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Research Article

Analysis of genetic parameters, trait association and genetic diversity in fodder cowpea [*Vigna unguiculata* (L.) Walp.]

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Abstract
Fodder cowpea (*Vigna ungiculata* (L.) Walp.) is regarded as one of the most important leguminous fodders due to its high biomass yield, high protein content and rapid growing nature. A study to analyze different genetic parameters, trait association and diversity was carried out with 79 fodder cowpea genotypes. The mean performances of the genotypes showed wide variation for all the traits studied. Plant height, the number of primary branches, the number of leaves per plant, leaf length, leaf breadth, leaf area index and dry matter yield were found to have a substantial and positive relationship with green fodder yield. Path coefficient analysis revealed that the leaf area index needs to be given due weightage for improving green fodder yield in cowpea. The 79 fodder cowpea genotypes were grouped into 10 clusters of which three were solitary which confirmed the presence of wide genetic diversity among the fodder cowpea germplasm lines. The maximum intra cluster distance was exhibited by cluster III followed by clusters IX, II, I, IV, V and VII, whereas the cluster II and cluster IX recorded the greatest inter-cluster distance. Based on mean performance for green fodder production, the genotypes GETC 54, GETC 46, TNFC 0926, and GETC 53 were observed to be better prospects for exploitation in future breeding programs.

Keywords: Fodder cowpea, genetic parameters, trait association, path analysis, genetic diversity

INTRODUCTION

India's livestock sector is the largest in the world, with 11.6 per cent of the world's cattle herds and it ranks first in milk production. According to 20th Livestock Census, 2019, 57.3 per cent of the world's buffalo population and 14.7 per cent of the world's cattle population is in India. To sustain this, the production of higher-quality feed at a lower cost is a prerequisite (Kumari *et al*., 2017). The green fodder availability to the cattle population during 1990s was to the tune of 60 per cent. Due to the increase in animal population and dwindling resources, the availability has come down by 50 per cent of the total requirement (Agrawal *et al*., 2008). Presently the net deficiency in availability of green fodder and dry fodder is 35.6 and 10.95 per cent, respectively (Singh *et al.,* 2022). As per the IGFRI Vision 2050 document, the demand for green fodder is projected to increase to 1012 million tonnes and dry fodder demand could be 631 million tonnes in the year 2050. Dagar (2017), has reported that the net green forage supply has to be increased at the rate of 1.69 per cent per annum to bridge the demand supply gap. In India, forage enhancement work began several decades ago and has resulted in the development of numerous improved fodder crops. Even though some fodder crops have significant promise in the Indian forage context, they are nevertheless underutilized. One of these crops is fodder cowpea.

Cowpea [*Vigna unguiculata* (L.) Walp., Fabaceae (2n=2x=22)] is one of the most widely adopted, early, multi-season and multipurpose pulse crops grown extensively throughout the tropical and subtropical regions of Africa, Asia, Nigeria and America (Ehlers and Hall, 1997; Singh *et al.,* 1997). Africa and China were considered as main centers of origin. Evidence suggests that cowpea originated and domesticated in Western or Central Africa very likely in Nigeria, where a plethora of wild and weedy species are observed in both Savannah and forest zones. In India, it is grown as a minor pulse in arid and semi-arid regions of Rajasthan, Gujarat, Maharashtra, Karnataka and Tamil Nadu in a total area of 407.93 lakh ha with a production of 7925.25 lakh tonnes and productivity of 19.47 tonnes/ha (Kumar *et al.,* 2020). Cowpea provides high quality protein rich food for people, fodder for livestock and fixes nitrogen for improving the soil fertility (Murdock *et al*., 2008). Its ability to adapt to hot, low, and unpredictable rainfall is one of its distinctive characteristics. As the duration of the crop is less, it can be ideally accommodated in any cropping sequence.

For successful cowpea breeding work, the availability of diverse parents is of paramount importance. When the parents used in crossing are genetically diverse, it is widely recognized that better segregants are more likely obtained (Jain, 1975). So, the selection of parents is the foundation of any crop improvement programme. Estimating the association among the yield contributing variables is required to identify the direction of selection and to maximize yield in the shortest time possible. In the present study, 75 fodder cowpea germplasm accessions were subjected to variability parameters and genetic diversity analyses for the identification of promising and diverse accessions for exploitation in future breeding programs.

MATERIALS AND METHODS

The experiment comprising of 75 fodder cowpea genotypes along with four checks (CO 5, CO 8, CO 9, TNFC 0926) was carried out in Randomized Block Design with two replications at New Area farm, Department of Forage Crops, Tamil Nadu Agricultural University, Coimbatore, India, during *Rabi*, 2021. Individual genotype in each replication was raised in two rows, of 4m in length with a spacing of 30 x 10 cm. Standard crop management practices were followed for proper growth and establishment of the crop.

Data was recorded on five random competitive plants per replication for seven morphometric parameters *viz*., the number of branches per plant, the total number of leaves per plant, plant height (cm), leaf length (cm), leaf breadth (cm), green fodder yield per plant (g), dry fodder yield per plant (g) and leaf area index was calculated from leaf length and leaf breadth. The data for days to first flowering and days to 50% flowering was recorded on a whole plot basis. Mean and range was calculated as per the method proposed by Panse and Sukhtame (1967), Phenotypic Coefficient of Variability (PCV) and Genotypic Coefficient of Variability (GCV) was calculated using the procedure developed by Fisher *et al.* (1932). The PCV and GCV were categorized as low (less than 10%), moderate (10-20%), and high (more than 20%) as per Sivasubramanian and Menon (1973). Heritability (h^2) was worked out according to Lush *et al*. (1940) and the values were categorized as low (30 per cent), moderate (30-60 per cent) and high (> 60 per cent) as per Johnson *et al*. (1955) and Genetic Advance as per cent over Mean (GAM) was estimated using the method suggested by Johnson *et al.* (1955). The range of genetic advance as per cent of the mean was classified as high (> 20%), moderate (10-20 %) and low (<10%) (Johnson *et al.,* 1955).

Computation of correlation coefficient for all the traits was done as recommended by Singh and Chaudhary (1979). To partition the direct correlation between variables into indirect effects, path coefficient analysis was carried out as per the method proposed by Dewey and Lu (1959). Genetic diversity among the accessions was studied by D^2 analysis as proposed by Mahalanobis (1936). Statistical analyses for PCV, GCV, GA, correlation coefficient, path coefficient and D^2 statistics were carried out using TNAUSTAT software (Manivannan, 2014).

RESULTS AND DISCUSSION

The mean sum of squares for all the attributes tested among the various genotypes was significant. This indicated the prevalence of wide variation among the genotypes, thus necessitating further study (**Table 1**). The mean performances of the fodder cowpea genotypes showed wide variation for all the characters studied among the genotypes (**Table 2**). Days to first flowering ranged from 52.50 days (GETC 53) to 63.00 days (GETC 31). Days to 50% flowering varied from 56.00 (GETC 53) to 66.00 days (GETC 40). Plant height differed from 36.00 cm (GETC 11) to 122.40 cm (TNFC 0926). The number of primary branches ranged from 2.18 (GETC 44) to 5.30 (GETC 51). The number of leaves per plant was maximum in GETC 66 (19.90) and minimum in TNFC 0926 (50.90). Leaf length ranged from 7.35 cm (GETC 16) to 10.86 cm (GETC 46). Leaf breadth varied from 3.86 cm (GETC 13) to 8.39 cm (TNFC 0926). Leaf area index differed from 5.54 (GETC 66) to 31.70 (TNFC 0926). Green fodder yield ranged from 65.00 gm (GETC 44) to 329.00 gm (GETC 54). Dry fodder yield ranged from 24.00 gm (GETC 55) to 75.00gm (GETC 54). Thus, wide variation was observed among the genotypes for the traits plant height, the number of leaves per plant, leaf area index and green fodder yield, presenting good scope for selection.

The PCV, GCV, h^2 and GAM for different characters are presented in **Table 3**. For the traits days to first flowering, days to 50% flowering, the number of primary branches, leaf length, leaf area index and dry fodder

Table 1. ANOVA for quantitative traits in fodder cowpea genotypes

S.No.	Characters	Mean sum of squares			CV%
		Replication	Genotypes	Error	
	Degrees of freedom	**1**	**78**	**78**	
1	Days to first flowering	40.50	10.42**	3.89	3.36
2	Days to 50% flowering	77.98	9.50*	5.75	3.89
3	Plant height	81.12	721.33**	33.15	8.82
4	Number of primary branches	0.03	0.83**	0.13	8.91
5	Number of leaves per plant	0.25	69.21**	5.95	7.53
6	Leaf length	2.08	1.09*	0.64	9.15
7	Leaf breadth	0.15	1.49**	0.02	2.76
8	Leaf area index	1.89	36.16**	2.30	12.03
9	Green fodder yield	3.96	4234.26**	194.80	10.64
10	Dry matter yield	22.79	141.62**	11.44	9.52

** Significant at p = 0.01

Table 2. Mean performance of 79 fodder cowpea genotypes for 10 quantitative traits

S. No.	Traits	Mean	Minimum	Maximum	S.E.	C.D. 5%	C.D. 1%
1	Days to first flowering	58.63	52.5 (GETC 53)	63 (GETC 31)	1.39	3.91	5.19
2	Days to 50% flowering	61.60	56 (GETC 53)	66 (GETC 40)	1.70	4.75	6.31
3	Plant height (cm)	65.29	36 (GETC 11)	122.4 (TNFC 0926)	4.07	11.40	15.14
4	Number of primary branches	3.97	2.175 (GETC 44)	5.3 (GETC 51)	0.25	0.70	0.93
5	Number of leaves per plant	32.38	19.9 (GETC 66)	50.9 (TNFC 0926)	1.73	4.83	6.42
6	Leaf length (cm)	8.76	7.35 (GETC 16)	10.86 (GETC 46)	0.57	1.59	2.11
7	Leaf breadth (cm)	5.45	3.855 (GETC 13)	8.39 (TNFC 0926)	0.11	0.30	0.40
8	Leaf area index	12.59	5.54 (GETC 66)	31.7 (TNFC 0926)	1.07	3.00	3.98
9	Green fodder yield (g)	131.28	65 (GETC 44)	329 (GETC 54)	9.87	27.64	36.71
10	Dry matter yield (g)	35.54	24 (GETC 55)	75 (GETC 54).	2.39	6.70	8.89

yield, wide difference was observed between PCV and GCV with PCV value being greater. This suggests that the expression of the above characters is highly influenced by the environment. This result is in accordance with Malarvizhi *et al.* (2005). For plant height, the number of leaves per plant, leaf breadth and green fodder yield, the difference between PCV and GCV is narrow indicating a greater influence of genetic background on the expression of the traits. The PCV and GCV values were categorized according to Sivasubramanian and Menon (1973). High PCV values were recorded for plant height (29.75), leaf area index (34.82), green fodder yield (35.87) and dry fodder yield (24.61). Moderate PCV values were recorded for the number of primary branches (17.41), the number of leaves per plant (18.93), leaf length (10.61) and leaf breadth (15.95) and low PCV values were recorded for days to first flowering (4.56) and days to 50% flowering (4.48). Characters with a high GCV have greater potential for progress than those with moderate GCV (Gandhi *et al*., 2001; Thirupathi Reddy *et al*., 2012). In the present study, high GCV values were recorded for green fodder yield (34.26), leaf area index (32.68), plant height (28.41) and dry fodder yield (22.7) and therefore these traits can be exploited for fodder cowpea improvement. The number of primary branches (14.96), the number of leaves per plant (17.37) and leaf breadth (15.71) showed moderate values and days to 50% flowering (2.22), days to first flowering (3.08) and leaf length (5.39) exhibited low GCV values (**Table 3**).

Apart from PCV and GCV, heritability and genetic advance as per cent of mean are also important genetic

Table 3. Variability parameters of various characters in fodder cowpea genotypes

S. No.	Traits	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
1	Days to first flowering	4.56	3.08	45.62	4.29
2	Days to 50% flowering	4.48	2.22	24.61	2.27
3	Plant height	29.75	28.41	91.21	55.90
4	Number of primary branches	17.41	14.96	73.82	26.48
5	Number of leaves per plant	18.93	17.37	84.16	32.82
6	Leaf length	10.61	5.39	25.75	5.63
7	Leaf breadth	15.95	15.71	97.00	31.88
8	Leaf area index	34.82	32.68	88.06	63.18
9	Green fodder yield	35.87	34.26	91.20	67.39
10	Dry matter yield	24.61	22.70	85.05	43.12

parameters to be taken into consideration during crop breeding programs. In the present study, high heritability values were observed for leaf breadth (97.00), plant height (91.21), green fodder yield (91.20), leaf area index **(**88.06**),** dry fodder yield (85.05) the number of leaves per plant (84.16) and the number of primary branches (73.83), which implied that the influence of environment is less for the above traits and the variability is heritable due to high genetic control. Moderate heritability value was recorded for days to first flowering (45.62**)** and low heritability values were observed for days to 50% flowering (24.61) and leaf length (25.75) and so selection for these characters may not be fruitful. Heritability is a mixture of fixable (additive) and non-fixable (dominant and epistatic) variances, hence it should not be employed exclusively in determining the genetic potentials (Olayiwola and Soremi, 2014). Johnson *et al.* (1955) proposed that using estimates of heritability and genetic advance together to anticipate the value of selection is more valuable than using heritability alone.Genetic advance is defined as the difference between the mean genotypic value of the selected lines and the mean genotypic value of the parental population. In the present study, GAM was observed to be high for green fodder yield (67.39), leaf area index (63.18), plant height (55.90), dry fodder yield (43.12), the number of leaves per plant (32.82), leaf breadth (31.88), the number of primary branches (26.48) and low for days 50% flowering (2.27), days to first flowering (4.29) and leaf length (5.63) (**Table 3**). The high GAM indicated that those characters may have high additive genetic variance which is due to additive gene effects. These results were similar to the findings of Ponmariammal and Vijendra Das (1996) for the traits the number of primary branches, the number of leaves per plant, plant height, green fodder yield and dry matter yield.

The characters plant height(r=0.52), the number of primary branches (r=0.41), the number of leaves per plant (r=0.57), leaf length (r=0.35), leaf breadth (r=0.39), leaf area index (r=0.57) and dry matter yield (r=0.93) exhibited significant and positive correlation with the green fodder yield **(Table 4).** This corroborates with the findings of

Table 4. **Simple correlation between green fodder yield and its component traits in fodder cowpea**

Traits	Days to first flowering	Days to 50% flowering	Plant height	Number of primary branches	Number of leaves per plant	Leaf length	Leaf breadth	Leaf area index	Dry matter yield	Green fodder yield
Days to first flowering	**1.00**									
Days to 50% flowering	0.97**	**1.00**								
Plant height	-0.10	-0.06	**1.00**							
Number of primary branches	-0.07	-0.05	0.32**	**1.00**						
Number of leaves per plant	-0.13	-0.12	0.58**	0.69**	**1.00**					
Leaf length	-0.17*	-0.15	0.63**	0.12**	0.35**	**1.00**				
Leaf breadth	-0.29**	-0.27**	0.57**	0.16**	0.34**	0.63**	**1.00**			
Leaf area index	-0.23**	-0.21**	0.74**	0.45**	0.79**	0.74**	0.76**	**1.00**		
Dry matter yield	-0.15	-0.14	0.57**	0.41**	0.51**	0.37**	0.44**	0.57**	**1.00**	
Green fodder yield	-0.12	-0.12	0.52**	0.41**	0.57**	0.35**	0.39**	0.57**	0.93**	**1.00**

**significance at 1% level; *significance at 5% level

Dangi and Paroda (1974), Sheela and Gopalan (2006), Singh *et al.* (2010), Navaselvakkumaran *et al.* (2019). The same set of traits *i.e.,* plant height, the number of primary branches, the number of leaves per plant, leaf length, leaf breadth, leaf area index and green fodder yield also exhibited a significant positive correlation with the dry matter yield. This could be the result of linkage disequilibrium of the genes determining the above traits and the biological pleiotropy of genes. Similar findings were reported by Chopra and Singh, (1977) and Sahai *et al*. (2013). The character plant height had a positive inter-correlation with the number of primary branches, the number of leaves per plant, leaf length, leaf breadth and leaf area index. Days to 50% flowering were highly significant and positively correlated with days to first flowering but showed a significant negative correlation with leaf breadth and leaf area index and exhibited a non-significance with other green fodder yield contributing characters. These results were in consonance with those of Bashir *et al.* (2001).

Path analysis reveals direct and indirect effects of different biometrical traits on yield, by partitioning genotypic correlation coefficients using partial and multiple regression techniques. The results of partitioning of a direct correlation between yield contributing traits and green fodder yield revealed that dry matter yield (r = 0.98) recorded the highest positive direct effect (Phogat *et al.,* 2017) followed by the trait leaf area index (r = 0.28) (**Table 5**). Direct effects of the number of primary branches, leaf length and leaf breadth towards green fodder yield per plant were negligible and negative. The direct effect for the trait number of leaves per plant is negligible and positive but had a significant positive indirect effect on green fodder yield through the leaf area index and dry matter yield. The trait plant height had a significant negative direct effect but had a greater significant positive indirect effect through the leaf area index and dry matter yield. The traits leaf length and leaf breadth had negative direct effects but positive indirect effects through the traits leaf area index and dry matter yield. The number of primary branches had a positive negligible direct effect and exhibits a significant indirect effect through dry matter yield (Kumar *et al.,* 2002). Thus, the study revealed that for improvement of green fodder yield in cowpea, leaf area index could be given due weightage. The residual effect of path analysis at the genotypic level was recorded as 0.25.

The 79 fodder cowpea genotypes were grouped into 10 clusters of which three were solitary (**Table 6**). This confirms the presence of wide genetic diversity among the fodder cowpea germplasm lines.

In the current study, the maximum intra cluster distance was exhibited by cluster III followed by cluster IX, II, I, IV, V and VII. This indicated that genotypes within these clusters were highly diverse. Maximum inter cluster distance was registered between cluster II and cluster IX indicating that genetic divergence was high between these clusters. With respect to clustering pattern, GETC 13, GETC 38, GETC 2, GETC 21 of cluster II had a wider genetic divergence from Co 9, TNFC 0926 of cluster IX (**Table 7**). Hybridization between genotypes of these two clusters could result in heterotic F_1 and could yield better recombinants in the F_2 generation (Narayanankutty *et al., 2003).* Likewise, hybridization between the genotypes of cluster I and cluster IX, cluster VI and cluster IX also could be useful in obtaining heterotic combinations and desirable recombinants with high green fodder yield.

In the present study, the character leaf breadth was observed to contribute maximum towards diversity. This was followed by green fodder yield and plant height (**Table 8**). This clearly indicates that there was wide variation among the accessions for leaf breadth and this presents ample scope for selection for the trait.

Table 5. Direct and indirect effects of other component traits on green fodder yield at genotypic level

	Days to first flowering	Days to 50% flowering	Plant height	Number of primary branches	Number of leaves per plant	Leaf length	Leaf breadth	Leaf area index	Dry matter yield	Simple correlation with green fodder yield
Days to first flowering	**-0.0248**	0.0621	0.0269	0.0064	-0.0125	0.0082	0.051	-0.0881	-0.2066	-0.12
Days to 50% flowering	-0.0276	**0.0559**	0.0248	0.0061	-0.0139	0.0085	0.0597	-0.1026	-0.2309	-0.12
Plant height	0.0035	-0.0072	**-0.1926**	-0.026	0.0479	-0.0199	-0.0787	0.2127	0.5941	0.52**
Number of primary branches	0.002	-0.0042	-0.0625	**-0.0801**	0.0582	-0.0023	-0.0219	0.1275	0.4318	0.41**
Number of leaves per plant	0.0039	-0.0098	-0.1157	-0.0584	**0.0797**	-0.0114	-0.0482	0.2249	0.5237	0.57**
Leaf length	0.0096	-0.0222	-0.1794	-0.0085	0.0426	**-0.0213**	-0.1228	0.3013	0.5658	0.35**
Leaf breadth	0.0095	-0.025	-0.1134	-0.0131	0.0288	-0.0196	**-0.1335**	0.2177	0.448	0.39**
Leaf area index	0.0079	-0.0206	-0.147	-0.0366	0.0643	-0.023	-0.1043	**0.2787**	0.5728	0.57**
Dry matter yield	0.0052	-0.0132	-0.1166	-0.0353	0.0426	-0.0123	-0.061	0.1627	**0.9811**	0.93**

Residual effect: 0.2545

Table 6. Distribution of fodder cowpea genotypes into different clusters

Cluster	Number of genotypes	Name of genotypes
Cluster 1	48	GETC 17, GETC 41, GETC 32, GETC 19, GETC 14, GETC 1, GETC 5, GETC 27, GETC 11, GETC 28, GETC 7, GETC 20,GETC 49, GETC 25, AVTC1- 2,GETC 26, GETC 18, GETC 23, GETC 50, GETC 12, GETC 48, GETC 68, GETC 53, GETC 30, GETC 40, GETC 39, GETC 44, GETC 15, GETC 10, GETC 60, AVTC1- 3, GETC 66, GETC 4, GETC 31, GETC 37, GETC 9, GETC 29, GETC 67, GETC 34, GETC 47, GETC 36, GETC 6, GETC 22, GETC 3, GETC 35, GETC 16, GETC 33, GETC 58
Cluster 2	4	GETC 13, GETC 38, GETC 2, GETC 21
Cluster 3	9	IVTC 3, AVTC1-1, AVTC1-4, GETC 56, GETC 65, GETC 42, GETC 63, GETC 24, GETC 8
Cluster 4	4	IVTC 1, IVTC 2, GETC 55, GETC 59
Cluster 5	6	GETC 43, GETC 45, GETC 61, GETC 51, GETC 64, GETC62
Cluster 6	1	GETC 57
Cluster 7	3	CO 8, Co5, IVTC 4
Cluster 8	1	GETC 46
Cluster 9	2	CO 9, TNFC 0926
Cluster 10	1	GETC 54

Table 7. Intra cluster (diagonal values) and inter cluster distances based on D^2 values

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX	X
I	54.53	127.46	143.34	187.68	126.58	102.86	330.94	308.87	748.84	375.51
II		56.51	353.15	398.18	241.54	193.67	643.69	513.14	1154.20	539.83
III			68.45	103.50	106.11	128.11	131.62	182.77	371.99	243.67
IV				53.65	119.59	238.74	95.70	81.54	323.96	361.82
V					53.50	99.94	222.76	188.50	482.74	189.95
VI						0.00	357.33	324.16	702.93	131.97
VII							50.19	118.72	161.18	398.53
VIII								0.00	282.69	379.05
IX									59.89	550.69
X										0.00

Table 8. Contribution of various traits towards divergence

S.No.	Traits	Contribution (%)
1	Days to first flowering	1.36
2	Days to 50% flowering	0.00
3	Plant height	14.54
4	Number of primary branches	5.13
5	Number of leaves per plant	5.65
6	Leaf length	0.26
7	Leaf breadth	54.72
8	Leaf area index	1.27
9	Green fodder yield	16.00
10	Dry matter yield	1.07

The selection of genotypes as parents, based on desirable cluster mean could help to improve the particular trait in breeding programmes (Panigrahi and Baisakh, 2014). It was observed that cluster IX recorded the least number of days to first flowering and days to 50% flowering (**Table 9**). Hence, the genotypes in this cluster can be utilized in a hybridization programme to develop short duration varieties. Plant height, the number of primary

Table 9. Mean performance of characters in various clusters

Cluster number	Days to first flowering	Days to 50% flowering	Plant height(cm)	Number of primary branches	Number of leaves per plant	Leaf length (cm)	Leaf breadth (cm)	Leaf area index	Green fodder yield (g)	Dry matter yield (g)
I	58.99	61.91	55.24	3.88	30.67	8.49	5.08	10.65	117.38	32.41
II	58.00	60.63	61.23	3.49	31.14	8.70	4.07	10.83	97.75	30.13
III	56.89	59.94	69.47	4.34	34.71	9.08	6.22	15.34	167.17	41.78
IV	59.13	62.00	83.49	3.88	30.23	8.83	6.24	13.26	95.50	30.75
V	60.08	63.58	96.41	4.63	39.32	9.14	5.60	15.92	167.50	43.25
VI	57.00	60.50	73.55	4.10	31.30	8.30	5.23	11.57	223.00	51.00
VII	58.33	61.33	73.26	3.70	35.81	9.18	7.13	17.95	133.33	41.00
VIII	57.00	60.50	99.10	2.20	24.80	10.86	6.60	13.24	101.00	33.00
IX	55.25	58.25	109.20	4.45	44.35	10.66	8.26	28.37	197.50	45.75
X	60.00	62.00	112.80	4.70	40.00	9.51	6.08	18.39	329.00	75.00

branches, green fodder yield and dry fodder yield recorded high cluster mean values in cluster X. Leaf length recorded higher cluster mean value in cluster VIII. The number of leaves, leaf breath and leaf area index recorded high cluster mean values in cluster IX. Hence, the genotypes of these clusters can be used in a hybridization programme in fodder cowpea to improve those traits which have the highest cluster mean.

In the present study, the 79 fodder cowpea genotypes used were found to have significant variability for most of the characters. Trait association studies revealed that more emphasis could be placed on plant height, the number of leaves per plant, leaf length, leaf breadth, leaf area index, dry fodder yield and green fodder yield. Based on mean performance for green fodder yield and components with better correlation with green fodder yield, the genotypes GETC 54, GETC 46, TNFC 0926 and GETC 53 were found as better candidates, suggesting that they could be used as genetic stocks for crop improvement. Genetic diversity analysis also suggested the presence of genetic diversity among the lines. Hybridization of lines from divergent clusters could result in superior segregants with high green fodder yield.

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