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GENETIC PARAMETERS FOR VARIOUS FODDER TRAITS AMONG THE ELITE COWPEA S (*Vigna unguiculata L.Walp*) GENOTYPES

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ABSTRACT
In this experiment correlation, heritability, genetic advance were studied in twenty elite fodder cowpea genotypes in randomized block design with three replications for various fodder related traits at two environments; Hisar (E_1) and Rohtak (E_2). Out of these genotypes GFC-2 showed maximum green fodder yield per plant followed by EC 3941-1, IC528491, GFC-4, TVv92-2 and GFC-3 in both the environments *i.e.* E_1 & E_2. This indicated that the genotypes can be used in breeding programme for improvement. High heritability coupled with high genetic advance as percent of mean was observed for the characters like green fodder yield per plant, leaf weight, stem weight, pod width, peduncle length, number of main branches per plant, terminal leaflet length, terminal leaflet width and plant height in both the environments indicating that these traits were under the strong influence of additive gene action and hence simple selection based on phenotypic performance of these traits would be more effective. Positive and significant correlations were recorded between green fodder yield with leaf weight, stem weight, number of main branches per plant, and terminal leaflet width indicating the importance of these traits in selection for yield. Direct selection based on these traits would result in concurrent improvement of a mentioned trait and yield per se in cowpea.

KEY WORDS: Heritability, correlation, genetic advance, fodder yield and selection.

INTRODUCTION

Among fodder legumes cowpea (*Vigna unguiculata* L.Walp) is grown for both grain and fodder in all tropical and sub-tropical climates. It can be eaten as a green bean, but it is more important as the source of green as well as dry fodder. Cowpea is most important crop as fodder purpose because cowpea is the only fodder crop which contains high protein content and rich in lysine and tryptophan amino acids as compared to other fodder crops (Bressani, 1985). Like grain yield, fodder yield in cowpea is also a complex character; a sum total of various independent characters. Therefore, selection on the basis of one or more characters may not necessarily lead to the improvement in forage yield. Moreover, improvement in forage crop has to be considered in term of quality of forage in additions to forage yield as it is the animal performance which is to be taken into consideration simultaneously. It is, therefore, essential to know the importance as well as association of various quantitative as well as quality characters in order to initiate an effective selection programme aiming at the improvement in both the forage yield as well as quality of the forage. Better knowledge of the genetic similarity of breeding materials could help to maintain genetic diversity and sustain long term selection gain. Hence, any breeding programme aiming at increasing yield should consider association between yield and its attributes through estimation of genotypic and phenotypic correlation, which help a great deal in formulating selection indices to aid in selection programmes. An understanding of the variability existing in a crop is necessary to formulate and accelerate conventional breeding programme. Germplasm collection, evaluation, quantification for existing genetic variability for different characters and its classification into groups help in identifying better genotypes. This enables the breeder to operate selection efficiently. Keeping these aspects in view, the present study was initiated for evaluating the extent of genetic variability existing for different characters in cowpea germplasm collected from different environments which will be of immense practical use for plant breeders to choose the plant of interest for different breeding programmes. Importance of genotype-environment interactions has widely been realised in plant breeding. Results from studies on association between component characters carried out in different environments are therefore, essential to come to a fairly reasonable conclusion. Keeping in view the above facts the present study was undertaken to estimate genotypic; phenotypic coefficient of variation and heritability for various traits and to access association between fodder yield and its components traits.

MATERIALS & METHODS

Experimental design and Plant material

Twenty elite fodder cowpea genotypes were used as plant material in present investigation. They were phenotyped using the randomized block design with three replications in single row of 2m length with 60cm row to row spacing. The experiment was conducted during 2011-12 *kharif* season at two different locations at Dry land research area of Forage Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar and Research farm of Krishi Vigyan Kendra, Rohtak (Haryana) India. The source of these genotypes is presented in Table 1.

TABLE 1: Source of genotypes used in present investigation

S.No.	Genotype	Source	S. No.	Genotype	Source
1	COFC8	TNAU, Coimbature	11	GFC-3	AAU,Gujrat
2	EC101980	NBPGR, Delhi	12	EC 4216	NBPGR, Delhi
3	IC249141	NBPGR, Delhi	13	EC3941-1	NBPGR, Delhi
4	KOHINOOR	NBPGR, Delhi	14	HC46	HAU, Hisar
5	CO4	TNAU, Coimbature	15	BL2	IGFRI, Jhansi
6	CO5	TNAU, Coimbature	16	CO(CP)-7	TNAU, Coimbature
7	TVU 92-2	KAU, Vellanikkara	17	KBC-2	UAS, Bangalore
8	NDFC-15	NDUA&T, Faizabad	18	CS88	HAU, Hisar
9	GFC-1	AAU,Gujrat	19	GFC-4	AAU,Gujrat
10	GFC-2	AAU,Gujrat	20	IC528491	NBPGR, Delhi

Phenotyping of Morpho-physiological traits

Observations of various morpho-physiological traits were recorded in present investigation. Fodder yield/plant (g) (FY) was recorded at the flower initiation stage. Weight of total leaf in plant and weight of the stem was separately estimated six weeks after planting to find out leaf weight (g) (LW) and stem weight (g) (SW). Leaf: stem ratio (L: S) were estimated as a ratio of leaf weight and stem weight. Number of main branches/plant (NBP) arising directly from the main stem was counted six weeks after planting. Terminal leaf length (TLL) and width (TLW) (mm) was measured six weeks after planting from the typical leaflet. Plant height (cm) (PH) was measured six weeks after planting from base of the plant to tip of the plant.

Quality traits

Protein Content (%): It was estimated using Micro-kjeldahl technique (AOAC, 1990).

IVDMD (*In vitro* dry matter digestibility %) The digestibility was estimated using the method described by Tilley and Terry (1963) and modified by (Barnes *et.al*,. 1971)

Statistical analysis

Analysis of variance was performed using method described by Panse and Sukhatme (1967). Phenotypic coefficient of variance and genotypic coefficient of variability were calculated by the method explained by Singh and Chaudhary (1985). Heritability in broad sense and genetic advance were calculated by method given by (Burton and Devane, 1953) as given below: Heritability in broad sense H (bs): Vg / Vp or Vg / Vg + Ve. Correlation coefficients at phenotypic and genotypic level were calculated using the variances and co-variances according to Al-Jibouri *et al*., (1958).

RESULTS & DISCUSSION

Analysis of variance and Mean performance

Analysis of variance for the various fodder traits of cowpea in present investigation showed significant variation among the genotypes in both the environments (Table 2 and 3). Mean performance of fodder yield/ plant ranged from 180.76 g (E_2) for CO5 to 694.4 g (E1) for GFC-2. The mean yield of the genotypes under study was 346.2 and 340.7 g in E_1 and E_2, respectively. While, Leaf: stem ratio ranged from 0.66 (HC46) to 0.85 (BL 2) in both the environments. Number of branches/ plant ranged from 1.49 (E_2) to 5.1 (E_1) for HC46 and EC3941-1, respectively. Terminal leaf length and width also showed significant differences among the genotypes in present investigation. The leaf length ranged from 8.13 (E_1) to 29.58 (E_2). Similarly leaf width ranged from 15.26 to 37.93 in E_2. Protein content and IVDMD are key quality traits for fodder production. Mean protein content among the genotypes in present study ranged from 13.46 % to 20.81 % in E_1, while in E_2 it was from 13.76 to 20.8 %. Likewise IVDMD ranged from 48.06 to 57.06 % in E_1 and 47.03 to 56.76% in E_2.

Significant differences were observed among the genotypes for all the characters studied. This indicated that these characters were responsible for wide variation among the genotypes. These results are in agreement with finding of Gupta and Lodhi 1979; Dwivedi *et al*., 1999; Borah and Khan, 2000; Kumar *et al*., 2002; Kohli, 2002; Malarvizshi *et al*., 2005; Lohithaswa *et al*., 2009 and Singh *et al*., 2010) .

Genetic components of various traits

Fodder yield/plant, green leaf weight, stem weight, no of main branches, terminal leaflet width and length, plant height. It showed high heritability, GCV, PCV and genetic advance in both the environments. Leaf: stem ratio exhibited high heritability (92.24%), low GCV (7.51%), low PCV (7.82%) and moderate genetic advance as percent of mean (14.86%). Green leaf weight revealed high heritability (99.51%), GCV (37.57%), PCV (37.66%) and genetic advance as percent of mean (77.22%).

TABLE 2: Analysis of variance for various traits associated with fodder yield in elite cowpea genotypes during *Kharif* 2011-12 crop seasons

Source of variation	D.F	Fodder yield/plant		Leaf: Stem ratio		Leaf weight (g)		Stem weight (g)		No. of main Branches/plant		Terminal leaf length (mm)		Terminal Leaf width (mm)		Plant Height (cm)		Protein Content (%)		IVDMD (%)	
		E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2
Replication	2	42467.4	61006.2	0.002	0.01	883.1	100.19	44.05	24.75	0.05	0.06	0.001	59.17	56.81	69.36	45.41	50.45	1.06	4.39	2.4	1.86
Treatment	19	66,817.7*	63,371.3*	0.01*	0.01*	10,827.8*	10566.6*	21,280.5*	21,005.9*	3.9*	3.7*	71.6*	73.7*	110.2*	99.4*	1,094.5*	684.3*	12.0*	10.2*	23.0*	26.9*
Error	38	923.46	1,275.93	0.002	0.001	17.4	11.97	8.47	12.16	0.03	0.02	0.15	0.94	0.86	3.54	84.08	97.99	0.44	0.51	0.98	2.15
SE (m) ±		17.54	20.62	0.01	0.01	2.41	2.055	1.68	2.01	0.1	0.09	0.22	0.56	0.53	1.08	5.29	5.71	0.38	0.41	0.57	0.84
CV%		8.77	10.48	2.17	2.46	2.61	2.28	1.39	1.66	5.69	5.34	2.2	5	3.77	7.67	11.41	12.29	3.7	3.96	1.85	2.75
CD(P=0.5)		50.42	59.27	0.03	0.03	6.92	5.9	4.83	5.78	0.29	0.28	0.65	1.61	1.54	3.12	15.21	16.42	1.1	1.19	1.64	2.43

*** Significance at 0.01 LSD * significance at 0.05 LSD, E1: environment first, E2: environment second*

TABLE 3: Mean performance of different cowpea genotypes for various traits in environment first and second during kharif sesason 2011-12

Genotypes	Fodder yield /plant		Leaf: stem ratio		Leaf weight. (g)		Stem weight. (g)		No. of main Branches/plant		Terminal leaf length (mm)		Terminal leaf width (mm)		Plant Height (cm)		Protein Content (%)		IVDMD (%)	
	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2
COFC8	328.84	322.86	0.83	0.84	185.06	183.6	216.13	216.8	2.8	2.90	18.26	17.94	17.06	17.46	109.33	98.00	17.37	17.98	53.25	53.66
EC101980	294.66	289.6	0.77	0.78	113.6	111.93	142.93	143.6	3.6	3.66	27.53	29.58	35.6	34.73	60.00	68.33	15.86	15.74	51.83	51.66
IC249141	238.08	235.66	0.76	0.75	117.53	114.53	151.33	151.53	4.3	4.01	17.06	19.92	28.26	28.2	69.00	65.66	17.58	17.76	53.13	53.46
KOHINOOR	196.69	194.63	0.68	0.68	90.13	86.73	126.86	127.06	1.6	1.65	20.60	21.48	24	23.13	53.66	62.33	20.28	20.01	55.5	55.6
CO4	200.45	197.16	0.71	0.70	85.6	82.66	115.73	116.8	4.3	4.25	14.13	16.17	22.53	21.93	100.6	103.00	18.36	18.91	54.96	55.13
CO5	183.53	180.76	0.8	0.79	86.46	83.66	105.86	105.53	2.4	2.4	15.13	16.45	20.73	20.73	54.00	57.33	18.38	18.64	54.9	55.13
TVu92-2	442.8	437.36	0.67	0.68	216.33	211.33	309.2	310	4.3	4.25	25.13	26.14	29.6	28.33	75.66	83.00	19.78	19.72	49.3	49.3
NDFC-15	348.06	345	0.79	0.79	181.8	177.53	225.6	224.6	1.5	1.57	15.40	17.74	25.46	24.26	101.3	95.00	18.95	18.9	55.66	56
GFC-1	305.64	301.63	0.8	0.79	170.33	164.73	207.5	206.46	2.4	2.41	8.13	10.05	15.93	16.46	64.33	71.66	20.47	20.14	54.43	54.63
GFC-2	694.4	677.93	0.71	0.72	267.13	262.13	363.73	361.4	4.3	4.32	15.46	16.82	21.06	20.6	113.3	104.33	16.53	17.27	54.26	53.86
GFC-3	380.93	375.2	0.81	0.81	181.53	179.33	216.86	219.6	3.5	3.58	24.40	25.42	27.33	26.66	96	95.66	19.75	19.41	57.06	56.76
EC 4216	231.12	228.43	0.74	0.74	113.33	111.06	149.06	149	1.5	1.49	17.26	18.34	21.86	23.33	67.66	68	17.9	18.02	50.3	49.53
EC3941-1	684.13	669.63	0.7	0.71	283.33	274.73	388.93	388.6	5.1	5.08	26.06	28.97	38.2	37.93	67.33	63.66	17.59	17.83	52.7	53.76
HC46	230.86	229.03	0.66	0.66	98.93	96.8	143.73	145.26	1.5	1.49	15.60	15.45	15.33	15.26	105.3	99.66	16.54	17.31	48.06	47.03
BL2	335.13	332.16	0.85	0.85	184.33	182.4	215.33	215.13	2.0	2.00	17.06	19.8	28.73	29.26	65.33	68.66	18.89	19.00	55.76	55.53
CO(CP)-7	325.93	321.46	0.71	0.7	133.73	130.06	182.9	184.2	3.6	3.58	19.00	21.45	28.93	28.66	85.33	82.00	20.81	20.8	56.6	56.33
KBC-2	254.73	252.33	0.74	0.74	112.06	109.13	145.1	146.06	2.8	2.82	17.53	20.42	28.33	27.86	75.66	77.66	19.45	19.43	55.58	55.6
CS88	253.4	248.06	0.8	0.79	134.46	131.06	163.46	165.86	3.6	3.58	13.06	14.9	19.66	22.46	94.66	90.66	14.16	14.47	48.43	47.56
GFC4	477.02	469.5	0.71	0.7	222.6	214.26	304.7	303.26	4.1	4.17	12.86	14.92	21.2	21.2	83.66	85.33	13.46	13.76	50.43	49.86
IC528491	518.46	506.16	0.68	0.67	216.6	209.2	310.83	311.06	3.7	3.76	15.53	17.21	23	22.03	65.00	70.00	16.73	16.76	55.5	53.96
Mean	**346.24**	**340.73**	**0.75**	**0.74**	**159.74**	**155.84**	**209.29**	**209.59**	**3.2**	**3.15**	**17.76**	**19.46**	**24.64**	**24.52**	**80.36**	**80.5**	**17.94**	**18.09**	**53.38**	**53.22**
SE (m) ±	**8.92**	**20.62**	**2.87**	**0.01**	**3.1**	**2.05**	**1.36**	**2.01**	**5.3**	**0.09**	**2.07**	**0.56**	**3.72**	**1.08**	**5.29**	**5.71**	**4.16**	**0.41**	**1.95**	**0.84**
CV	**16.75**	**10.48**	**0.01**	**2.46**	**2.7**	**2.28**	**1.54**	**1.66**	**0.1**	**5.34**	**0.21**	**5**	**0.53**	**7.67**	**11.41**	**12.29**	**0.43**	**3.96**	**0.61**	**2.75**
C.D. 5%	**47.63**	**59.27**	**0.04**	**0.03**	**7.67**	**5.9**	**4.37**	**5.78**	**0.2**	**0.28**	**0.6**	**1.61**	**1.5**	**3.12**	**15.21**	**16.42**	**1.23**	**1.19**	**1.74**	**2.43**

TABLE 4: Genetic components of various traits of cowpea genotypes on in environment first and second during kharif 2011-12 season

Characters	PCV (%)		GCV (%)		H^2 (%)		GAM	
Environment	E1	E2	E1	E2	E1	E2	E1	E2
Fodder yield/plant (g)	43.69	43.50	42.80	42.22	95.96	94.19	86.37	84.41
Leaf: stem Ratio	7.82	7.86	7.511	7.47	92.24	90.32	14.86	14.63
Leaf wt.(g)	37.66	37.65	37.57	37.58	99.51	99.63	77.22	77.28
Stem wt.(g)	40.25	39.94	40.23	39.91	99.88	99.82	82.83	82.14
No. of main branches/plant	36.64	35.40	36.02	35.00	97.56	97.72	73.29	71.28
Terminal leaflet length(mm)	27.55	25.79	27.46	25.30	99.36	96.23	56.39	51.13
Terminal leaflet width(mm)	24.79	24.28	24.50	23.04	97.67	90.00	49.88	45.02
Plant height(cm)	2.528	21.28	22.83	17.36	80.02	66.60	42.08	29.19
Protein content(%)	11.54	10.68	10.93	9.92	89.70	86.25	21.34	18.98
IVDMD(%)	5.40	6.06	5.07	5.39	88.20	79.27	9.82	9.98

PCV (%): Phenotypic component of Variation, GCV (%): Genetic component of variation, H^2 (%): Heritability (broad scene) and GAM: genetic advance as percent of mean

TABLE 5: Correlation coefficients of various traits of cowpea in environment first (below diagonal) and environment second (above diagonal) during *kharif* 2011-12 crop season

Characters	Fodder yield /plant (g)	Leaf: stem ratio	Leaf weight. (g)	Stem weight. (g)	No. of main Branches /plant	Terminal leaf length (mm)	Terminal leaf width (mm)	Plant Height (cm)	Protein content (%)	IVDMD (%)
Fodder yield/plant(g)		-0.180	0.934**	0.950**	0.584**	0.239	0.276*	0.128	-0.201	-0.005
Leaf-stem Ratio	-0.238		-0.004	-0.208	-0.23	-0.06	0.012	0.014	0.027	0.268*
Leaf wt.(g)	0.934**	-0.068		0.978**	0.501**	0.177	0.197	0.149	-0.177	0.023
Stem wt.(g)	0.956**	-0.247	0.981**		0.551**	0.193	0.204	0.125	-0.191	-0.039
No. of main branches/plant	0.576**	-0.239	0.493**	0.537**		0.350**	0.408**	0.096	-0.278*	-0.008
Terminal leaf length(mm)	0.225	-0.156	0.151	0.172	0.287*		0.801**	-0.217	0.106	0.117
Terminal leaf width(mm)	0.297*	-0.074	0.217	0.232	0.429**	0.777**		-0.345**	0.081	0.159
Plant height(cm)	0.154	0.181	0.194	0.151	-0.095	-0.155	-0.394**		-0.352**	-0.149
Protein content (%)	-0.21	0.06	-0.176	-0.194	-0.273*	0.158	0.158	-0.15		0.551**
IVDMD (%)	0.019	0.266*	0.012	-0.044	-0.054	0.002	0.188	0.009	0.560**	

*** Significance at 0.01 LSD * significance at 0.05 LSD,* Stem weight unveiled high heritability (99.88%), GCV (40.23%), PCV (40.25%) and genetic advance as percent of mean (82.83%). Number of main branches per plant showed high heritability (97.56%), GCV (36.02%), PCV (36.64%) and genetic advance as percent of mean (73.29%). Terminal leaflet length had high heritability (99.36%), GCV (27.46%), PCV (27.55%) and genetic advance as percent of mean (56.39%).

Terminal leaflet width had high heritability (97.67%), GCV (24.50%), PCV (24.79%) and genetic advance as percent of mean (49.88%). Plant height recorded high heritability (80.02%), GCV (22.83%), PCV (25.2%) and genetic advance as percent of mean (42.08%). Crude protein content in green plant recorded high heritability (89.70%), moderate GCV (10.93%), moderate PCV (11.54%) and high genetic advance as percent of mean (21.34%). IVDMD recorded high heritability (88.20%), low GCV (5.07%), low PCV (5.40%) and high genetic advance as percent of mean (98.2%).

In E_2 green fodder yield was found to have high heritability (94.19%), GCV (42.22%), PCV (43.50%) and genetic advance as percent of mean (84.41%). Leaf: stem ratio exhibited high heritability (90.32%), low GCV (7.47%), low PCV (7.86%) and moderate genetic advance as percent of mean (14.63%). Green leaf weight recorded high heritability (99.63%), GCV (37.58%), PCV (37.65%) and genetic advance as percent of mean (77.28%). Stem weight revealed high heritability (99.82%), GCV (39.91%), PCV (39.94%) and genetic advance as percent of mean (82.14%). Number of main branches per plant recorded high heritability (97.72%), GCV (35.00%), PCV (35.04%) and genetic advance as percent of mean (71.28%). Terminal leaflet length was found to have high heritability (96.23%), GCV (25.30%), PCV (57.79%) and genetic advance as percent of mean (51.13%). Terminal leaflet width recorded high heritability (90.00%), GCV (23.04%), PCV (24.28%) and genetic advance as percent of mean (45.02%). Plant height showed high heritability (66.60%), moderate GCV (17.36%), high PCV (21.28%) and genetic advance as percent of mean (29.19%). Crude protein content in green plant recorded high heritability (86.25%), low GCV (9.92%), moderate PCV (10.68%) and high genetic advance as percent of mean (18.98%). IVDMD showed high heritability (79.27%), low GCV (5.39%), low PCV (6.06%) and low genetic advance as percent of mean (9.98%).

Lohithaswa *et al*. (2009) agreed to the high heritability of plant height, number of branches per plant, green fodder yield per plant and number of pod per plant. (Borah and Khan, 2000) also reported the high heritability for plant height, green fodder yield per plant, number of main branches per plant, leaf weight and stem weight.

The results were supported by (Thiyagarajan *et al.,* 1989) for plan height, number of seed per pod and 100 seed weight. (Roquib and Patnaik *et al*., 1990) showed similar results for plan height, number of seed per pod, seed yield per plant, pod length, whereas (Thaware *et al*., 1991) showed moderate PCV and GCV estimates for plant height conversely to the present study. Nath and Tajane (2014) also reported high GCV and PCV for green fodder yield/plant in cowpea.

The result of the present study are similar to the finding of Lohithaswa *et al*. (2009) for high GAM of plant height, number of branches per plant, green fodder yield per plant and number of pod per plant. Gupta and Lodhi (1979) reported high genetic advance for stem weight. Borah and Khan (2000) for high GAM of plant height, green fodder yield per plant, number of main branches per plant, leaf weight and stem weight. Kumar *et al*., (2002) for the high GAM of days to first flower, green fodder yield per plant height and Adu. Danah *et al*., (2005) for high GAM for leaf weight.

Correlation

In environment (E1) correlation was found to be positive and highly significant between fodder yield per plant and leaf weight (0.934) and stem weight (0.956) and number of branches per plant (0.576). The terminal leaf width was found to have positive and significant correlation with fodder yield /plant (0.297). Negative and significant correlation was found between protein content and number of branches/plant. Similar results were observed in environment (E_2) where genotypic correlation coefficient was found to be positive and highly significant between fodder yield/plant and leaf weight (0.934), stem weight (0.950) and number of branches/plant (0.584). Terminal leaf width was found to have positive and significant correlation with fodder yield/plant (0.276). Protein content (%) was found to have negative and highly significant correlation with plant height (-0.352) and significant negative correlation with number of branches/plant.

Green fodder yield per plant recorded significant positive correlation with green leaf weight, green stem weight, number of main branches per plant and terminal leaflet width indicating the importance of these traits in selection for yield. Direct selection based on these traits would result in simultaneous improvement of aforesaid traits and yield per se in cowpea. Similar results in cowpea were reported by Chauhan *et al*., (2003); Adu. Dapaah *et al*., (2005); Singh *et al*., (2010) and Nath and Tajane (2014).

CONCLUSION

Genotypes GFC-2 showed maximum green fodder yield per plant and followed by EC 3941-1, IC528491, GFC-4, TVv92-2 and GFC-3 in both the environments *i.e*. E_1 & E_2. This indicated that the genotypes can be used in breeding programme for improvement. High heritability coupled with high genetic advance as percent of mean was observed for the characters like green fodder yield per plant, green leaf weight, stem weight, pod width, peduncle length, number of main branches per plant, terminal leaflet length, terminal leaflet width and plant height in both the environments indicating that these traits were under the strong influence of additive gene action and hence simple selection based on phenotypic performance of these traits would be more effective. High heritability and low GAM values were observed for days to first flower, days to first ripe pod, number of pod per peduncle, number of locules per pod, pod length, number of node per branches and curde protein content in green plant in both environments. This indicates the influence of non-additive gene action and considerable influence of environment on the expression of these traits. These traits could be exploited through manifestation of dominance and epistatic components through heterosis. Positive significant correlation were recorded between green fodder yield with leaf weight, stem weight, number of main branches per plant, and terminal leaflet width indicating the importance of these traits in selection for yield. Direct selection based on these traits would result in concurrent improvement of a mentioned trait and yield per se in cowpea.

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