among different characters is essential for any systematic breeding programme. The success of good breeding programme usually depends on the genetic variability present in the breeding material. Thus, knowledge of genetic variability, heritability and genetic advance in cowpea is essential for a breeder to choose good genotypes for its improvement.

### Divergence analysis

Among several statistical methods developed for measuring the divergence between populations, multivariate analysis or D<sup>2</sup> statistics has been effectively used for quantitative estimate of genetic variability. In this context, Mahalonobis's D<sup>2</sup> statistics is an effective tool in quantifying the degree of divergence at genetic level and it also provides a quantitative measure of association between geographic and genetic diversity based on genotype distance Mahalonobis (1936) [25]. He introduced the idea of statistical field in which each point represented the centre of density cluster belonging to a particular normal population specified by

1. The means of the characters and
2. The measure of covariances at the particular point in the field.

The advantage with D<sup>2</sup> statistics is that it enables us to obtain an indication of the distances in the p-dimensional shape in which samples are most distinct as also to obtain an estimate of the extent to which the sets in multiple measurements differ. Genetic divergence among the genotypes was measured by the Euclidian distance method of Cruz and Regazzi (1994) [8] as cited by Oliveira and Valls (2003) [32]. Euclidean distance was remarked by Hoque and Rahman (2007) [15] as a suitable method of measuring distances

between would be parents.

A brief review of divergence analysis in cowpea based on D<sup>2</sup> statistic is summarized below.

Genetic divergence was assessed by Dharmalingam and Kadambavanasundaram (1989) [10] among the 13 clusters formed. The genotypes CO2 and G5 in cowpea belonging to the two most divergent clusters were recommended as suitable for inclusion in heterosis breeding programmes. Thiyagarajan and Natarajan (1989) [44] revealed that on the basis of multivariate analysis the number of pods per plant, number of seeds per pod and seed yield per plant made a large contribution to the genetic divergence. There was no parallelism between geographic and genetic diversity. Hazra *et al.* (1993) [13] grouped cowpea genotypes belonging to three cult groups (*unguiculata*, *bio flora* and *sesquipedalis*) into four clusters using D<sup>2</sup> statistics. Maximum inter cluster distance between cluster I and IV and minimum between III and IV was observed. The clustering pattern revealed that genetic diversity was not related to geographical diversity. The characters like plant height/ vine length, pod length, pod weight, 100 seed weight and pod yield per plant will offer good scope for rational selection because of their important contribution towards genetic divergence of cowpea. They also concluded that genotypes of same culti group did not necessary clustered together which might have arisen due to presence of number of intermediate types. Rewale *et al.* (1996) [36] observed that multivariate analysis grouped the genotypes into 19 clusters, of which 11 had only one genotype each. There was no relationship between geographical origin and genetic diversity. Hazra *et al.* (1996) [14] used genetic divergence technique for choosing parents for hybridization with a view for improving vegetable cowpea involving three cult groups viz *unguiculata*, *bioflora* and *sesquipedalis*. Impact of environment on the composition of clusters was evident. Genotypes stable in their grouping in

both the environments were considered as good breeding material. Crosses involving the genotypes of *bioflora* and *sesquipedalis* were likely to produce recombinants with desirable characters of both cultigroup because of very high order to divergence between the genotypes of these cultigroups.

According to Anbuselvam *et al.* (2000) [2] observed that analysis of variance revealed significant variability among genotypes for all traits studied. The highest inter cluster distance (924.80) was observed between clusters II and IV, indicating high genetic divergence between genotypes belonging to these clusters. Awopetu and Aliyu (2000) [3] studied genetic diversity within 25 cowpea accessions originating from different ecological areas. The results showed dissimilar biotypes that can be tentatively categorized into early, intermediate and late flowering and eventual pod-maturity groups for further selection. It was observed that geographical distribution as well as previous improvement status or genetic background of the materials basically affected the genotypic relationships among and within the groups and subgroups respectively. Ushakumari *et al.* (2000) [45] employed D<sup>2</sup> analysis in fifty genotypes of cowpea and grouped all into 13 clusters. IT-86-F-310-6 gave the highest values for number of branches, pod length, and seeds per pod, while IT-87-D-272 gave the highest values for plant height, clusters per plant, pods per cluster, and single plant yield. The highest contributions towards divergence were recorded for plant height (22.69%), seeds per pod (17.63%), number of branches (16.82%), number of pods per cluster (15.27%) and pod length (13.47%). Kapoor *et al.* (2000) [17] evaluated sixty genotypes of cowpea were sown in randomized block design with four replication to assess genetic divergence for fourteen traits *viz.* green fodder yield, seed yield and their component traits. Through Mahalanobis's D<sup>2</sup> technique, all the sixty genotypes were grouped into fifteen clusters depending upon their genetic distances. The divergent genotypes 86-B, V-9-A, 221-1-B in cluster III and 229-B, 221-B, 25-1-B and cowpea-88 in cluster VII were identified and are expected to perform better and give transgressive segregation in their progenies. Borah and Khan (2001) [6] evaluated 60 cowpea cultivars for genetic diversity. The grouping of cultivars into 10 clusters indicated high genetic divergence among the cultivars. The clustering pattern showed that geographic diversity was not an index of genetic diversity. Based on inter cluster distance and cluster means for 13 characters (plant height, number of branches and leaves, leaflet length and width, stem thickness, days to 50% flowering, dry matter and green fodder yields, dry weight of leaves and stems, leaf/stem ratio, and crude protein content), clusters I, II, IX, and X were the most genetically diverse. Dry matter yield, green fodder yield and plant height recorded the highest contribution to total genetic divergence, suggesting that these traits are good criteria for the selection of parents for hybridization programmes. Neema and Palaniswami (2003) [30] employed D<sup>2</sup> to cluster eight parents and twenty eight hybrids at two locations to assess the relation between the genetic divergence and heterotic expression. Six clusters were made for each location which differs in constitution. The hybrids produced by selection of parents based on D<sup>2</sup> clustering showed high heteroticeffect. Narayanankutty *et al.* (2003a) [28] conducted genetic variability and divergence studies on thirty-seven genotypes of vegetable cowpea. The thirty-seven genotypes were grouped into eleven clusters using D<sup>2</sup> statistics. In general, the inter cluster distances were higher than intra cluster distances. The maximum inter cluster distance was between clusters

VIII and X, followed by clusters VI and X and clusters VIII and IX, respectively. The intra cluster distance was maximum in cluster VII. Venkatesan *et al.* (2004) [48] grouped the cowpea population into six clusters, of which clusters II and III had the maximum number of genotypes. Analysis collaborated the absence of parallelism between geographic origin and genetic diversity. Intra cluster distance was maximum in cluster V and minimum in cluster II. The inter cluster distance was maximum between II and VI. Clusters per plant, pods per cluster, pods per plant and seed yield per plant had the maximum contribution towards total divergence. Nigude *et al.* (2004b) [31] studied the nature of magnitude of genetic diversity in a set of 45 cowpea genotypes from indigenous and exotic sources. The genotypes were grouped into five clusters using Mahalanobis D<sup>2</sup> statistics. Cluster I was the largest with 28 genotypes followed by cluster II with 11 genotypes and cluster III with 4 genotypes. The clusters IV and V were mono-genotypic. The maximum inter-cluster distance was observed between clusters III and V followed by distance between clusters II and III. Clusters I and III exhibited the minimum inter-cluster distance. The number of branches per plant, test weight, biomass (dry weight) at harvesting and number of pods per plant had contributed considerably towards divergence. Kumari *et al.* (2004) [19] grouped fifty genotypes of cowpea into four clusters on the basis of D<sup>2</sup> values. Maximum numbers of genotypes (45) were included in cluster I, while cluster II and III had two genotypes each, and cluster IV had only one genotype. The cluster pattern of genotypes revealed that the genetic diversity was not always related with geographical diversity. Genotypes in cluster IV recorded high mean values for number of clusters, number of pods, 100-seed weight, seed yield per plant, dry weight per seedling, vigour index and *in vitro* protein digestibility, with low values for pod length and tannin content. Genotypes in cluster I showed maximum mean values for standard germination and shoot length. Divergent parents from cluster I, cluster III and cluster IV may be used in hybridization programmes to get transgressive segregants for high seed yield and quality traits in cowpea. Saini *et al.* (2004) [37] evaluated one hundred and fifty-five cowpea germplasm lines for their genetic divergence by D<sup>2</sup> analysis for a set of eight quantitative characters. The D<sup>2</sup> analysis revealed that genotypes exhibited considerable diversity and were grouped in 10 clusters. Cluster I exhibited maximum number of germplasm lines. Inter-cluster distance was maximum between clusters IV and X followed by clusters IX and X. Cluster IX recorded highest mean seed yield per plant, 100-seed weight and also the intra-cluster distance. The genotypes belonging to these clusters *viz.*, GC 3 and DCP 10 may be useful in multiple breeding programme to recover transgressive segregants with the desirable combinations of yield components. Kumawat and Rajee (2005a) [20] evaluated fifty genotypes of cowpea for yield and its components and grouped the genotypes into 6 clusters. Average intra-cluster distance ranged from 0.00 (cluster IV) to 5.622 in (cluster II). Seed yield per plant had the highest contribution towards the total genetic divergence followed by seeds per pod, days to 50% flowering, plant height and reproductive period. Madheshia and Pandey (2005) [22] reported that sixty-five genotypes were grouped into 24 clusters. Significant differences were observed for each character under study. The maximum intra cluster distance was observed in cluster VIII, whereas inter cluster distance between clusters XVII and XXII. The days to first flowering and number of pods per plant contributed towards maximum

divergence. Based on cluster mean and cluster distance desirable and promising genotypes were also identified. Magloire (2005) <sup>[24]</sup> worked out genetic divergence of 20 genotypes the results showed a relatively high level of dissimilarity among the accessions for most of the morphological traits analyzed, especially for accessions from different countries. Mandavi (2005) <sup>[26]</sup> carried out divergence study on 20 collected germplasm reported presence of appreciable amount of genetic diversity for green pod yield and its components and observed non inter allelism among the genotypes and place of collection, showing lot of scope for selection for green pod yield and reported that D<sup>2</sup> value recorded for different characters for varying genotypes in cowpea revealed the presence of appreciable genetic diversity in the genotypes included in the investigation and geographical distribution had no relation to genetic diversity. Narayanankutty *et al.* (2005) <sup>[29]</sup> evaluated sixty-three accessions of vegetable cowpea for 12 quantitative characters including yield. The genotypes were grouped into 8 clusters with variable number of genotypes. Clustering pattern indicated no association between geographical distribution of accessions and genetic divergence. The characters like pod weight, pod yield, number of pods per plant and pod length had the highest contribution to genetic divergence. Jain *et al.* (2006) <sup>[6]</sup> One hundred and twenty-seven cowpea germplasm lines were grouped into 10 clusters on the basis of D<sup>2</sup> analysis. Cluster I exhibited maximum number of genotypes. Inter-cluster distance was maximum between clusters VIII and X followed by clusters IV and VIII. Intra-cluster distance was maximum in cluster VIII. The observed distances showed the genetic diversity among and within the clusters and clustering was useful to identify the diverse genotypes. Cluster IX registered the highest mean value for plant height (88.74 cm), seed yield per plant (35.69 g) and 100-seed weight (14.93 g). Divergent parents from various clusters can be used in hybridization programme to get transgressive recombinants for grain yield and its component traits. Girish *et al.* (2006) <sup>[12]</sup> evaluated one hundred cowpea genotypes for 11 quantitative characters to quantify the genetic diversity existed among them by using Mahalanobis D<sup>2</sup> statistics. The genotypes fell into 11 clusters. Among the 11 quantitative characters studied, fodder yield contributed highest (75.73%) towards the divergence followed by plant height (8.28%) and seed yield (6.3%). Lesly *et al.* (2006) <sup>[21]</sup> applied D<sup>2</sup> statistics in 169 cowpea genotypes and grouped it all into 46 clusters. Significant differences were observed for all the characters under study. The inter cluster distance was maximum between cluster 11 and 42 followed by 34 and 42. The number of pods per plant contributed maximum divergence which was followed by harvest index and days to flower termination. They further suggested based on cluster distance and performance of genotypes, selection can be made to get intercrosses to recover good recombinants and desirable segregants. Pandey (2007) <sup>[33]</sup> grouped forty-four cowpea genotypes into nine clusters. Cluster III had minimum days to first flower opening in addition to maximum number of pods per plant and primary branches. Cluster II, V, VII had maximum yield per plant, 100 seed weight, pod length and number of seeds per pod respectively. Cluster II had minimum days to maturity whereas VII had maximum days to maturity. He further suggested that genotypes from high and low cluster mean were most promising for hybridization programme. Suganthi *et al.* (2007) <sup>[42]</sup> carried out D<sup>2</sup> statistics among thirty genotypes which were grouped into eleven clusters. Maximum inter cluster distance was found between

cluster I and XI, indicating that genotypes of these clusters were more divergent. The diversity among the genotypes measured by inter cluster distance was adequate for improvement of cowpea by hybridization and selection. Valarmathi *et al.* (2007) <sup>[46]</sup> evaluated sixty genotypes of *Vigna unguiculata* var. *Unguiculata* and nine genotypes of *Vigna unguiculata* var. *sesquipedalis*. All the accessions were grouped into 12 clusters. Both the varieties were grouped in distinctly different clusters. Days to maturity contributed maximum to the genetic divergence followed by 100 seed weight, number of branches per plant and number of seeds per pod. Bhandari and Verma (2007) <sup>[5]</sup> evaluated twenty advanced generation forage cowpea genotypes alongwith two released varieties for genetic divergence and correlation analysis. Based on divergence analysis of pooled data, the 22 genotypes were grouped into seven clusters. Cluster 1 had maximum number of genotypes 10, clusters II and III had five and three genotypes, respectively. Maximum intra cluster distance was in cluster III and maximum inter cluster distance was between clusters V and VII. Crude protein content, dry matter digestibility, dry matter yield and number of leaves per plant were major contributors towards genetic divergence. Sulnathi *et al.* (2007) <sup>[43]</sup> genetic diversity assessed in 56 genotypes of cowpea using D<sup>2</sup> statistics for thirteen yield contributing characters showed grouping of genotypes into nine clusters. Cluster I had the maximum number of genotype. Characters *viz.*, days to maturity, 100-seed weight and days to flowering were the highest contributors to D<sup>2</sup> values. The geographical diversity was not related to genetic diversity. Dalsaniya *et al.* (2009) <sup>[9]</sup> field experiment was conducted with 60 genotypes of cowpea to study the diversity among the genotypes which were grouped in to 12 clusters revealing the presence of considerable diversity in the material. The clustering pattern of the varieties usually did not confirm to geographical distribution. Inter cluster distance and mean cluster character values indicated that hybridization of cluster X variety (JCPL-134) with cluster IV varieties (JCPL-1, JCPL-13 and JCPL-21) and cluster V varieties (JCPL-50 and JCPL-133) with cluster III varieties (JCPL-26 and JCPL-131) would exhibit high heterosis and also result in transgressive segregants with higher yield. It was also noted that genotypes of cluster-X which had higher cluster mean values for yield and other desired characters like leaf area, ten pods weight, number of pods per plant and green pod yield per plant etc. could be directly tested in multiplication trials for their suitability or could be used as a donor parent in breeding programme. The characters like plant height, green pod yield per plant, protein content and leaf area were found to contribute much to the total genetic divergence in cowpea. Francisco *et al.* (2009) <sup>[11]</sup> Twenty eight lines of the gene bank included for the analysis of genetic divergence the canonical variables, Mahalanobis' distance and the Tocher cluster method were used. Most of the maximum distances were observed when combined with CE-46 genotypes. The crosses between the groups VIII and XI and groups VII and VIII may result in new gene combinations. The variables beginning of flowering and crop cycle contributed most to the genetic divergence among the genotypes. According to Adewale *et al.* (2011) <sup>[1]</sup> reported the mean Euclidean distance between the genotypes was 3.7479, the least (0.9494) was between 25016-2 and 24901-1 and the highest (6.4590) was between 24884-1 and 24881-2. Studies nine breeding lines of cowpea and a common cowpea cultivar were evaluated in a RCBD. The phenotypic traits measured includes plant height at 4 week, number of pods per plant, pod

length, number of days to first flower, number of days to first ripe pod number of peduncles per plant, peduncle length and number of branches per plant. Group I had genotype with high pod productivity but late flowering and ripening. The genotypes in group II flowered and produced ripen pods much earlier. Pandiyan *et al.* (2012) [34] studies genetic diversity among thirty six accessions of cultivated and wild *Vigna* species. The cluster analysis resulted in eight clusters for the morphological traits and the accessions of the *V. dalzelliana*, *V. unguiculata*, *V. trilobata*, *V. mungo* var. *V. mungo* and, *trinervia* var and *bourneae* were clustered in separate groups. Hence the variation was found at species level. More intensive collection, characterization and conservation of diverse species and accumulation of variations within the species, predominantly of the close wild relatives of Asian *Vigna* species specific characters great importance in crop improvement programmes. Nancee *et al.* (2013) [27] grouped forty six genotypes into eight clusters based on  $D^2$  values, containing two to fifteen genotypes. These clusters consisted of genotypes with different geographical origins and indicated no correlation between genetic and geographical divergence. The genotypes of cluster VIII showed maximum genetic divergence with cluster V followed by cluster II, hence, the genotypes belonging to cluster VIII and cluster V may be selected for generating genetic variability and hybridization. Cluster II having two genotypes was found to be the best performing for agronomic characters followed by cluster I with three genotypes and cluster V with three genotypes. Thus, to generate desirable genetic variability, the crossing between cluster II, I and V genotypes would be useful. Brahmaiah *et al.* (2014) [7] evaluated 40 cowpea genotype for 18 quantitative character to estimate the genetic diversity using Mahalanobis  $D^2$  statistics and grouped them into 6 cluster. The cluster strength varied from single genotype (clusters III, IV and V) to 25 genotype (cluster I). Clusters IV and VI had high inter cluster distance. Clusters II, III and I had maximum 100-seed weight, number of seeds per pod and seed yield respectively. Cluster IV had maximum seedling vigour index, germination percent, peduncle length, number of clusters per plant and number of primary branches. The genotypes from clusters IV and IV may be inter-crossed to obtain high variation. Sandeep *et al.* (2014) [38] studied genetic divergence using  $D^2$  analysis was carried out in 50 diverse genotype of cowpea. All the 50 genotype were grouped into twelve clusters. Cluster I was largest comprising of twenty seven genotypes followed by cluster II with twelve genotype, cluster IV with three genotype and cluster III, V, VI, VII and VIII, IX, X, XI, XII were represented each by single genotype. Intra-cluster  $D^2$  values ranged from 0 to 38.06. The inter-cluster  $D^2$  value ranged from 44.08 to 276.55. The maximum inter cluster distance was observed between VII and XII clusters followed by clusters IV and XII and cluster X and VII. The maximum contribution towards genetic divergence in by days to 50% flowering (25.22%) followed by plant height (12.44%) and biological yield per plant. Patil *et al.* (2015) grouped the twenty genotypes could be into 6 clusters on the basis of  $D^2$  analysis. Cluster II had the highest number of genotypes (8) followed by cluster I (5). The cluster III and IV included 3 genotypes each. Remaining clusters were mono-genotypic. The highest intra-cluster distances were recorded in cluster II followed by cluster III. Among the 20 genotypes, C-152 showed the highest cluster mean for days to maturity. The characters 100-seed weight (71.58%) was the main contributor to the total genetic divergence. Biological yield per plant (9.47%), pod length (5.26%),

number of branches per plant (5.26%), plant height (4.21%) and days to flowering (2.63%) contributed moderately and pods per plant shown small contribution, while the characters days to maturity, seeds per pod and harvest index showed 0.00% contribution towards total genetic divergence. Wamalwa *et al.*, (2016) [51] evaluate genetic diversity in 19 cowpea genotypes. These genotypes were clustered into two major groups. High divergence was observed between accessions from Ethiopia and Australia and those from Western Kenya. Upper Volta accessions were closely related to those from Western Kenya. Low variation was observed between accessions from Eastern and Rift Valley than those from Western and Coastal regions of Kenya. Koolwal, Mafakheri *et al.*, (2017) [23] studied 58 genotypes (accessions and mutants of cowpea variety RC-101 and RC-19) of cowpea for seed storage protein profile using Sodium Dodecyl Sulphate polyacrylamide gel electrophoresis (SDS-PAGE) to study diversity among the genotypes. Singh *et al.*, (2018) [40] studied Thirty-eight accessions of cowpea were evaluated for nine quantitative characters and grouped into ten clusters. On the basis of inter-cluster distances, cluster VII and X in  $E_1$  environment and cluster II and III in  $E_2$  environment were found to be most divergent. Cluster VII had the genotype with the highest mean value for number of seed yield per plant, number of pods per plant and number of clusters per plant in  $E_1$  environment, while cluster I had the genotypes which showed maximum mean value for seed yield per plant, number of pods per plant, peduncle length, and number of clusters per plant in  $E_2$  environment. Praveena *et al.*, (2019) evaluated  $D^2$  analysis for the thirty genotypes grouped into 11 clusters. The maximum intra-cluster  $D^2$  value was shown by cluster IV (146.57), followed by cluster I (127.52), cluster II (101.49) and cluster III (55.47). Highest inter-cluster  $D^2$  values among genotypes existed between cluster VIII and cluster X (1559.98), followed by cluster VIII and cluster XI (1480.33), cluster VIII and cluster II (1367.65), and cluster VIII and cluster IV (1309.08). Minimum inter-cluster  $D^2$  values among genotypes existed between cluster XI and cluster IX (160.10) followed by cluster I and cluster III (164.51), cluster XI and cluster IV (167.47). The analysis clearly shows the existence of significant difference between the 30 genotypes under study for the 14 characters.

## Conclusion

The literature reviewed in this paper highlighted the genetic divergence available in cowpea genotypes. Knowledge of genetic divergence between forage yield, seed yield and its components is very useful for efficient selection of desirable plant type. Therefore, genetically divergent genotypes could be utilized for cowpea crop improvement for the future. Generally it has been reported that as cowpea is one important legume crop that has a vital role in economic value, nutrition value and as it adds nitrogen fertilizer to soil through bacterial symbiosis. It also has large genetic diversity whether it is wild or cultivated which its production is high in different countries However, cowpea is very improved cultivar which can tolerate to different geographical location, resistant to diseases and insects, produce high yield and nutrition quality. There were many studies which deal with genetic divergence and forage yield and seed yield related traits of cowpea which based on quantitative trails cowpea genotypes.

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